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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:27:07 ; Search time 111.01 Seconds
(without alignments)
501.665 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISYPLTFGGTKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/pct_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1011.5	79.1	244	5	US-09-791-537-121728
2	1001	78.3	240	5	US-09-791-537-22737
3	993	77.7	242	5	US-09-791-537-115236
4	992	77.6	240	5	US-09-511-939-2
5	992	77.6	240	5	US-09-968-561A-2
6	991	77.5	239	5	US-09-791-537-121731
7	938	73.4	248	5	US-09-791-537-115235
8	901.5	70.5	240	6	US-10-127-890-148
9	898.5	70.3	243	5	US-09-791-537-34222
10	888.5	69.5	224	5	US-09-791-537-128071
11	886	69.3	232	5	US-09-791-537-128029
12	885.5	69.3	243	5	US-09-791-537-9775
13	882	69.0	243	5	US-09-791-537-18026
14	880	68.9	232	5	US-09-791-537-128028
15	878	68.7	244	5	US-09-791-537-22734
16	873	68.3	248	6	US-10-113-996-22
17	871.5	68.2	229	5	US-09-791-537-128087
18	871.5	68.2	298	5	US-09-791-537-131629
19	869.5	68.0	268	5	US-09-791-537-850
20	869	68.0	240	1	PCT-US02-16106-22
21	869	68.0	240	6	US-10-151-882-22
22	865.5	67.7	238	5	US-09-791-537-78382
23	864	67.6	248	6	US-10-113-996-23
24	861.5	67.4	241	1	PCT-US02-16106-21
25	861.5	67.4	241	6	US-10-151-882-21
26	860.5	67.3	238	5	US-09-791-537-78362

27	858.5	67.2	238	5	US-09-791-537-78383	Sequence 78383, A
28	857.5	67.1	238	5	US-09-791-537-78381	Sequence 78381, A
29	857.5	67.1	239	1	PCT-US02-16106-23	Sequence 23, Appl
30	857.5	67.1	239	6	US-10-151-882-23	Sequence 23, Appl
31	854.5	66.9	238	5	US-09-791-537-78345	Sequence 78345, A
32	854.5	66.9	238	5	US-09-791-537-78380	Sequence 78380, A
33	851.5	66.6	238	5	US-09-791-537-78364	Sequence 78364, A
34	851.5	66.6	238	5	US-09-791-537-78365	Sequence 78365, A
35	849	66.4	232	5	US-09-791-537-128045	Sequence 128045, A
36	848.5	66.4	238	5	US-09-791-537-78361	Sequence 78361, A
37	846.5	66.2	243	5	US-09-791-537-55358	Sequence 55358, A
38	846	66.2	248	5	US-09-791-537-55353	Sequence 55353, A
39	843	66.0	240	6	US-10-110-174-2	Sequence 2, Appli
40	842.5	65.9	238	5	US-09-791-537-78827	Sequence 78827, A
41	828.5	64.8	272	5	US-09-417-478-183	Sequence 183, App
42	823	64.4	240	5	US-09-791-537-138788	Sequence 138788, A
43	819.5	64.1	277	5	US-09-522-727D-54	Sequence 54, Appl
44	815.5	63.8	294	5	US-09-661-992-100	Sequence 100, Appl
45	815.5	63.8	732	5	US-09-661-992-90	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-09-791-537-121728
; Sequence 121728, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121728
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-121728

Query Match 79.1%; Score 1011.5; DB 5; Length 244;
Best Local Similarity 79.5%; Pred. No. 1.8e-53;
Matches 194; Conservative 21; Mismatches 26; Indels 3; Gaps 2;
QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVROAPKGLBWSGTMWNSGICY 60
Db 1 QVQLVQSGGGLVQHGGSLRLSCAASGFTFSSEMMVROAPKGLBWSGSGSGSTYY 60
QY 61 ADSVKGRTISRDNKNSLYLQMNLSRAEDTAVYYCAREP--HNTD-AFDINGRGLTVTV 117
Db 61 ADSVKGRTISRDNKNSLYLQMNLSRAEDTAVYYCARDGWELTDWYFDLWGRGTMVTV 120
QY 118 SSGGGPGGGGGGGGGSDVVMVQSPFLSAFVQDITITCRASQGIYNYLAWYQKPGKA 177
Db 121 SSGGGGGGGGGGGGGSDTQMTQSPSTLSASIGDRVITTCRASEGIYHWLAWYQKPGKA 180
QY 178 PKLLIYAASTLOGVPSRFSRSGSGSGTEFTLTSSLPQDPDFGTYTCOOLISYPLTFGGGTK 237
Db 181 PKLLIYKASSLASGAPSRFSRSGSGSGTDFLTITSSLPQDDFATYYCOQYSNYPLTFGGGTK 240
QY 238 VEIK 241
Db 241 LEIK 244

RESULT 2
US-09-791-537-22737
; Sequence 22737, Application US/09791537

GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22737
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22737

Query Match 78.3%; Score 1001; DB 5; Length 240;
Best Local Similarity 78.8%; Pred. No. 7.4e-53;
Matches 190; Conservative 22; Mismatches 27; Indels 2; Gaps 1;
QY 1 QVRLQSGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGICY 60
DB 1 QVQLVQSGGGLVQPGSLRLSCAASGFTFSYGMHWVRQAPGKLEWVAISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAPDINGRGTLTVTSSG 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARD--WGDSLDPMGKGTLTVTSSG 118
QY 121 GGGPGGGGGGGSDVVMVTQSPFSFAFVGDITITTCRASQGIYNYLAWYQOKPKAPKL 180
DB 119 GGGSGGGGGGGSDIQMTQSPSTLSASIGCDRVTITCRASEGIRYRLAWYQOKPKAPKL 178
QY 181 LIYAASLTQSGVPSRFGSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGTKEI 240
DB 179 LIYKASSLASRAPSRFGSGSGTDFTLTISLQPDFAFYTCQYSNPLTFGGGTKEI 238
QY 241 K 241
DB 239 K 239

RESULT 3
US-09-791-537-115236
; Sequence 115236, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 115236
; LENGTH: 242
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-115236

Query Match 77.7%; Score 993; DB 5; Length 242;
Best Local Similarity 79.7%; Pred. No. 2.2e-52;
Matches 192; Conservative 18; Mismatches 31; Indels 0; Gaps 0;
QY 1 QVRLQSGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGICY 60
DB 1 QVQLVQSGGGLVQPGSLRSCAASGFTFSYAMHWVRQAPGKLEWVSGISGANTYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAPDINGRGTLTVTSSG 120

DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKASSLGYYFDYWGQGTLTVTSSG 120
QY 121 GGGPGGGGGGGSDVVMVTQSPFSFAFVGDITITTCRASQGIYNYLAWYQOKPKAPKL 180
DB 121 RGGSGGGGGGGSDVVMVTQSPFSFAFVGDITITTCRASQGIYNYLAWYQOKPKAPKL 180
QY 181 LIYAASLTQSGVPSRFGSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGTKEI 240
DB 181 LIYKASSLASGVPSRFGSGSGTDFTLTISLQPDFAFYTCQYSNPLTFGGGTKEI 240
QY 241 K 241
DB 241 K 241

RESULT 4
US-09-511-939-2
; Sequence 2, Application US/09511939
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GH98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-511-939-2

Query Match 77.6%; Score 992; DB 5; Length 240;
Best Local Similarity 80.6%; Pred. No. 2.6e-52;
Matches 195; Conservative 16; Mismatches 27; Indels 4; Gaps 2;
QY 1 QVRLQSGGGLVQPGSRSLRSCAASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGICY 60
DB 1 EVQLLESGGGLVQPGSLRSCAASGFTFSYAMSWVRQAPGKLEWVAISGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAPDINGRGTLTVTSSG 120
DB 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK---SYGAFDYWGQGTLTVTSSG 117
QY 121 GGGPGGGGGGGSDVVMVTQSPFSFAFVGDITITTCRASQGIYNYLAWYQOKPKAPKL 179
DB 118 GGGSGGGGGGGSDIQMTQSPSSLSASVSGDRVTITCRASQSISSYLAHWYQOKPKAPKL 177
QY 180 LIYAASLTQSGVPSRFGSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGTKEI 239
DB 178 LIYAASLTQSGVPSRFGSGSGTDFTLTISLQPEDFAFYTCQYSNPLTFGGGTKEI 237
QY 240 IK 241
DB 238 IK 239

RESULT 5
US-09-968-561A-2
; Sequence 2, Application US/09968561A
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M

```

; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

```

Query Match	77.6%;	Score 992;	DB 5;	Length 240;
Best Local Similarity	80.6%;	Pred. No. 2.6e-52;		
Matches 195;	Conservative 16;	Mismatches 27;	Indels 4;	Gaps 2;
Qy	1	QVRLOQSGGLVQPGRSRLSCAASGFTFDYAHWVQAPGKGLEWYSGMTWNSGSLCY	60	
Db	1	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSVRQAPGKGLEWYSAISGGSGSTYY	60	
Qy	61	ADSVKGRFTISRDAKNSLYIQMNSLRADFAVYCAAREPHNTDAFDLWGRCTLVTVSSG	120	
Db	61	ADSVKGRFTISRDNKNTLYIQMNSLRADFAVYCAK---SYGAFDWGGTLLTVTVSSG	117	
Qy	121	GGGPGGGSGGGGS--DVVMTQSPFSLFAFGDTTITCRASQGINYLAWTQKPGKAPK	179	
Db	118	GGGSGGGSGGGGGTDTQMTQSPSLASVGRVTITCRASQSSISSYLNWTQKPGKAPK	177	
Qy	180	LLIYAASLTQGVSPRFSGSGSGTEFTTIISSLQPEDFGTYCYCOOLISYPLTFGGGTAVE	239	
Db	178	LLIYAASLSQGVSPRFSGSGSGTDFTLTIISSLQPEDFAITYCOOSYSTPNTFGGTAVE	237	
Qy	240	IK 241		
Db	238	IK 239		

```

RESULT      6
US-09-791-537-121731
; Sequence 121731, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121731
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-791-537-121731

```

Query Match 77.5%; Score 991; DB 5; Length 239;
Best Local Similarity 77.6%; Pred. NO. 2.9e-52;
Matches 187; Conservative 24; Mismatches 28; Indels 2; Gaps 1;

Qy	1	QVR	QQSGGLVQPG	RLRLSCA	SQFTFD	YAHMV	VRQAP	KGLEW	VSGMTW	NSGSIGY	60
Db	1	QVQ	VQSGGLVPR	PGGSL	SLSCAV	SGITL	TYGNH	VRQAP	KGLEW	AGISF	60
Qy	61	ADV	KGRFTT	SRONAK	NLSYLQ	WNSLR	APTYV	YCA	REPHNT	DAFD	120
Db	61	ADV	QGRFTT	SRSSK	NWTLYLQ	WNSLR	APET	TAYVY	CARG	AHY--	118
Qy	121	GGP	GGGGGGGG	GVVMT	QSPFL	SAPV	GDTT	ITCR	ASQGY	NYLAWY	180
Db	119	GGC	GGGGGGGG	SDIQ	MTQSP	SLAS	IGDRV	TITCR	ASEGY	YHWLAWY	178
Qy	181	LIYA	ASTLQ	SGVPS	RRSSG	SGSTF	TLT	ISSLP	EDPG	TYVY	240
Db	179	LIY	KASSL	ASGAP	RRFSG	SGSGD	FTLT	ISSLP	DDP	PATYV	238
Qy	241	K	241								
Db	239	K	239								

```

RESULT 7
US-09-791-537-115235
; Sequence 115235, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115235
; LENGTH: 248
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-115235

```

Query Match 73.4%; Score 938; DB 5; Length 248;
Best Local Similarity 74.9%; Pred. No. 4.4e-49;
Matches 185; Conservative 20; Mismatches 36; Indels 6; Gaps 2;

Qy	1	QVRLQSGGGGLVQGRSLRLSCAASGFTFDDYAHHWYRQAPGKLEWVSCM--TWNSGSI	56
		: : : : : : : : : : : :	
Db	1	QVQLQESGGGLVLPKGGSLRLSCAASGFTFSYSNHWYRQAPGKLEWVGKSKTDGGTT	60
		: : : : : : : : : : : :	
Qy	59	GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC---AREPHNTDAFDIWRGTL	114
		: : : : : : : : : : : :	
Db	61	DYAAPVKGRFTISRDTSKNTLYLQMNLSLKTEDTAVYYCTTRMYRGVITGRWDFPWGGTL	120
		: : : : : : : : : : : :	
Qy	115	VTVSSGGGGGGGGGGGGSDVVMQSPFLSPAVPGDTITITCRASGIIYNYLAWYQQKP	174
		: : : : : : : : : : : :	
Db	121	VTVSSGGGGGGGGGGGGSDIQMTQSPFLSLASVSGDKVITITCRASGSI SYLYNWTQQKP	180
		: : : : : : : : : : : :	
Qy	175	GKAPKLLIYAASTLQSGVPSRFSFGSGSGTGFETLTISSLQPEDFGTYCQQLISVPLTFGG	234
		: : : : : : : : : : : :	
Db	181	GKAPKLLIYAASSLQSGVPSRFSFGSGSGTGFETLTISSLQPDDFATYYCQQYNSYWFQ	240
		: : : : : : : : : : : :	
Qy	235	GTRVEIK 241	
		:	
Db	241	GTKLEIK 247	
		:	

RESULT 8
US-10-127-890-148
; Sequence 148, Application US/10127890
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.

Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 148:
US-10-127-890-148

Query Match 70.5%; Score 901.5; DB 6; Length 240;
Best Local Similarity 70.1%; Pred. No. 6.5e-47;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHVRQAPGKGLVWVSGMTWNSGSIGY 60
Db 1 EIQLVQSGGGLVQGRSVRISCAASGYTFYNGMNVVRQAPGKGLVWVSGMTWNSGSIGY 60
QY 61 ADSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYICAREPHTDINGRGTLVTSSG 120
Db 61 ADSFKGRFTSLDDSKNTAYLQINSLRRAEDTAVYICAREPHTDINGRGTLVTSSG 119
QY 121 GGGPGGGGGGGSDVMTQSPFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPKL 180
Db 120 GGGGGGGGGGGSDVMTQSPFLSAFVGDITITCRASQGIYNYLAWYQKPGKAPKL 179
QY 181 LIYAASTLQSGVPSRFGSGSGTFTLTITSSLPQEDFGTYVCOQLISYPLTFGGGKVEI 240
Db 180 LIYRANRLESQVPSRFGSGSGTFTLTITSSLPQEDFGTYVCOQLISYPLTFGGGKVEI 239
QY 241 K 241

Db 240 K 240
RESULT 9
US-09-791-537-34222
; Sequence 34222, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34222
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-34222
Query Match 70.3%; Score 898.5; DB 5; Length 243;
Best Local Similarity 70.0%; Pred. No. 9.8e-47;
Matches 170; Conservative 32; Mismatches 38; Indels 3; Gaps 2;
QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHVRQAPGKGLVWVSGMTWNSGSIGY 60
Db 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHVRQAPGKGLVWVSGMTWNSGSIGY 59
QY 61 ADSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYICAREP--HNTDAFDIWRGTLVTVS 118
Db 60 PDSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYICAREP--HNTDAFDIWRGTLVTVS 119
QY 119 SGGGGPGGGGGSDVMTQSPFLSAFVGDITITCRASQGIYNYLAWYQKPGKAP 178
Db 120 SGGGGPGGGGGSDVMTQSPFLSAFVGDITITCRASQGIYNYLAWYQKPGKAP 179
QY 179 KLLIYAASTLQSGVPSRFGSGSGTFTLTITSSLPQEDFGTYVCOQLISYPLTFGGGTKV 238
Db 180 QLLIYAASTLQSGVPSRFGSGSGTFTLTITSSLPQEDFGTYVCOQLISYPLTFGGGTKL 239
QY 239 EIK 241
Db 240 ELK 242
RESULT 10
US-09-791-537-128071
; Sequence 128071, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128071
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-128071
Query Match 69.5%; Score 888.5; DB 5; Length 224;
Best Local Similarity 74.0%; Pred. No. 3.6e-46;

Matches 179; Conservative 18; Mismatches 26; Indels 19; Gaps 4;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
 DB 1 QVQLVSGGGVQVQGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLWVAVISDGNKYY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDINGRGLTVTVSSG 120
 DB 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCARN-GDPEAFDYWGQGLTVTVS-- 117

QY 121 GGGPGGGGGGGSDVVMQSPSFLSAFYGDITITCRASQGIYNYLAWYQKPKAPKL 180
 DB 118 -----SDIQMTQSPSLASVGDRTITCRASQSIISTYLNMYQKPKGOAPKL 164

QY 181 LIYAASLTQSGVPSRFGSGSGTEFTLTITSSLPQDEFGTYTCQOLISY-PLTFGGGKTVE 239
 DB 165 LIYGASSLTQSGVPSRFGSGSGTDFLTITSSLPQDEFGTYTCQOLISY-PLTFGGGKTVE 222

QY 240 IK 241
 DB 223 IK 224

RESULT 11
 US-09-791-537-128029
 ; Sequence 128029, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 128029
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-791-537-128029

Query Match 69.3%; Score 886; DB 5; Length 232;
 Best Local Similarity 70.9%; Pred. No. 5.3e-46;
 Matches 175; Conservative 23; Mismatches 27; Indels 22; Gaps 4;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
 DB 1 QVQLVSGGGVQVQGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLWVAVM-WFDGTEKY 59

QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPH-----NTDAFDINGRGLT 114
 DB 60 SAESVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHDMLLWGDRCALDVWGQGT 119

QY 115 VTVSSGGGPGGGGGSDVVMQSPSFLSAFYGDITITCRASQGIYNYLAWYQKPK 174
 DB 120 VTVS-----SDIVMTQSPSLASVGDRTITCRASQSIISTYLNMYQKPKGOAPKL 164

QY 175 GKAPKLLIYAASLTQSGVPSRFGSGSGTEFTLTITSSLPQDEFGTYTCQOLISYPLTFGG 234
 DB 165 GKAPKLLMYEASSLESQVPSRFGSGSGTEFTLTITSSLPQDPAFYTCQHYNTYPTFGQ 224

QY 235 GTKLEIK 241
 DB 225 GTKLEIK 231

RESULT 12
 US-09-791-537-9775
 ; Sequence 9775, Application US/09791537
 ; GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.
 APPLICANT: Debe, Derek
 APPLICANT: Danzer, Joseph
 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 FILE REFERENCE: 261/210
 CURRENT APPLICATION NUMBER: US/09/791,537
 CURRENT FILING DATE: 2001-02-22
 NUMBER OF SEQ ID NOS: 153055
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 9775
 LENGTH: 243
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-791-537-9775

Query Match 69.3%; Score 885.5; DB 5; Length 243;
 Best Local Similarity 68.2%; Pred. No. 5.9e-46;
 Matches 165; Conservative 30; Mismatches 46; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
 DB 1 QVQLQSGGAEVKPKGSSVKVSKTSGYTFGYMHWVRQAPGQGFENMGWIDPNSGATY 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTD-AFDINGRGLTVTVSS 119
 DB 61 AQKFGRLILSRDTSINTAYMELRLTSDTAVYYCAKKTQTWTGPPFWGQGTTVTVSS 120

QY 120 GGGPGGGGGGGSDVVMQSPSFLSAFYGDITITCRASQGIYNYLAWYQKPKAPK 179
 DB 121 GGGGGGGGGGGSDIVMTQSPSLASVGDRTITCRASQGIYNYLAWYQKPKAPN 180

QY 180 LLIYAASLTQSGVPSRFGSGSGTEFTLTITSSLPQDEFGTYTCQOLISYPLTFGGGKTVE 239
 DB 181 LLIYKASHLYNGVPSRFGSGSGTDFLTITSSLPQDPAFYTCQOLISYPLTFGGGKTVE 240

QY 240 IK 241
 DB 241 IK 242

RESULT 13
 US-09-791-537-18026
 ; Sequence 18026, Application US/09791537
 ; GENERAL INFORMATION:
 ; APPLICANT: Bionomix, Inc.
 ; APPLICANT: Debe, Derek
 ; APPLICANT: Danzer, Joseph
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
 ; FILE REFERENCE: 261/210
 ; CURRENT APPLICATION NUMBER: US/09/791,537
 ; CURRENT FILING DATE: 2001-02-22
 ; NUMBER OF SEQ ID NOS: 153055
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 18026
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Mus sp
 US-09-791-537-18026

Query Match 69.0%; Score 882; DB 5; Length 243;
 Best Local Similarity 69.2%; Pred. No. 9.5e-46;
 Matches 166; Conservative 30; Mismatches 42; Indels 2; Gaps 1;

QY 2 VRLQSGGGLVQGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 61
 DB 3 VOLVESGGGLVQPGSLKLSCAASGDFSRYYMSWVRQAPGKGLWIGEINPDSSITNYT 62

QY 62 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDINGRGLTVTVSSGG 121
 DB 62 DSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDINGRGLTVTVSSGG 121

Db 63 PSLKDKFIISDNANKNTLYLQMSKVRSEDTALYYCARRGY--AMDYWGQGTSTVTSSGG 120
QY 122 GPGGGGGGGSDVVMVTQSPFLSAFVGTITITCRASOGIYNYLAWYQKPGKAPKLL 181
Db 121 GSGGGGGGGSDVVMVTQSPASLSVGTVTITCRASENIYSYLAHYQKQKSPQLL 180
QY 182 IYAASTLQSGVPRFSGSGGTFTLTITSSLPEDFGTYTCQQLISYPLTFGGTKVEIK 241
Db 181 VYNAKTLAEGVPSRFSGSGGTQFSLKINSLPEDFGSYVQHHYGPFTFGSGTKLEIK 240

RESULT 14

US-09-791-537-128028
; Sequence 128028, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128028
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-128028

Query Match 68.9%; Score 880; DB 5; Length 232;
Best Local Similarity 70.4%; Pred. No. 1.2e-45;
Matches 174; Conservative 23; Mismatches 28; Indels 22; Gaps 4;

QY 1 QVRLQSGGGLVQGRSLRLSCASGTFDDYAMHWYRQAPGKLEWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGGAVKPKGDSVKVSKASGYTFSDHYMHYRQAPGQGLEWGWIDPNNGDTRF 59
QY 61 -ADSVKGRFTISRDNANKNSLYLQMSLRADETAVYYCAREPH-----NTDAFDIWRGTL 114
Db 60 SAESVKGRTISRDNKNSNTLFLQMSLRADDTAVYYCAREPDWLLGDRGALDVWGQGT 119
QY 115 VTVSSGGGPGGGGGSDVVMVTQSPFLSAFVGTITITCRASOGIYNYLAWYQKQP 174
Db 120 VTVS-----SDIVMTQSPSTLSASVGRVITITCRASQSISSWLAHYQKQP 164
QY 175 GKAPKLLIYAASTLQSGVPSRFSGSGGTFTLTITSSLPEDFGTYTCQQLISYPLTFGG 234
Db 165 GKAPKLLMYEASDESQVPSRFSGSGGTFTLTITSSLPEDFAAAYYQHYNTVPYTFGQ 224
QY 235 GTRKVEIK 241
Db 225 GTRKLEIK 231

RESULT 15

US-09-791-537-22734
; Sequence 22734, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22734
; LENGTH: 244

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-22734

Query Match 68.7%; Score 878; DB 5; Length 244;
Best Local Similarity 66.3%; Pred. No. 1.7e-45;
Matches 161; Conservative 40; Mismatches 40; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCASGTFDDYAMHWYRQAPGKLEWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGAEVKKPKGDSVKVSKASGYTFSDHYMHYRQAPGQGLEWGWIDPNNGDTRF 60
QY 61 -ADSVKGRFTISRDNANKNSLYLQMSLRADETAVYYCAREPHNTDAF--DIWGRGTLTVTS 118
Db 61 AQRFGCRVTWTRDTISISAAWYEVSRLSDDTAVYYCAREGTGSAIYGMVWGQGTTLTVTS 120
QY 119 SGGGGPGGGGGGGSDVVMVTQSPFLSAFVGTITITCRASOGIYNYLAWYQKPGKAP 178
Db 121 SGGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHHLAWYQKPGKAP 180
QY 179 KLLIYAASTLQSGVPSRFSGSGGTFTLTITSSLPEDFGTYTCQQLISYPLTFGGTKV 238
Db 181 KFLIYKRASSLASGAPSRFSGSGGTFTLTITSSLPQDDFAFYTCQYSNPLTFGGGTKL 240
QY 239 EIK 241
Db 241 EIK 243

Search completed: August 15, 2002, 16:27:07
Job time: 372 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:15 ; Search time 39.61 Seconds
(without alignments)
148.613 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISPLTFGGTKVEIK 241

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1010.5	79.1	245	4	US-08-918-148-75
2	1002.5	78.4	245	4	US-08-918-148-78
3	987.5	77.3	245	4	US-08-918-148-76
4	987.5	77.2	244	4	US-08-918-148-77
5	939.5	73.5	284	4	US-08-564-164A-2
6	901.5	70.5	240	1	US-08-488-113B-148
7	901.5	70.5	240	1	US-08-477-484B-148
8	901.5	70.5	240	2	US-08-646-360-148
9	901.5	70.5	240	4	US-08-839-765-148
10	901.5	70.5	240	4	US-09-136-389-148
11	882	69.0	243	1	US-07-958-140-2
12	882	69.0	243	5	PCR-US93-09166-2
13	879	68.8	301	2	US-08-661-052-14
14	879	68.8	301	4	US-09-188-082-14
15	879	68.8	553	2	US-08-661-052-16
16	879	68.8	553	4	US-09-188-082-16
17	873	68.3	248	2	US-08-887-352B-22
18	873	68.3	248	4	US-09-109-207C-22
19	873	68.3	248	4	US-09-296-005-22
20	868.5	68.0	281	4	US-09-025-769B-178
21	864	67.6	248	2	US-08-887-352B-23
22	864	67.6	248	4	US-09-109-207C-23
23	864	67.6	248	4	US-09-296-005-23
24	847.5	66.3	277	2	US-08-256-790-2
25	825	64.6	255	4	US-09-553-498-8
26	817.5	64.0	282	2	US-08-860-174A-10
27	817	63.9	236	2	US-08-190-199A-65

28	808.5	63.3	246	1	US-07-843-125-1	Sequence 1, Appl
29	805	63.0	240	2	US-08-956-047-25	Sequence 25, Appl
30	792.5	62.0	247	4	US-09-227-693-34	Sequence 34, Appl
31	792.5	62.0	248	1	US-08-331-398A-34	Sequence 34, Appl
32	792.5	62.0	248	2	US-08-331-397B-34	Sequence 34, Appl
33	792.5	62.0	248	2	US-08-759-804A-34	Sequence 34, Appl
34	784	61.3	309	4	US-09-079-029-9	Sequence 9, Appl
35	783.5	61.3	310	4	US-09-079-029-11	Sequence 11, Appl
36	783	61.3	269	4	US-08-646-265A-109	Sequence 109, App
37	779.5	61.0	246	1	US-07-843-125-11	Sequence 11, Appl
38	777	60.8	264	4	US-08-564-164A-4	Sequence 4, Appl
39	769.5	60.2	267	4	US-09-485-737B-2	Sequence 2, Appl
40	769.5	60.2	541	4	US-09-485-737B-85	Sequence 85, Appl
41	769.5	60.2	711	4	US-09-485-737B-90	Sequence 90, Appl
42	766	59.9	239	2	US-08-553-497A-18	Sequence 18, Appl
43	762	59.6	637	1	US-08-235-838-14	Sequence 14, Appl
44	762	59.6	637	2	US-08-465-473B-14	Sequence 14, Appl
45	762	59.6	711	1	US-08-235-838-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-75

Query Match 79.1%; Score 1010.5; DB 4; Length 245;
Best Local Similarity 79.3%; Pred. No. 3.6e-72;
Matches 191; Conservative 23; Mismatches 26; Indels 1; Gaps 1;
QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTDDYAMHWVROAPGKGLVWVSGMTWNSGSIGY 60
Db 3 EVLVOSGGGLVKPGGSLRLSCAASGFTFSDYMTSMVROAPGKGLVWVSYISSGSIYY 62
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIMGRGLTVTVSSG 120
Db 63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARW-SGEDAFDIMGQGTMTVSSG 121
QY 121 GGGPGGGGGGGSDVVMVQSPFLSAFVGDITITTCRASQGIYNYLAWYQKPKRAPKL 180
Db 122 GGGSGGGGGGGSDIVMTQSPSTLSASVGDRAITTCRASEGIYHNLAWYQKPKRAPKL 181
QY 181 LIYAASTLQSGVPSRFRSGSGSGTEFTLTITSSLOPEFGIYYCOOLISYPLTFGGGKVEI 240
Db 182 LIYKASSLASGAPSRFRSGSGSGADFTLTITSSLOPDDFATYYCOQSNYPLTFGGGKLEV 241
QY 241 K 241
Db 242 K 242
RESULT 2
US-08-918-148-78
; Sequence 78, Application US/08918148A

;; TITLE OF INVENTION: Thereof
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.
;; STREET: 500 Arcola Road, 3C43
;; CITY: Collegeville
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19426-0107
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/564,164A
;; FILING DATE: 28-DEC-1995
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/FR94/00714
;; FILING DATE: 15-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 93/07241
;; FILING DATE: 16-JUN-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Savitzky, Martin F.
;; REGISTRATION NUMBER: 29,699
;; REFERENCE/DOCKET NUMBER: ST93030-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (610)454-3816
;; TELEFAX: (610)454-3808
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 284 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-564-164A-2

Query Match 73.5%; Score 939.5; DB 4; Length 284;
Best Local Similarity 72.7%; Pred. No. 1.5e-66;
Matches 176; Conservative 29; Mismatches 36; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLSCAASGTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
Db 28 QVKLQSGGGLVQPGRSRLSCVSGTFNSYGMNWIOTPGKGLWVAYISSGSYLYY 87

QY 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCAR-EPHNTDAFDIWRGRTLVTVSS 119
Db 88 AETVKGRTTISRDNKNTLYLQMTSLRSEDALYYCARHEGTTDFDYWGOGTTVTYSS 147

QY 120 GGGPGGGGGGGSDVVMQTQSPFLSAFVGDITITCRASQGIYNLAWYQKPKAPK 179
Db 148 GGGSGGGGGGGSDVLTQSPHLSASLGETVSECLASBSISNLYAWYQKPKGSPQ 207

QY 180 LLIYAASTLQSGVPSRFGSGGTEFTLTISLPDFTGTYTCQQLISYPLTFGGGKVE 239
Db 208 LLIYAASSLQDGVPSRFGSGSGTQPSLKNMQPDEGVYTCQAYKYPFTFGAGTKLE 267

QY 240 IK 241
Db 268 IK 269

RESULT 6
US-08-488-113B-148
; Sequence 148, Application us/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.

;; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;; TITLE OF INVENTION: Proteins
;; NUMBER OF SEQUENCES: 169
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;; STREET: 500 West Madison Street, 34th floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60661
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,113B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/425,336
;; FILING DATE: 18-APR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/064,691
;; FILING DATE: 12-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/988,430
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEFAX: 312/707-9155
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 148:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 240 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-488-113B-148

Query Match 70.5%; Score 901.5; DB 1; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLSCAASGTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
Db 1 EQLVQSGGGLVQPGRSVRISCAASGYFTYGMNWRQAPGKGLWGWINTHTGEPTY 60

QY 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCARPHNTDAFDIWRGRTLVTVSS 120
Db 61 ADSFKGRTTSLDSDSKNTAYLQINLSRAEDTAVYFCTRRGVDW-YFDVWGOGTTVTYSS 119

QY 121 GGGPGGGGGGGSDVVMQTQSPFLSAFVGDITITCRASQGIYNLAWYQKPKAPK 180
Db 120 GGGSGGGGGGGSDIQMTQSPSSLASVGDVITCRASQDINSYLSWFOQKPKAPKT 179

QY 181 LLIYAASTLQSGVPSRFGSGGTEFTLTISLPDFTGTYTCQQLISYPLTFGGGKVEI 240
Db 180 LLIYRANLESQVPSRFGSGSGCTDTLTITSSLOYEDFGIYYCQYDESPWTFGGGCKLEM 239

QY 241 K 241

Query Match 70.5%; Score 901.5; DB 2; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;
QY 1 QVRLOQSGGLVQPGSRSLRLSCAAGFTFDDYAMHVRQAPGKLEWYSGMTWNSGSIGY 60
DB 1 ETQLVQSGGLVQPGSVRISCAASGYFTNGMNVVRQAPGKLEWGWINTHTGEPTY 60
QY 61 ADSVGRFTISRDNAKNSLYLQMSLRABDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120
DB 61 ADSFGKGRFTSLDDSKNTAYLQINSRLABDTAVYFCTRRGYDW-YFDVWGQGTTVTVSSG 119
QY 121 GGGPGGGGGGGSDVWMTQSPSFLSAFYVDRTITTCRASQGIYNYLAWYQOKPKAPKL 180
DB 120 GGGGGGGGGGGSDIQTQSPSSLSASVGDRTVITTCRASQDINSYLSWFOQPKAPKT 179
QY 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEI 240
DB 180 LIYRANRLESQVPSRFSGSGTDTLTISLQYEDFGIYTCQYDESPWTFGGGKLEM 239
QY 241 K 241
DB 240 K 240
RESULT 9
US-08-839-765-148
; Sequence 148, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889

TELEFAX: 312/707-9155
TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-148
Query Match 70.5%; Score 901.5; DB 4; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;
QY 1 QVRLOQSGGLVQPGSRSLRLSCAAGFTFDDYAMHVRQAPGKLEWYSGMTWNSGSIGY 60
DB 1 ETQLVQSGGLVQPGSVRISCAASGYFTNGMNVVRQAPGKLEWGWINTHTGEPTY 60
QY 61 ADSVGRFTISRDNAKNSLYLQMSLRABDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120
DB 61 ADSFGKGRFTSLDDSKNTAYLQINSRLABDTAVYFCTRRGYDW-YFDVWGQGTTVTVSSG 119
QY 121 GGGPGGGGGGGSDVWMTQSPSFLSAFYVDRTITTCRASQGIYNYLAWYQOKPKAPKL 180
DB 120 GGGGGGGGGGGSDIQTQSPSSLSASVGDRTVITTCRASQDINSYLSWFOQPKAPKT 179
QY 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYTCQQLISYPLTFGGGKVEI 240
DB 180 LIYRANRLESQVPSRFSGSGTDTLTISLQYEDFGIYTCQYDESPWTFGGGKLEM 239
QY 241 K 241
DB 240 K 240
RESULT 10
US-09-136-389-148
; Sequence 148, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430

;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/901,707
;; FILING DATE: 19-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,567
;; FILING DATE: 04-NOV-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McNicholas, Janet M.
;; REGISTRATION NUMBER: 32,918
;; REFERENCE/DOCKET NUMBER: 200-70-P4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/707-8889
;; TELEX: 650 388-1248
;; INFORMATION FOR SEQ ID NO: 148:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 240 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-136-389-148

Query Match 70.5%; Score 901.5; DB 4; Length 240;
Best Local Similarity 70.1%; Pred. No. 1.2e-63;
Matches 169; Conservative 33; Mismatches 38; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVQPGRSRLSLCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSGY 60
DB 1 ETQLVSGGGLVKPGGSRVISCASGTTTNGMNVVRQAPGKGLWGWINTHTGEPT 60

QY 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 120
DB 61 ADSEFKGRTFSLDDSKNTAYLQINSRAEDTAVYFCTRRGYDW-YFDVNGQGTTVTVSSG 119

QY 121 GGGPGGGGGGGSDVVMVQSPFLSAFVGDITITCRASQGIYNYLAWYQOKPKAPKL 180
DB 120 GGGGGGGGGGGSDIQMTQSPSLASASGDRVTITCRASQDINSYLSWFOQKPKAPKT 179

QY 181 LIYAASLTQSGVPSRFGSGSGTEFTLTSSLPQEDFGYVYCOOLISYPLTFGGGPKVEI 240
DB 180 LIYRANLESVPSRFGSGSGTDYTLTSSLPQEDFGYVYCOOYDESWTFGGGKLEM 239

QY 241 K 241
DB 240 K 240

RESULT 11
US-07-958-140-2
; Sequence 2, Application US/07958140
; Patent No. 5489525
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,140
; FILING DATE: 19921008
; CLASSIFICATION: 436

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 15280-77
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 243 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-07-958-140-2

Query Match 69.0%; Score 882; DB 1; Length 243;
Best Local Similarity 69.2%; Pred. No. 4.1e-62;
Matches 166; Conservative 30; Mismatches 42; Indels 2; Gaps 1;

QY 2 VRLQSGGGLVQPGRSRLSLCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSGY 61
DB 3 VQLVESGGGLVQPGGSLKLSLCAASGDFDSRYWMSVVRQAPGKGLWIGEINPDSSITNT 62

QY 62 DSVKGRFTTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLTVTVSSG 121
DB 63 PSLKDKFTTSSDNKNTLYLQMSKVRSEDYLYYCARRGY--AMDYWGQGTSTVTVSSG 120

QY 122 GPGGGGGGGGGSDVVMVQSPFLSAFVGDITITCRASQGIYNYLAWYQOKPKAPKL 181
DB 121 GSGGGGGGGGGSDIVMTQSPASLSASVGETVTITCRASENIYSLAWYQOKGKSPQL 180

QY 182 IYAASLTQSGVPSRFGSGSGTEFTLTSSLPQEDFGYVYCOOLISYPLTFGGGPKVEIK 241
DB 181 VYNKTLAEGVPSRFGSGSGTQFSLKINSLOPDEGSGYVYCOHHYCTPTFTFGSGTKLEIK 240

RESULT 12
PCT-US93-09166-2
; Sequence 2, Application PC/TUS9309166
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira H.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO PROSTATE CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US93-09166-2

Query Match 69.0%; Score 882; DB 5; Length 243;
Best Local Similarity 69.2%; Pred. NO. 4.1e-62;
Matches 166; Conservative 30; Mismatches 42. Indels

[illegible]

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RESULT 13
US-08-661-052-14
; Sequence 14, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chetan Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-14

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Qy 2 VRLQQSGGLVQPGRSURLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSGIYA 61
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Db 21 IQLVESGGGVVQPGRSURLSCSSSGEFTSDNYMYWVRQAPGKGLEWVATISDGGSYTYP 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREPHNTD-AFDIWRGGLVTVSSG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 DSVKGRFTISRDNKNTFLFQMDSLRPEDTGVYFCARGYYRYEGAMDYWCQGTPTVTVSSG 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 121 GGGPGGGGGGGGSDVVMVTQSPSLSAFVGDTTITTCRASQGIY-----NYLAWYQQRP 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 GGGSGGGGGGGGSDIQLTQSPSSLASVGDRTVITCKSSQSVLYSSNOKNYLAWYQQRP 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175 GKAPKLLIYAASLTQSGVPSRFSGSGSGTEFTLTISLQPEDFGTYTTCOOLISYPLTFGG 234
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Db 201 GKAPKLLIYWASTRESGVPSRFSGSGSGTDTFTTISLQPEDIATYVYCHQYLS-SWTFQG 259
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RESULT 14
US-09-188-082-14
; Sequence 14, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-188-082-14

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QY 2 VRLQQSGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGYA 61

Db 21 IQLVESGGGVQGRSLRLSCSSSGIFSDNYMYVRQAPGKGLEWVATISDGGSYTYP 80
QY 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-AFDIWRGTLVTVSSG 120
Db 81 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-AFDIWRGTLVTVSSG 140
QY 121 GGGPGGGGGGGSDVVMVMTQSPFSLAFVGDITITICRASQGIY-----NYLAWYQOKP 174
Db 141 GGGSGGGGGGGSDIQLTQSPSSLSASVGDRTVITCKSSQSVLYSSNOKNYLAWYQOKP 200
QY 175 GKAPKLLIYAASLTQSGVPSRFGSGSGTEFTLTITSSLOPEDFGTYCCOOLISYPLTFGG 234
Db 201 GKAPKLLIYWASTRESGVPSRFGSGSGTDFTTISSLOPEDIATYYCHQYLS-SWTFGQ 259
QY 235 GTRKVEIK 241
Db 260 GTRKVEIK 266

RESULT 15
US-08-661-052-16
; Sequence 16, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chезian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,052
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-661-052-16

Query Match 68.8%; Score 879; DB 2; Length 553;
Best Local Similarity 69.6%; Pred. No. 1.8e-61;
Matches 172; Conservative 27; Mismatches 40; Indels 8; Gaps 3;
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Db 21 IQLVESGGGVQGRSLRLSCSSSGIFSDNYMYVRQAPGKGLEWVATISDGGSYTYP 80

QY 62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTD-AFDIWRGTLVTVSSG 120
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QY 121 GGGPGGGGGGGSDVVMVMTQSPFSLAFVGDITITICRASQGIY-----NYLAWYQOKP 174
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QY 175 GKAPKLLIYAASLTQSGVPSRFGSGSGTEFTLTITSSLOPEDFGTYCCOOLISYPLTFGG 234
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QY 235 GTRKVEIK 241
Db 260 GTRKVEIK 266

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Job time: 425 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:04 ; Search time 101.13 Seconds
(without alignments)
264.697 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
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Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1040	81.4	242	21 AAY58236	Internalising anti
3	1023.5	80.1	248	13 AAR20059	Recombinant sc3D6
4	1010.5	79.1	245	20 AAY06714	Antibody 5E5 singl
5	1009.5	79.0	245	20 AAY06717	Antibody 12B5 sing
6	993.5	77.7	293	22 AAG65715	Amino acid sequenc
7	992	77.6	240	20 AAY02472	A single chain ant
8	988	77.3	240	22 AAB46044	Human TF anti-idio
9	988	77.3	240	22 AAB46045	Human TF anti-idio
10	987.5	77.3	245	20 AAY06715	Antibody 10D10 sin
11	987	77.2	244	20 AAY06716	Antibody 12B5 sing

12	985	77.1	240	22 AAB46040	Human TF anti-idio
13	984	77.0	240	22 AAB45992	Human MUC-1 scfv c
14	977	76.4	240	22 AAB46039	Human TF anti-idio
15	977	76.4	240	22 AAB46048	Human TF anti-idio
16	976	76.4	240	22 AAB46010	Human MUC-1 scfv c
17	976	76.4	240	22 AAB46042	Human TF anti-idio
18	975	76.3	240	22 AAB45997	Human MUC-1 scfv c
19	975	76.3	240	22 AAB46007	Human MUC-1 scfv c
20	975	76.3	240	22 AAB46018	Human MUC-1 scfv c
21	975	76.3	240	22 AAB46020	Human MUC-1 scfv c
22	974	76.2	240	22 AAB46050	Human TF anti-idio
23	972	76.1	240	22 AAB46004	Human MUC-1 scfv c
24	972	76.1	240	22 AAB46038	Human TF anti-idio
25	971	76.0	240	22 AAB46051	Human TF anti-idio
26	970	75.9	240	22 AAB45991	Human MUC-1 scfv c
27	970	75.9	240	22 AAB46043	Human TF anti-idio
28	969	75.8	240	22 AAB46005	Human MUC-1 scfv c
29	969	75.8	240	22 AAB46046	Human TF anti-idio
30	968	75.7	240	22 AAB45993	Human MUC-1 scfv c
31	966	75.6	240	22 AAB45996	Human MUC-1 scfv c
32	966	75.6	240	22 AAB46003	Human MUC-1 scfv c
33	966	75.6	240	22 AAB46006	Human MUC-1 scfv c
34	966	75.6	240	22 AAB46047	Human TF anti-idio
35	964	75.4	240	22 AAB46021	Human MUC-1 scfv c
36	962	75.3	240	22 AAB45999	Human MUC-1 scfv c
37	962	75.3	240	22 AAB46002	Human MUC-1 scfv c
38	962	75.3	240	22 AAB46019	Human MUC-1 scfv c
39	961	75.2	240	22 AAB46009	Human MUC-1 scfv c
40	961	75.2	240	22 AAB46041	Human TF anti-idio
41	960	75.1	240	22 AAB46001	Human MUC-1 scfv c
42	959	75.0	240	22 AAB46012	Human MUC-1 scfv c
43	956	74.8	240	22 AAB45994	Human MUC-1 scfv c
44	955	74.7	240	22 AAB46014	Human TF anti-idio
45	954	74.6	240	22 AAB46011	Human MUC-1 scfv c

ALIGNMENTS

RESULT 1
AAW24063
ID AAW24063 standard; Protein; 241 AA.
XX AC AAW24063;
XX DT 17-MAR-1998 (first entry)
XX DE Human WSX receptor agonist antibody clone #17.
XX KW Human; WSX receptor; clone #17; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.
XX OS Homo sapiens.
XX PN WO9725425-A1.
XX PD 17-JUL-1997.
XX PF 07-JAN-1997; 97WO-US00325.
XX PR 20-JUN-1996; 96US-0667197.
XX PR 08-JAN-1996; 96US-0585005.
XX (GETH) GENENTECH INC.
XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI Rodrigues ML;
XX

DR WPI; 1997-372864/34.

XX WSX receptor and related antibodies and ligands - used to develop

PT products for diagnosis and therapy, e.g. for improving

PT haematopoiesis or for treating tumours

XX

XX Example 14; Pages 122-123; 219pp; English.

PS

XX The present sequence is an agonist antibody clone to the human WSX

CC receptor, which can be used to identify and purify ligands and

CC activators. An anti-WSX receptor antibody can be used as an agonist

CC to activate the WSX receptor, leading to enhanced proliferation or

CC differentiation of a cell expressing the WSX receptor. It can also

CC be used to decrease body weight and/or fat-depot weight and/or food

CC intake in an obese mammal. WSX receptor ligands can be used to

CC enhance proliferation or differentiation of lymphoid, myeloid or

CC erythroid blood cell lineages. This is useful when a mammal,

CC especially a human, is suffering from decreased blood cell levels,

CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone

CC marrow transplantation therapy. It can also be used to repopulate

CC blood cells in a mammal. The products can also be used to treat,

CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,

CC polycystic ovarian disease, cardiovascular diseases,

CC osteoarthritis, dermatological disorders, hypertension, insulin

CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer

CC and cholelithiasis.

XX

SQ Sequence 241 AA;

Query Match 100.0%; Score 1278; DB 18; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.1e-78;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OVRLOQSGGLVQGRSLRCAASGFTFDDYAMHWVROAPCKGLEWVSGMTWNSGICY 60

Db 1 qvrllqsgggglvqgrslriscasagftfddyamhwvrdpdkglewvsgmtwnsgsigy 60

OY 61 ADSVKGRTISRDNKNSLYLQMSLRARDTAVYYCAREPHNTDAFDIWRGRTLVTVSSG 120

Db 61 adsvkgtrfisdndknsllylqmslraedtavyycatephntdafdiwrgrtlvtvssg 120

OY 121 GGGPGGGGGGGSDVWQTSPSFLSAFVGDTITTCRASQGIYNYLAWYQKPKAPKL 180

Db 121 gggpgggsgggsgdsvwtqspfsfaisfvgdtititcrasqgiynylawyqkpgkpl 180

OY 181 LIYAASTLQSGVPSRFGSGSGCTERTLTSSLPQDFGYVYCCQLISYPLTFGGTKVEI 240

Db 181 liyaastlqsgvpsrfgsgsgctertlttsslpqdfgtyccqlisypitfgggckvei 240

OY 241 K 241

Db 241 k 241

RESULT 2

AAV58236

ID AAV58236 standard; Protein; 242 AA.

XX

AC AAV58236;

XX

XX 27-MAR-2000 (first entry)

XX Internalising anti-c-erbB-2 receptor antibody scFv C1.

XX Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;

KW HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.

XX Synthetic.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

PH Region 31..35

FT

FT /note= "Heavy chain variable region (VH) complementarity

FT determining region 1 (CDR1)"

FT Misc-difference 37 /note= "Encoded by GTN"

FT Region /note= "VH-CDR2"

FT Region /note= "VH-CDR3"

FT Region /note= "VH-CDR3"

FT Region /note= "Light chain variable region (VL) complementarity

FT determining region 1 (CDR1)"

FT Region /note= "VL-CDR2"

FT Region /note= "VL-CDR3"

XX WO955367-A1.

PN 04-NOV-1999.

XX 23-APR-1999; 99WO-US07395.

XX 24-APR-1998; 98US-0082953.

PR 12-FEB-1999; 99US-0250056.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Poul MA;

XX WPI; 2000-072168/06.

DR N-PSDB; AA255615.

XX Novel internalizing antibodies used to treat cancer cells -

PT Claim 3; Page 82; 85pp; English.

PS This sequence represents an internalising humanised antibody,

XX scFv C1, which specifically binds to the extracellular domain

CC of the c-erbB-2 receptor, the protein product of the HER/neu oncogene.

CC The scFv C1 antibody binds to the epitope of the c-erbB-2 receptor that

CC is bound by C1 antibodies. On binding the c-erbB-2 receptor, the

CC antibody is transported into the cell. The c-erbB-2 receptor is a marker

CC protein which is overexpressed by 30-50% of breast carcinomas and other

CC adenocarcinomas, and thus provides a useful cell surface marker for

CC specifically targeting tumour cells. The antibodies of the invention

CC are used as tumour-targeting molecules for diagnosis and treatment. The

CC antibodies can be attached to effector molecules. The effector molecules

CC may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin;

CC radionuclides; ligands such as growth factors; therapeutic agents such

CC as vinblastine, vindesine or melphalan; ribozymes; or antisense

CC molecules. The antibodies may also be used for in vivo or in vitro

CC detection and/or quantitation of the c-erbB-2 receptor and thus diagnosis

CC and/or localisation of cancers characterised by expression of c-erbB-2.

CC Although antibodies have previously been used to target tumour cells,

CC their success has been limited. The utility of prior art antibodies has

CC been hampered by the paucity of tumour specific antibodies, antibody

CC immunogenicity, low binding affinity, and poor tumour penetration.

CC Immunogenicity could be avoided and toxicity reduced if high affinity

CC tumour specific human antibodies were available. However, the production

CC of human monoclonal antibodies using conventional hybridoma technology

CC has proven difficult. Also, most of the antibodies produced react with

CC antigens that are also common to non-malignant cells, which makes them

CC unsuitable for use as tumour-targeting molecules. The antibodies of the

CC invention overcome these difficulties, as they are targeted to a

CC tumour-specific antigen, and avoid the problem of immunogenicity as they

CC are human in origin.

XX

SQ Sequence 242 AA;

Query Match 81.4%; Score 1040; DB 21; Length 242;

Best Local Similarity 83.0%; Pred. No. 1.1e-62;

Matches 200; Conservative 15; Mismatches 26; Indels 0; Gaps 0;


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QY 1 QVRLQSGGGLVQPGRLSLRSCAASGFTDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 1 qvqlvesggglvqpggslrlscaasgftfssyamgwvraqpgkglwvssisgssryiy 60
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSLRADTAAYYCAREPHNTDAFDIWRGRTLVTVSSG 120
Db 61 adsvkgrftisrdnksnlylqmnslrdaetavyycaKmdasgsyfnfwggglvtvssg 120
QY 121 GGGPGGGGGGGSDVMTQSPSFSLSAFVGDITITCRASQGIYNYLAWYQOKPGKAPKL 180
Db 121 gggsgggsgggsettlitqpsfslsafvgdrtitcraspgirnylawyqkpgkapkl 180
QY 181 LIYAASTLQSGVPSRFSGSGTETLTLSLQPEDFGYTCQQLISYPLTFGGGTVKVEI 240
Db 181 liyaastlqsgvpsrfsfgsgsgtdltlsslqpedfatyycqqynsyplsfgggkvei 240
QY 241 K 241
Db 241 k 241
RESULT 3
AAR20059
ID AAR20059 standard; Protein; 248 AA.
AC AAR20059;
XX
XX
DT 25-MAR-1992 (first entry)
DE Recombinant sc3D6 anti-HIV gp160 antibody.
XX
KW Plasmid pUC3D6LC; pUC3D6HC; human immunodeficiency virus; AIDS;
KW complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT /label= Framework_1_heavy_chain
FT /label= Framework_1_heavy_chain
FT /label= CDR_1_heavy_chain
FT /label= Framework_2_heavy_chain
FT /label= CDR_2_heavy_chain
FT /label= Framework_3_heavy_chain
FT /label= CDR_3_heavy_chain
FT /label= Framework_4_heavy_chain
FT /label= Framework_4_heavy_chain
FT /label= linker
FT /label= Framework_1_light_chain
FT /label= Framework_2_light_chain
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FT /label= CDR_2_light_chain
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FT /label= Framework_4_light_chain
XX
PN WO9118983-A.
XX
PD 12-DEC-1991.
XX

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PF 28-MAY-1991; 91WO-1000067.
XX
PR 29-MAY-1990; 90AT-0001178.
XX
PA (JUNG/) JUNGBAUER A.
XX
PI Felgenhauer M, Himmeler G, Kohl J, Steindl F;
XX
DR WPI; 1992-007468/01.
XX
DR N-PSDB; AAQ20068.
XX
PT Recombinant protein which binds to complex viral antigen and
PT HIV-1 - contains variable region of antibody derived from 3D6
PT cell line, used for detecting HIV-1 antigen
XX
PS Claim 4; Page 31; 52pp; German.
XX
CC The cell line 3D6 (87110301; Porton Down) produces a MAb of the
CC IgG1/kappa type that reacts specifically with HIV-1 gp41 and also
CC IgG1 cross-reacts with HIV-1 gp120. Gene construct sc3D6 was
CC engineered using the variable region coding regions of the heavy
CC and light chains of antibody 3D6, joined by a linker. The
CC recombinant protein binds to HIV gp160.
CC See also AAQ20066 and AAQ20067.
XX
XX Sequence 248 AA;
XX
Query Match 80.1%; Score 1023.5; DB 13; Length 248;
Best Local Similarity 79.4%; Pred. No. 1.4e-61;
Matches 197; Conservative 20; Mismatches 22; Indels 9; Gaps 2;
QY 1 QVRLQSGGGLVQPGRLSLRSCAASGFTDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 2 evqlvesggglvqpggslrlscaasgftfndyamhwvraqpgkglwvsgiswdsssigy 61
QY 61 ADSVKGRFTISRDNKNSLYLQMNLSLRADTAAYYCAREPHNTDAFDIWRGRT 113
Db 62 adsvkgrftisrdnksnlylqmnslrdaetavyycaKmdasgsyfnfwggglvtvssg 121
QY 114 LVTVSSGGGGGGGGSDVMTQSPSFSLSAFVGDITITCRASQGIYNYLAWYQOK 173
Db 122 mvtvssggggsgggsgggsggsgdiqmtqpsstlsasvdrvtitcrasqsisrlawyqqk 181
QY 174 PGKAPKLLIYAASTLQSGVPSRFSGSGTETLTLSLQPEDFGYTCQQLISYPLTFG 233
Db 182 pgkvpklliykasslesgvpsrfsfgsgsgtftltlsslqpedfatyycqqynsy--sfg 239
QY 234 GGTKEIK 241
Db 240 pgtkvdik 247
RESULT 4
AAV06714
ID AAY06714 standard; Protein; 245 AA.
XX
AC AAY06714;
XX
DT 17-JUN-1999 (first entry)
DE Antibody 5E5 single chain Fv (scFv) fragment.
XX
KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
KW neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS Homo sapiens.
XX
PN WO910494-A2.
XX

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Db 63 adsvkgrftisrdnaknsllylgnmslraedstavyycardgst-gmdvwgrgtlvtvssg 121
QY 121 GGGPGGGGGGGSDVMTQSPSFSLSAFYGDRITITCRASOGIYNYLAWYQOKPGKAPKL 180
Db 122 gggsgggsgggsgdqmtpstlsasigdrvtitcrasegiyhwlavyqkpgkpkpl 181
QY 181 LIYAASTLQSGVPSRPSGSGTETTLTSSLOPEDFGYNYCQQLISYPLTFGGGTKVEI 240
Db 182 llykassiasgapsrfsfgsgsgtdftxttisslqpddfatyyccqysnypltfgggkklai 241
QY 241 K 241
Db 242 k 242

RESULT 6
AAG65715
ID AAG65715 standard; protein; 293 AA.
XX AC AAG65715;
XX DT 07-JAN-2002 (first entry)
XX DE Amino acid sequence of secreted form of scFv 4A.
XX KW Polymeric immunoglobulin receptor; pIgR; ligand; therapeutic;
XX OS carcinoma diagnosis; veterinary; scFv 4A.
XX FH Synthetic.
XX FT Key
XX FT Location/Qualifiers
XX FT 1..22 "Peptide leader"
XX FT 23..27 "Peptide"
XX FT 28..58 "Region"
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Matches 193; Conservative 15; Mismatches 30; Indels 4; Gaps 2;

Qy 1 QVRLQSGGLVQPGRLSCAASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIQY 60
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 Db 1 evqllesggglvqpgsrlscaasgftfssyamsvwrqapkglewsaigwsgestwy 60
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 Qy 61 ADSVKGRFTISRDNKNSLYLQMSLRADTAAYVCAREPHNTDAFDIWRGTLVTVSSG 120
 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||
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 Qy 121 GGGPGGGSGGGGS-DVVMQTQSPFLSAFVGDTITITCRASQGIYNYLAWYQQRPGKAPK 179
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 Qy 240 IK 241
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 Db 238 lk 239

RESULT 9
 AAB46045
 ID AAB46045 standard; Peptide; 240 AA.
 XX AAB46045;
 AC AAB46045;
 DT 23-MAR-2001 (first entry)
 XX Human TF anti-idiotypic antibody fragment K3 #2.
 DE MUCL; human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW antidiotopic antibody; cytostatic; virucidal; antibacterial; TF antigen;
 KW antiparasitic; infectious disease.
 XX Homo sapiens.
 OS WO200073430-A2.
 PN 07-DEC-2000.
 XX 29-MAY-2000; 2000WO-DE01809.
 PF 27-MAY-1999; 99DE-1024405.
 PR 09-SEP-1999; 99DE-1043016.
 XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 PA Goletz S, Karsten U;
 PI WPI; 2001-049937/06.
 DR Vaccines against conformation-dependent or non-peptide antigens, based
 XX on DNA encoding peptide which mimics the antigen, useful e.g. as
 XX antitumor vaccines -
 PS Disclosure; Page 11; 36pp; German.
 CC This invention describes a novel vaccine (V1) against
 CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
 CC antibody, or peptide which immunologically imitates CDA, is new. (I)
 CC encodes a region of an antidiotopic antibody (Ab2) or another peptide
 CC which: (a) specifically binds to the binding site of an antibody (Ab1)
 CC or an antigen binding molecule; and (b) immunologically mimics the
 CC initial antigen. The epitope is partially or completely
 CC conformation-dependent, and has an immunogenic structure defined by a
 CC specific spatial conformation of amino acids. (I) is used in the form
 CC of linear or circular naked DNA and/or with a viral vector and/or
 CC adjuvants. The products of the invention have cytostatic, virucidal,
 CC antibacterial and antiparasitic. The invention also describes (I) a
 CC corresponding vaccine (V2) against antigens which are not proteins or

CC peptides, as defined above but which have epitopes which show an
 CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
 CC antidiotopic antibody fragments against the MUC1-conformation epitope
 CC having one of 31 approximately 60 residue amino acids sequences, all
 CC fully defined in the specification; (4) MUC1-conformation epitope mimics
 CC having one of 16 9-17 residue amino acid sequences, all fully in the
 CC specification; (5) antidiotopic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible.
 XX
 SQ Sequence 240 AA;

Query Match 77.3%; Score 988; DB 22; Length 240;
 Best Local Similarity 79.8%; Pred. No. 3.3e-59;
 Matches 193; Conservative 15; Mismatches 30; Indels 4; Gaps 2;

Qy 1 QVRLQSGGLVQPGRLSCAASGFTFDDYAMHWVRQAPGKLEWVSGMTWNSGSIQY 60
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 Db 1 evqllesggglvqpgsrlscaasgftfssyamsvwrqapkglewsaigwsgestwy 60
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 Qy 61 ADSVKGRFTISRDNKNSLYLQMSLRADTAAYVCAREPHNTDAFDIWRGTLVTVSSG 120
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 Qy 121 GGGPGGGSGGGGS-DVVMQTQSPFLSAFVGDTITITCRASQGIYNYLAWYQQRPGKAPK 179
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 Db 118 999sgggsgggsgtdqmtqspsslsasvgrvttitcrasqssylnwyqkpgkpk 177
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 Qy 240 IK 241
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 Db 238 lk 239

RESULT 10
 AAY06715
 ID AAY06715 standard; Protein; 245 AA.
 XX AAY06715;
 AC AAY06715;
 XX 17-JUN-1999 (first entry)
 DT Antibody 10D10 single chain Fv (scFv) fragment.
 DE Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
 XX megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
 KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
 KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
 KW neuromuscular; muscular dystrophy; complementarity determining region.
 XX Homo sapiens.
 XX WO9910494-A2.
 PN 04-MAR-1999.
 PD 21-AUG-1998; 98WO-US17364.
 PF 25-AUG-1997; 97US-0918148.
 PR (GETH) GENENTECH INC.
 XX Adams CW, Carter PJ, Fendly BM, Gurney AL;

AA046040	ID	AA046040 standard; Peptide: 240 AA.	
XX	AC	AA046040;	
XX	DT	23-MAR-2001 (first entry)	
XX	DE	Human TF anti-idiotypic antibody fragment P8.	
XX	MU	MU01; human; vaccine; conformation-dependent antigen; antibody; cancer;	
XX	KW	antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;	
XX	KW	antiparasitic; infectious disease.	
XX	OS	Homo sapiens.	
XX	PN	W0200073430-A2.	
XX	PD	07-DEC-2000.	
XX	PF	29-MAY-2000; 2000WO-DE01809.	
XX	PR	27-MAY-1999; 99DE-1024405.	
XX	PR	09-SEP-1999; 99DE-1043016.	
XX	PA	(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX	GO	Goletz S, Karsten U;	
XX	WI	WPI; 2001-049937/06.	
XX	PT	Vaccines against conformation-dependent or non-peptide antigens, based	
XX	PT	on DNA encoding peptide which mimics the antigen, useful e.g. as	
XX	PT	antitumor vaccines -	
XX	PS	Disclosure; Page 11; 36pp; German.	
XX	CC	This invention describes a novel vaccine (V1) against	
XX	CC	conformation-dependent antigens (CDA) comprising DNA (I) and/or an	
XX	CC	antibody, or peptide which immunologically imitates CDA, is new. (1)	
XX	CC	encodes a region of an antidiotypic antibody (Ab2) or another peptide	
XX	CC	which: (a) specifically binds to the binding site of an antibody (Ab1)	
XX	CC	or an antigen binding molecule; and (b) immunologically mimics the	
XX	CC	initial antigen. The epitope is partially or completely	
XX	CC	conformation-dependent, and has an immunogenic structure defined by a	
XX	CC	specific spatial conformation of amino acids. (1) is used in the form	
XX	CC	of linear or circular naked DNA and/or with a viral vector and/or	
XX	CC	adjuvants. The products of the invention have cytostatic, virucidal,	
XX	CC	antibacterial and antiparasitic. The invention also describes (1) a	
XX	CC	corresponding vaccine (V2) against antigens which are not proteins or	
XX	CC	peptides, as defined above but which have epitopes which show an	
XX	CC	immunogenic structure; (2) preparing (V1) and (V2); (3) human	
XX	CC	antidiotypic antibody fragments against the MUC1-conformation epitope	
XX	CC	having one of 31 approximately 60 residue amino acid sequences, all	
XX	CC	fully defined in the specification; (4) MUC1-conformation epitope mimics	
XX	CC	having one of 16 9-17 residue amino acid sequences, all fully in the	
XX	CC	specification; (5) antidiotypic antibody fragments against the TF	
XX	CC	antigen having one of 24 approximately 200 residue amino acid sequences,	
XX	CC	fully defined in the specification; (6) TF carbohydrate epitope mimetics	
XX	CC	having one of 25 7-13 residue amino acid sequences, all fully defined in	
XX	CC	the specification; and (7) DNA sequences encoding the fragments and	
XX	CC	derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat	
XX	CC	cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria	
XX	CC	and parasites. The vaccines are effective in cases where vaccination has	
XX	CC	previously not been possible.	
XX	SQ	Sequence 240 AA;	
XX	QM	Query Match 77.1%; Score 985; DB 22; Length 240;	
XX	BM	Best Local Similarity 79.8%; Pred. No. 5, 3e-59;	
XX	MA	Matches 193; Conservative 16; Mismatches 29; Indels 4; Gaps 2;	
XX	QY	1 QVRLQSGGGLVPGHSLRSLCAASGFTDDYAMHWVRQAPGKGLWVSGMTWNSGSIY 60	

CC having one of 31 approximately 60 residue amino acids sequences, all
 CC fully defined in the specification; (4) MUC1-conformation epitope mimics
 CC having one of 16 9-17 residue amino acid sequences, all fully in the
 CC specification; (5) anti-idiotypic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible.

XX SQ Sequence 240 AA;

Query Match 77.0%; Score 984; DB 22; Length 240;
 Best Local Similarity 78.9%; Pred. No. 6.2e-59;
 Matches 191; Conservative 18; Mismatches 29; Indels 4; Gaps 2;
 QY 1 QVRLQSGGLVQPGKSLRLSCAASGFTFDDYAMHWVRQAPGKGLVWYSGMTWNSGSIGY 60
 Db 1 evqllesgeglvqpggsirlscasagffssyamsvvrqapkgilewvssinyngdatsy 60
 QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYVCAREPHNTDAFDIWRGTLTVVSSG 120
 Db 61 adsvkgrftisrdnsknltlylqmnsraedtavvycaak---ssstfdywgqgtlvtvssg 117
 QY 121 GGGPGGGGGGGGS-DVWMTQSPSFLSAFVGDITITCRASGIVNYLAWYQKPKGKAP 179
 Db 118 999sgggsgggsggsgtdlqmtqpslsasvsgdvltitcrasqslssylnwyqqkpgkpk 177
 QY 180 LLIYAASLTQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYVCOQLISYPLTFGGGTVKE 239
 Db 178 lliysastlqsgvpsrfrsgsgsgtdftltisslqpedfatyycqqtspatfsggtkve 237

QY 240 IK 241

Db 238 lk 239

RESULT 14
 AAB46039

ID AAB46039 standard; Peptide; 240 AA.

XX AC AAB46039;

XX DT 23-MAR-2001 (first entry)

XX DE Human TF anti-idiotypic antibody fragment P3.

XX MUCL; human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW anti-idiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;
 KW antiparasitic; infectious disease.

XX OS Homo sapiens.

XX PN WO200073430-A2.

XX PD 07-DEC-2000.

XX PF 29-MAY-2000; 2000WO-DE01809.

XX PR 27-MAY-1999; 99DE-1024405.

XX PR 09-SEP-1999; 99DE-1043016.

XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX PI Goletz S, Karsten U;

XX DR WPI; 2001-049937/06.

XX PT Vaccines against conformation-dependent or non-peptide antigens, based

PT on DNA encoding peptide which mimics the antigen, useful e.g. as
 XX antitumor vaccines -
 XX Disclosure; Page 10; 36pp; German.

XX This invention describes a novel vaccine (V1) against
 CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
 CC antibody, or peptide which immunologically imitates CDA, is new. (1)
 CC encodes a region of an anti-idiotypic antibody (Ab2) or another peptide
 CC which: (a) specifically binds to the binding site of an antibody (Ab1)
 CC or an antigen binding molecule; and (b) immunologically mimics the
 CC initial antigen. The epitope is partially or completely
 CC conformation-dependent, and has an immunogenic structure defined by a
 CC specific spatial conformation of amino acids. (I) is used in the form
 CC of linear or circular naked DNA and/or with a viral vector and/or
 CC adjuvants. The products of the invention have cytostatic, virucidal,
 CC antibacterial and antiparasitic. The invention also describes (1) a
 CC corresponding vaccine (V2) against antigens which are not proteins or
 CC peptides, as defined above but which have epitopes which show an
 CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
 CC anti-idiotypic antibody fragments against the MUC1-conformation epitope
 CC having one of 31 approximately 60 residue amino acids sequences, all
 CC fully defined in the specification; (4) MUC1-conformation epitope mimics
 CC having one of 16 9-17 residue amino acid sequences, all fully in the
 CC specification; (5) anti-idiotypic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible.

XX SQ Sequence 240 AA;

Query Match 76.4%; Score 977; DB 22; Length 240;
 Best Local Similarity 79.0%; Pred. No. 1.8e-58;
 Matches 192; Conservative 18; Mismatches 27; Indels 6; Gaps 3;

QY 1 QVRLQSGGLVQPGKSLRLSCAASGFTFDDYAMHWVRQAPGKGLVWYSGMTWNSGSIGY 60

Db 1 evqllesgeglvqpggsirlscasagffssyamsvvrqapkgilewvssisysgatkny 60

QY 61 ADSVKGRFTISRDNKNSLYLQMNSLRADTAIVYVCAREPHNTDA-FDIWRGTLTVVSS 119

Db 61 adsvkgrftisrdnsknltlylqmnsraedtavvycaak----sdasfdywgqgtlvtvss 116

QY 120 GGGPGGGGGGGGS-DVWMTQSPSFLSAFVGDITITCRASGIVNYLAWYQKPKGAP 178

Db 117 999sgggsgggsggtdlqmtqpslsasvsgdvltitcrasqslssylnwyqqkpgkap 176

QY 179 LLIYAASLTQSGVPSRFRSGSGSGTEFTLTISLQPEDFGTYVCOQLISYPLTFGGGTVK 238

Db 177 klllydasslqsgvpsrfrsgsgsgtdftltisslqpedfatyycqdygggttfggtkv 236

QY 239 EIK 241

Db 237 eik 239

RESULT 15

AAB46048

ID AAB46048 standard; Peptide; 240 AA.

XX AC AAB46048;

XX DT 23-MAR-2001 (first entry)

XX DE Human TF anti-idiotypic antibody fragment J6.

XX MUCL; human; vaccine; conformation-dependent antigen; antibody; cancer;

...

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:35:37 ; Search time 91.6 Seconds
(without alignments)
455.150 Million cell up

Title: US-08-779-457-50
 Perfect score: 1278
 Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISYPITFGGKTKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

```
Minimum DB seq length: 0
Maximum DB seq length: 20
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
STREMBL_19:*
1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_tvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query #		DB	ID	Description
		Match	Length			
1	871.5	58.2	298	11	Q9QYF0	Q9QYF0 mus musculus
2	728	57.0	241	11	Q92IA6	Q92IA6 mus musculus
3	589.5	46.1	218	11	Q925S1	Q925S1 mus musculus
4	490.5	38.4	112	4	Q9HCCI	Q9HCCI homo sapien
5	478	37.4	121	4	Q9UL71	Q9UL71 homo sapien
6	468	36.6	597	4	Q96B89	Q96B89 homo sapien
7	467.5	36.6	118	4	Q9UL91	Q9UL91 homo sapien
8	452	35.4	108	4	Q9UL79	Q9UL79 homo sapien
9	451	35.3	104	4	Q9UL87	Q9UL87 homo sapien
10	450.5	35.3	107	4	Q96SA9	Q96SA9 homo sapien
11	449	35.1	108	4	Q9UL70	Q9UL70 homo sapien
12	446	34.9	113	4	Q9UL90	Q9UL90 homo sapien
13	440	34.4	108	4	Q9UL77	Q9UL77 homo sapien
14	440	34.4	116	4	Q9UL93	Q9UL93 homo sapien
15	439.5	34.4	494	4	Q96K68	Q96K68 homo sapien
16	435.5	34.1	118	4	Q9UL72	Q9UL72 homo sapien

17	433.5	33.9	473	11	Q91205	Q91205 mus musculus
18	432.5	33.8	122	4	Q9UL84	Q9UL84 homo sapien
19	426.5	33.4	147	4	Q9Y509	Q9Y509 homo sapien
20	424.5	33.2	107	4	Q9UL81	Q9UL81 homo sapien
21	414	32.4	109	11	Q920E6	Q920E6 mus musculus
22	403	31.5	479	11	Q91WP5	Q91WP5 mus musculus
23	401.5	31.4	487	11	Q99XA4	Q99XA4 mus musculus
24	392	30.7	119	11	Q920E7	Q920E7 mus musculus
25	390	30.5	95	4	Q9ULB6	Q9ULB6 homo sapien
26	384	30.0	211	11	Q91XL0	Q91XL0 mus musculus
27	381.5	29.9	109	4	Q9UL85	Q9UL85 homo sapien
28	381.5	29.9	437	11	Q9LIA4	Q9LIA4 mus musculus
29	381	29.8	116	4	Q96PF6	Q96PF6 homo sapien
30	379	29.7	108	4	Q9ULB3	Q9ULB3 homo sapien
31	378	29.6	486	11	Q91Z07	Q91Z07 mus musculus
32	377.5	29.5	109	4	Q9UL78	Q9UL78 homo sapien
33	377	29.5	233	11	Q91WS9	Q91WS9 mus musculus
34	375	29.3	131	4	Q9ULB8	Q9ULB8 homo sapien
35	366	28.6	112	4	Q9UGP3	Q9UGP3 homo sapien
36	364	28.5	480	11	Q91XPI	Q91XPI mus musculus
37	363	28.4	214	11	Q9RIA5	Q9RIA5 mus musculus
38	361	28.2	170	11	Q925S2	Q925S2 mus musculus
39	357	27.9	111	11	Q920E9	Q920E9 mus musculus
40	356.5	27.9	109	4	Q9ULB6	Q9ULB6 homo sapien
41	356	27.9	107	11	Q9JL84	Q9JL84 mus musculus
42	354	27.7	473	11	Q9UD8L4	Q9UD8L4 mus musculus
43	353	27.6	125	4	Q9UL95	Q9UL95 homo sapien
44	351.5	27.5	234	6	Q9N0W6	Q9N0W6 oryctolagus
45	350	27.4	124	11	Q9LWF8	Q9LWF8 mus musculus

ALIGNMENTS

RESULT 1

Q9QYF0	PRELIMINARY;	PRT;	298 AA.
ID	Q9QYF0		
AC	Q9QYF0;		
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	GN 8 SCFV.		
DE	GN 8		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX	NCBI_TaxID=10090;		
[1]	SEQUENCE FROM N.A.		
RN	STRAIN-BALB/C; TISSUE=SPLEEN;		
RP	MEDLINE=20183931; PubMed=10706631;		
RC	Shinohara N.; Demura T.; Fukuda H.;		
RA	Isolation of a vascular cell wall-specific monoclonal antibody		
RT	recognizing a cell polarity by using a phage display subtraction		
RT	method.;		
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).		
RL	EMBL; AB036341; BAA88633.1; ..		
DR	HSP; P01607; IREI.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 2.		
DR	SMART; SM00406; IGV; 2.		
DR	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;		

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Query Match      68.2%; Score 871.5; DB 11; Length 298;
Best Local Similarity 68.2%; Pred. No. 4.6e-66;
Matches 165; Conservative 33; Mismatches 41; Indels 3; Gaps 2;

Qy 1 QVRQQSGGGLVQGRSLRLSCAASGFTDDYAMHWVRQAPCKGLEWYSGMTWNSGSICY 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 QVKLOOSGGGLVQPGGSLKLSLCAASGSDFSRYKWSWVRQAPCKGLEWIEINPDSTSLNY 99
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 61 ADSVKGRTTISRDNKNSLYLQWNSLRADTAVVYCARP-HNTDAFDIWRGTLTVSS 119
||:| |||||:||||: |||||:||||: ||: |||||
Db 100 TSLDKFTISRDNKNTLYLQWNSLRSEDTALYCARASYGHSAY--WGQTTTVTVSS 157

QY 120 GGGGPGGGGGGGGVVMTQSPSFLSAFVGTITITCRASOGIYNYLAWYQKPKAPK 179
||||| |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:
Db 158 GGGGPGGGGGGGGGDIETQSPASLASVGETVITTCRASGNIHNYLAWYQKQKSPQ 217

QY 180 LLIYAASTLQSGVPSRFSGSGGTFTLTISISLQPEDFGTYCQQLISYPLTFGGGKVE 239
||:| || ||||| |||||: |||||:||||: |||||:||||: |||||:||||: |||||:
Db 218 LLIYNAKTLADGVPSPSFGSGGTQYSLKINSLOPEDFGSYVCOHFWTPTPTFGGKLE 277

QY 240 IK 241
||
Db 278 IK 279

RESULT 2
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218
FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 46.1%; Score 589.5; DB 11; Length 218;
Best Local Similarity 51.6%; Pred. No. 2.4e-42;
Matches 112; Conservative 42; Mismatches 58; Indels 5; Gaps 2;

QY 1 QVRLQSGGGLVQPGSRSLRSCAASGFTDDYAMHVRQAPGKLEWVSGMTWNSGICY 60
||:||||| ||:| ||||| |||||: |||||:||||: |||||:||||: |||||:
Db 3 QVKLQSGGPELKKPGTETVTRISKASGYTFTAGMQMVQKMPGKGLKMGWINTHSGVPKY 62

QY 61 ADSVKGRTTISRDNKNSLYLQWNSLRADTAVVYCARPHTNTDAFDIWRGTLTVSSG 120
||:| ||||| ||:| |||||: |||||: |||||: |||||: |||||: |||||:
Db 63 AEEFKGRFAFSLTASATAYLOISNLKNETATYFCMRWDYD-GGFAYWGQGTTVTVSSG 121

QY 121 GGGPGGGGGGGGVVMTQSPSFLSAFVGTITITCRASOGIYN----YLAWYQKPK 176
||||| ||||| |||||:||||: ||: |||||: |||||: |||||: |||||:
Db 122 GGGGGGGGGGGSDIVLTQSPASLAIVSLQGRATISCRASEVDNIGISFMNFQKPKQ 181

QY 177 APKLLIYAASTLQSGVPSRFSGSGGTFTLTITSSLQ 213
||||| ||||| |||||: |||||: |||||: |||||: |||||: |||||:
Db 182 PPKLLIYASKOGSGVPGALLASGSGTDFSLNIYPWE 218

RESULT 4
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragment2A3 specific for native lysozyme : Isolation from a
RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
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QY 61 ADSVKGRTTISRDNKNSLYLQWNSLRADTAVVYCARP-HNTDAFDIWRGTLTVSS 119
||:| |||||:||||: |||||:||||: ||: |||||
Db 100 TSLDKFTISRDNKNTLYLQWNSLRSEDTALYCARASYGHSAY--WGQTTTVTVSS 157

QY 120 GGGGPGGGGGGGGVVMTQSPSFLSAFVGTITITCRASOGIYNYLAWYQKPKAPK 179
||||| |||||:||||: |||||:||||: |||||:||||: |||||:||||: |||||:
Db 158 GGGGPGGGGGGGGGDIETQSPASLASVGETVITTCRASGNIHNYLAWYQKQKSPQ 217

QY 180 LLIYAASTLQSGVPSRFSGSGGTFTLTISISLQPEDFGTYCQQLISYPLTFGGGKVE 239
||:| || ||||| |||||: |||||:||||: |||||:||||: |||||:||||: |||||:
Db 218 LLIYNAKTLADGVPSPSFGSGGTQYSLKINSLOPEDFGSYVCOHFWTPTPTFGGKLE 277

QY 240 IK 241
||
Db 278 IK 279

RESULT 2
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218
FT SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 57.0%; Score 728; DB 11; Length 241;
Best Local Similarity 56.4%; Pred. No. 5.1e-54;
Matches 141; Conservative 41; Mismatches 48; Indels 20; Gaps 6;

QY 1 QVRLQSGGGLVQPGSRSLRSCAASGFTDDYAMHVRQAPGKLEWVSGMTWNSGICY 60
||:||||| ||:| ||||| |||||: |||||:||||: |||||:||||: |||||:
Db 1 QVKLQSGPELKKPGTETVTRISKASGYTFTDYGMNVKQAPGKGLKMGWINTYTGEPT 60

QY 61 ADSVKGRTTISRDNKNSLYLQWNSLRADTAVVYCARPHTNTDAFDIWRGTLTV 117
||:| ||||| ||:| |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 ADFKGRFAFSLTASATAYLOINLNKNETATYFCARK----DLRYFDYWGQGTTVTV 116

QY 118 SSGGGPGGGGGGGGVVMTQSPSFLSAFVGTITITCRASOGIYNYLAWYQKPKGA 177
||||| ||||| |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 117 SSGGGGGGGGGGGSDIELTQSPSLASLGKVTITCKASQDINKYIAWYQHKPGK 176

QY 178 PK----LLIYAASTLQSGVPSRFSGSGGTFTLTISISLQPEDFGTYCQQLISYP-IT 231
||:| || ||||| |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 177 PRSAHTLHY----IQGIPSRFSGSGGRDYSFSTISNLEPEDIATYYC---LHYDNLHT 229

QY 232 FGGGKTRVEIK 241
|||||:|:|
Db 230 FGGGKTRVEIK 239

RESULT 3
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
```

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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00406; IG; 1.
DR SMART: SM00410; IG_like; 1.
DR NON_TER 1
FT NON_TER 112
FT SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

Query Match 38.4%; Score 490.5; DB 4; Length 112;
Best Local Similarity 80.0%; Pred No. 2.6e-34;
Matches 92; Conservative 9; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVRLQSQGGGLVQGRSLRSLRSCAASGTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EVQLVESGGGVVPRGGSLRISCAASGTFDDYGSWVRQAPGKGLEWVSGINWNGSGTGY 60
QY 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDWGRGTLV 115
Db 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCARRY---ALDYWGQGTLLV 112

RESULT 5
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
FT NON_TER 1
FT NON_TER 121
FT SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 37.4%; Score 478; DB 4; Length 121;
Best Local Similarity 76.9%; Pred. No. 3.3e-33;
Matches 93; Conservative 12; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVRLQSQGGGLVQGRSLRSLRSCAASGTFDDYAMHWVRQAPGKGLEWVSGMTWNSGSIGY 60
Db 1 EVQLVESGGGVVPRGGSLRFLCAASGTFDDYAMHWVRQAPGKGLEWVSLISGGSGTYY 60
QY 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNT--DAFDWGRGTLVTS 118
Db 61 ADSVKGRTTISRDNKNSLYLQMNLSRAEDTALYYCAKGVTTIYDRFDWGGQGTMTVS 120
QY 119 S 119
Db 121 S 121

RESULT 6

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Query Match      36.6%; Score 467.5; DB 4; Length 118;
Best Local Similarity 78.0%; Pred. No. 2.5e-32;
Matches 92; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 1 QVRLQSGGGLVOPGKSLRLSCAASGFTTDDYAMHVVRQAPGKGLWVSGMTWNSGSIY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTTSSYSMNVVRQAPGKGLWVSVISITITIIY 60

QY 61 ADSVKGRTTISRDNKNSLYLQWNSLRADETAVYYCAREPHNTDAPDINGRGTLTIVS 118
Db 61 ADSVKGRTTISRDNKNSLYLQWNSLRADETAVYYCAR-GDSSEAFDINGQGTMTVTS 117

RESULT 8
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match      35.4%; Score 452; DB 4; Length 108;
Best Local Similarity 81.3%; Pred. No. 4.6e-31;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQOKPKAPKLLIYAASLTQSGVPS 194
Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQOKPKAPPELLIYAASLTQSGVPS 60

QY 195 RFSGSGSGTEFTLTISLQPEDFGYYCQQLISYPLTFGGGKVEIK 241
Db 61 RFSGSGSGTDFTLTISLQSEDFATYICQYYSFPPTFGGGKVEIK 107

RESULT 9
Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4B843E9C5B577F16 CRC64;

Query Match      35.3%; Score 450.5; DB 4; Length 107;
Best Local Similarity 84.1%; Pred. No. 6.1e-31;
Matches 90; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 135 DVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQOKPKAPKLLIYAASLTQSGVPS 194
Db 1 DIQMTQSPSSLSASVGRVITITCRASQSISSYLWYQOKPKAPKLLIYAASLTQSGVPS 60

QY 195 RFSGSGSGTEFTLTISLQPEDFGYYCQQLISYPLTFGGGKVEIK 241
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICQYYSTLTTFGGGKVEIK 106

RESULT 11
Q9UL70
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035027; AAD36263.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match      35.3%; Score 451; DB 4; Length 104;
Best Local Similarity 81.7%; Pred. No. 5.3e-31;
Matches 85; Conservative 7; Mismatches 6; Indels 6; Gaps 1;

QY 22 CAASGFTTDDYAMHVVRQAPGKGLWVSGMTWNSGSIYADSVKGRFTISRDNKNSLYL 81
Db 1 CAASGFTTDDYAMHVVRQAPGKGLWVSGISWNSGSIYADSVKGRFTISRDNKNSLYL 60

QY 82 QMNSLRADETAVYYCARE-----PHNTDAFDIWRGTLVTYSS 119
Db 61 QMNSLRADETALYYCAKANYGSGSYTFYFQHWGGTLVTYSS 104

RESULT 10
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4B843E9C5B577F16 CRC64;

Query Match      35.3%; Score 450.5; DB 4; Length 107;
Best Local Similarity 84.1%; Pred. No. 6.1e-31;
Matches 90; Conservative 5; Mismatches 11; Indels 1; Gaps 1;

QY 135 DVVMTQSPSFLSAFVGDITITCRASQGIYNYLAWYQOKPKAPKLLIYAASLTQSGVPS 194
Db 1 DIQMTQSPSSLSASVGRVITITCRASQSISSYLWYQOKPKAPKLLIYAASLTQSGVPS 60

QY 195 RFSGSGSGTEFTLTISLQPEDFGYYCQQLISYPLTFGGGKVEIK 241
Db 61 RFSGSGSGTDFTLTISLQPEDFATYICQYYSTLTTFGGGKVEIK 106

RESULT 11
Q9UL70
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ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 35.1%; Score 449; DB 4; Length 108;
Best Local Similarity 82.2%; Pred. No. 8.2e-31;
Matches 88; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTTITCRASQGIYNYLAWYQQRPGKAPKLLIYAASLTQSGVPS 194
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQGISNYLAWYQQRPGKPKSLIYAASLTQSGVPS 60

QY 195 RFSGSGSGTEFTLTISLQPEDFGTYCQQLISYPLTFGGGTKEIK 241
Db 61 RFSGSGSGTDFTLTISLQPEDVATYCYQKYNAPRTFGPGTKLEIK 107

RESULT 12
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 113
FT SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
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Query Match 34.9%; Score 446; DB 4; Length 113;
Best Local Similarity 71.4%; Pred. No. 1.6e-30;
Matches 85; Conservative 15; Mismatches 13; Indels 6; Gaps 1;

QY 1 OYVLOQSGGLYQPGSLRSLSCAASGTFDDYAMHVVRQAPGKGLWVSGMTWNSGISGY 60
Db 1 EVOLVESGGVQPGGSLRSLSCAASGTFSSYGMHVVRQAPGKGLWVAFIRYDGSNKYY 60

QY 61 ADSVKGRTISRDNKNSLYLQMNLSRAEDTAVYYCAREPHNTDAFDIWRGTLTVSS 119
Db 61 ADSVKGRTISRDNKNSLYLQMNLSRAEDTAVYYCAKD-----LNYWGQGLTVTVSS 113

RESULT 13
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 34.4%; Score 440; DB 4; Length 108;
Best Local Similarity 81.3%; Pred. No. 4.7e-30;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 135 DVVMTQSPSFLSAFVGDTTITCRASQGIYNYLAWYQQRPGKAPKLLIYAASLTQSGVPS 194
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQISSYLNWYQQRPGKAPNLLIYAASSLTQSGVPS 60

QY 195 RFSGSGSGTEFTLTISLQPEDFGTYCQQLISYPLTFGGGTKEIK 241
Db 61 RFSGSGSGTDFTLTISLQPEDFATYCYQOQSYSTSTFGEGTKEIK 107

RESULT 14
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=98277139; PubMed=9614934;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA  Young D.C.;
RT  *Myosin-reactive autoantibodies in rheumatic carditis and normal
RL  fetus.*;
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035021; AAD56257.1; -.
DR  HSSP; P01772; 2FB4.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_Y.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
FT  NON_TER 1
FT  NON_TER 116
SQ  SEQUENCE 116 AA; 12434 MW;  ODA0348154DD6061 CRC64;

Query Match      34.4%; Score 440; DB 4; Length 116;
Best Local Similarity 72.9%; Pred. No. 5.2e-30;
Matches 86; Conservative 13; Mismatches 17; Indels 2; Gaps 1;

QY  2 VRLQSGGGLVQPGSLRLSCAASGFTFDDYAMHWVRQAPGKGLVWSGWTNNSGIGYA 61
DB  1 VOLVESGGGVQPGSLRLSCAASGFTFSSYAMHWVRQAPGKGLVWSGWTNNSGIGYA 60
QY  62 DSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHNTDAFDIWRGTLTVTSS 119
DB  61 DSVKGRFTISRDNKNTLYLQMSLRAEDTAMYYCA--CGGGLGLGWGGTLTVTSS 116

RESULT 15
Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CDNA FJ114473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO
DE SAPIENS SNC73 PROTEIN (SNC73) MRNA..
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT *NEO human cDNA sequencing project.*;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027379; BAB55072.1; -.
SQ SEQUENCE 494 AA; 53088 MW;  9A1D7AEB5AEE4C0E CRC64;

Query Match      34.4%; Score 439.5; DB 4; Length 494;
Best Local Similarity 72.1%; Pred. No. 3.3e-29;
Matches 88; Conservative 11; Mismatches 20; Indels 3; Gaps 1;

QY  1 QYRLQSGGGLVQPGSLRLSCAASGFTFDDYAMHWVRQAPGKGLVWSGWTNNSGIGY 60
DB  20 EVOLVESGGGLVQPGSLRLSCAASGFTFSSYAMHWVRQAPGKGLVWSGWTNNSGIGY 79
QY  61 ADSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCAREPHN---TDAFDIWRGTLTVT 117
DB  80 RDSVKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARDSCNGAICYGFSWGQGLTVTV 139
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QY 118 SS 119
   ||
DB 140 SS 141

Search completed: August 15, 2002, 16:35:38
Job time: 798 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:36:09 ; Search time 28.14 Seconds
(without alignments)
331.607 Million cell updates/sec

Title: us-08-779-457-50

Perfect score: 1278

Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISYPLTFGGTKVEIK 241

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	455	35.6	121	1 HV3J_HUMAN	P01771 homo sapien
2	454.5	35.6	122	1 HV3G_HUMAN	P01768 homo sapien
3	446	34.9	108	1 KV1V_HUMAN	P04430 homo sapien
4	441.5	34.5	120	1 HV3D_HUMAN	P01782 homo sapien
5	439	34.4	119	1 HV3I_HUMAN	P01770 homo sapien
6	438	34.3	108	1 KVIG_HUMAN	P01599 homo sapien
7	437	34.2	108	1 KV1S_HUMAN	P01611 homo sapien
8	434	34.0	108	1 KV1R_HUMAN	P01610 homo sapien
9	433	33.9	129	1 KV1W_HUMAN	P04431 homo sapien
10	430	33.6	108	1 KV1H_HUMAN	P01600 homo sapien
11	427.5	33.5	116	1 HV3T_HUMAN	P01781 homo sapien
12	426	33.3	108	1 KV1Y_HUMAN	P80362 homo sapien
13	424.5	33.2	122	1 HV3H_HUMAN	P01769 homo sapien
14	422	33.0	129	1 KV1X_HUMAN	P04432 homo sapien
15	420	32.9	108	1 KV1L_HUMAN	P01604 homo sapien
16	419	32.8	108	1 KV1P_HUMAN	P01598 homo sapien
17	418	32.7	108	1 KV1Q_HUMAN	P01608 homo sapien
18	416	32.6	108	1 KV5D_MOUSE	P01636 mus musculus
19	415.5	32.5	126	1 HV3K_HUMAN	P01772 homo sapien
20	413	32.3	108	1 KV1E_HUMAN	P01597 homo sapien
21	413	32.3	108	1 KV1C_HUMAN	P01603 homo sapien
22	412	32.2	117	1 HV3C_HUMAN	P01764 homo sapien
23	411	32.2	108	1 KV1B_HUMAN	P01594 homo sapien
24	411	32.2	108	1 KV1Q_HUMAN	P01609 homo sapien
25	410.5	32.1	136	1 HV1E_MOUSE	P01783 mus musculus
26	410	32.1	108	1 KV1M_HUMAN	P01605 homo sapien
27	410	32.1	108	1 KV1O_HUMAN	P01607 homo sapien
28	409.5	32.0	107	1 KV1D_HUMAN	P01596 homo sapien
29	409	32.0	108	1 KV1N_HUMAN	P01606 homo sapien
30	409	32.0	115	1 HV3D_HUMAN	P01765 homo sapien
31	406.5	31.8	114	1 HV3B_HUMAN	P01763 homo sapien
32	405	31.7	117	1 KV1I_HUMAN	P01601 homo sapien
33	404.5	31.7	122	1 HV3A_HUMAN	P01762 homo sapien

34	404	31.6	108	1 KV1C_HUMAN	P01595 homo sapien
35	402	31.5	117	1 KV1J_HUMAN	P01602 homo sapien
36	401.5	31.4	109	1 KV1T_HUMAN	P01612 homo sapien
37	398	31.1	115	1 HV3F_HUMAN	P01767 homo sapien
38	395	30.9	119	1 HV3L_HUMAN	P01773 homo sapien
39	393.5	30.8	119	1 HV38_MOUSE	P01808 mus musculus
40	393	30.8	115	1 HV32_MOUSE	P01801 mus musculus
41	392.5	30.7	119	1 HV40_MOUSE	P01810 mus musculus
42	392	30.7	108	1 KV1A_HUMAN	P01593 homo sapien
43	392	30.7	120	1 HV3E_HUMAN	P01766 homo sapien
44	391.5	30.6	114	1 HV01_CANFA	P01784 canis famil
45	389	30.4	113	1 HV34_MOUSE	P01803 mus musculus

ALIGNMENTS

RESULT 1

HV3J_HUMAN
ID HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V-III region HIL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=79124695; PubMed=420800;

RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;

RT "Amino acid sequence of the VH region of human myeloma

RT cryoimmunoglobulin IgG Hil.";

RL Biochemistry 18:553-560(1979).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA

CC PIR: A02054; GIHUHL.

DR HSSP: P01772; 2FB4.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig: 1.

DR SMART: SM00406; IGV: 1.

KW Immunoglobulin V region.

FT MOD_RES 1

FT NON_TER 121 121

SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 35.6%; Score 455; DB 1; Length 121;

Best Local Similarity 71.1%; Pred. No. 6.7e-30;

Matches 86; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTDDYAMHWVRQAPGKLEWVGMTWNSGICY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 QVQLVQAGGCVQPGKSLRLSCLASGFTFSNFGMHWVRQAPGKLEWVAIVNGSRITY 60

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 ADSVKGRTISRDNAKNSLYLQMNSLRADETAVYICAREPHNTDA--FDIWGRGLTVTVS 118

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 GDSVKGRTISRDNSKRTLYM2MNSLRTEDTAVYICARDPDILTAFSPDYWGQGLVTVS 120

QY 119 S 119

Db 121 S 121

RESULT 2

HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.

AC P01768;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

	FT	DOMAIN	57	88	FRAMEWORK-3.
	FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING-3.
	FT	DOMAIN	98	107	FRAMEWORK-4.
	FT	DISULFID	23	88	BY SIMILARITY.
	FT	NON_TER	108	*	
	SQ	SEQUENCE	108 AA;	11840 MW; CD3FD944FE96FD37 CRC64;	
Query Match 34.9%; Score 446; DB 1; Length 108;					
Best Local Similarity 78.5%; Pred.No. 3.le-29;					
Matches 84; Conservative 9; Mismatches 14; Indels 0; Gaps					
QY	135	DVMTQPSPSLSAFGVTITTCRASGIINYLAWTQQKPGKAPELLIYAASTLQSGLVPSS	194		
DB	1	: : ::::: :: : : : : : : :	194		
DB	1	DIQLTQPSLSASVGDRVTITCRASGVSYNYVAWFQQPKGAPKAPKLIIIVDASTLQSGLVPSS	60		
QY	195	RFGSGSGETTIITISSLOPEDFTGYCQQLISPYLTFFGGGTKEIK	241		
DB	1	::: - :	241		
DB	61	NFTGSGSTDFILTSSLQPEDEATYYCCQYNYPYTFGGGTAVQIK	107		
RESULT	4				
ID	HV3U_HUMAN	STANDARD;	PRT;	120 AA.	
AC	P01782;				
DT	21-JUL-1986 (Rel. 01, Created)				
DD	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V-II region DOB.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
ON	NCBI_Taxid=9606;				
OX	[1]				
RP	SEQUENCE				
RX	MEDLINE=80020921; PubMed=114209;				
RA	Steiner L.A., Garcia Pardo A., Margollies M.N.;				
RT	"Amino acid sequence of the heavy-chain variable region of the				
RT	crystallizable human myeloma protein Dob.";				
RL	Biochemistry 18:4068-4080(1979).				
RN	[2]				
RP	CRYSTALLIZATION.				
RX	MEDLINE=80020920; PubMed=114208;				
RA	Steiner L.A., Lopes A.D.;				
RT	"The crystallizable human myeloma protein Dob has a hinge-region				
RT	deltion."				
RL	Biochemistry 18:4054-4067(1979).				
CC	-1 MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE				
CC	HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN				
CC	DISULFIDE BONDS.				
DR	PIR; AO2065; GIHUBD.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; IGv; 1.				
KW	Immunoglobulin V region.				
FT	NON_TER	120	120		
SQ	SEQUENCE	120 AA;	13440 MW; 880DDE307CAB2627 CRC64;		
Query Match 34.5%; Score 441.5; DB 1; Length 120;					
Best Local Similarity 70.8%; Pred.No. 7.9e-29;					
Matches 85; Conservative 13; Mismatches 21; Indels 1; Gaps					
QY	1	QVRLLQGSGGLVGPGRSLRLSCAAGSFDPDYAHMVHQAPRGLEWVSGMTWNSSIGY	60		
DB	:	: : :	60		
DB	1	EVLVESGGDLVGPGRSLRLSCAAGSNFYEHNMHLRQGGPDKPVSVITWGGSVLV	60		
QY	61	ADSVKGFTISRNAKNNSLYQNLRPAETAYTVYCAREPHNTDAFDIWGCTFLTVSS	119		
DB	61	ADSVKGFALSRNAQAOKTLYLQNLIRPDATFYCAKYINNNGNWFDWSHGQTFLT	120		

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RESULT 5
HV31_HUMAN
ID HV31_HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
CC PIR; A02053; GIHUNI.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; C96935A6E5E165B CRC64;

Query Match 34.4%; Score 439; DB 1; Length 119;
Best Local Similarity 71.4%; Pred. No. 1.2e-28;
Matches 85; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 QVRLQSGGGLVQPGKSLRLSCAASGFTFDDYAMHWYRQAPKGLWVSGMTWNSGSIGY 60
Db 1 QVQLVQSGGVSVPQGRSLRLSCAASGFTESRYTIHWYRQAPKGLWVAVMVGBBKH 60
QY 61 ADSVKGRTISRDNKNSLYLQMNLSRAEDTAVYICAREPHNTDAFDIWRGTLTVSS 119
Db 61 ADSVNGRTISRDNKNTLYLNMSLRPEDTAVYICARIDRTAMFPAHNGQGLTVSS 119

RESULT 6
KVIG_HUMAN
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;

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RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 34.3%; Score 438; DB 1; Length 108;
Best Local Similarity 81.3%; Pred. No. 1.3e-28;
Matches 87; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 135 DVVMTQSPFLSAFVGDITITCRASQGIYNYLAWTQKPGKAPKLLIYAASTLQSGVPS 194
Db 1 DIQMTQSPSLASVGDRTYITCRASQGINDLTWYQKPGKAPKELIYAASLQSGVPS 60
QY 195 RFGSGSGTEFTLTISLQPEDFGTYVCOQLSYPTFGGSGTKVEIK 241
Db 61 RFGSGGAGTEFTLTISLQPEDFATYVYCLQNSYPRSGGSGTKVEIK 107

RESULT 7
KVIS_HUMAN
ID KVIS_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01877; KIHWS.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=71032830; PubMed=4097974;
RX Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP; P80362; 1WT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW NON_TER 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 33.6%; Score 430; DB 1; Length 108;
Best Local Similarity 77.6%; Pred. No. 5,8e-28;
Matches 83; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 135 DVWVTQSFSLSAFVGDITTCRASQGIYNYLAWYQKPKAPKLLIYAASLTSGVPS 194
I: ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||||
DB 1 DIOMTQSPSSLSASGDRVTTCRASQSISSYLSYQKPKAPOVLIYAASLPSGVPS 60

QY 195 RFGSGSGTEFTLTSSLPQDEFGYQCQLSYPLTFGGGPKVEIK 241
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 RFGSGSGTDFLTSSLPQDEFATYICQNYITTSFGQGRVEIK 107

RESULT 11
HV3T_HUMAN
ID HV3T_HUMAN STANDARD; PRT; 116 AA.
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.); II: the amino acid sequence of the H-chain (mu-
type), subgroup H III. Architecture of the complete IgM-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP REVISION TO THE COMPOSITION OF 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S
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CC MACROGLOBULIN.
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW NON_TER 116
SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAAA1282 CRC64;

Query Match 33.5%; Score 427.5; DB 1; Length 116;
Best Local Similarity 69.7%; Pred. No. 9.9e-28;
Matches 83; Conservative 11; Mismatches 28; Indels 3; Gaps 1;

QY 1 QVRLQSGGLVQPGSLRLSCAASGFTDDYAMHWVRQAPGKLEWVSGMTWNSGSIQY 60
:|: ||| ||||| ||||| ||| ||| ||||| ||| ||| ||||| ||| ||| |||||
DB 1 EVQLVESGGLVQPGSLRLSCAASGFBFBGLGTWVRQAPGKLEWVANIKZBSZ2BY 60

QY 61 ADSVKGRTISRDNAKNSLYLQMNSLRLEDYAVYICAREPHNTDAFDINGRTLVTVSS 119
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 VDSVKGRTISRDNAKNSLYLQMNSLRVEDTALTYCAR---GMGGGDYWGQGLTVTVST 116

RESULT 12
KVLY_HUMAN
ID KVLY_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1WT. 01-NOV-94.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
```


-1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
CC PIR: A01870; KIHUKU.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Benice-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;

Query Match 32.9%; Score 420; DB 1; Length 108;
Best Local Similarity 75.7%; Pred. No. 3.6e-27;
Matches 81; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 135 DVMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQKPGKAPKLLIYAASLTQSGVPS 194
I: ||||| | ||| :||||||| | :||||||| ||||| |||||:|||||
Db 1 DIQMTQSPSTQPASVGDRTTTCRASQSIINILAWYQKPGKAPKLLIYKASTLETGVPS 60

Qy 195 RFGSGSGTEFTLTITSSLPQEDFGYYCQQLISYPLTFGGGPKVEIK 241
||||| |||||:||||| || ||||| || |||||:|
Db 61 RFGSGSGTEFTLTINSLQPDGFATYYCQYSRYPTTFQGGTKLDIK 107

Search completed: August 15, 2002, 16:36:10
Job time: 720 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:25:02 ; Search time 54.95 Seconds
(without alignments)
421.429 Million cell updates/sec

Title: US-08-779-457-50
Perfect score: 1278
Sequence: 1 QVRLQSGGGLVQGRSLRL.....CQQLISYPLTFGGTKVEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	704.5	55.1	249	2 S41374	single chain Fv an
2	697	54.5	268	2 A56446	Ig heavy chain V r
3	631.5	49.4	233	2 JG5322	p53 specific singl
4	562.5	44.0	128	2 S31595	Ig heavy chain V r
5	552	43.2	121	2 S31118	Ig heavy chain - h
6	543	42.5	121	2 S31104	Ig heavy chain (su
7	543	42.5	123	2 S30532	Ig heavy chain V r
8	527	41.2	120	2 S36273	Ig heavy chain V r
9	518.5	40.6	145	2 S11239	Ig heavy chain V r
10	498	39.0	119	2 F36005	Ig heavy chain V r
11	489	38.3	98	2 S26790	Ig heavy chain V r
12	487	38.1	123	2 PC4281	Ig heavy chain V r
13	487	38.1	132	2 S40334	anti-SS-A/Ro 60k p
14	482	37.7	119	2 S31107	Ig kappa chain - h
15	482	37.7	119	2 S31108	Ig heavy chain - h
16	480.5	37.6	141	2 S31669	Ig heavy chain V r
17	480	37.6	119	2 D36005	Ig heavy chain V r
18	479.5	37.5	137	2 S31701	Ig heavy chain V r
19	478.5	37.4	112	2 PH1654	Ig heavy chain V r
20	478.5	37.4	122	2 E36005	Ig heavy chain V r
21	478	37.4	108	2 S36279	Ig lambda chain V
22	478	37.4	120	2 S36278	Ig heavy chain V r
23	477.5	37.4	120	2 S44111	Ig heavy chain V-D
24	477.5	37.4	122	2 S31117	Ig heavy chain - h
25	476	37.2	108	2 S36277	Ig lambda chain V
26	475.5	37.2	124	2 S40336	Ig kappa chain V-J
27	475	37.2	138	2 S31666	Ig heavy chain V r
28	474	37.1	119	2 C36005	Ig heavy chain V r
29	473.5	37.1	118	2 S31105	Ig heavy chain (su

30 473 37.0 108 2 S19674 Ig kappa chain V r
31 473 37.0 134 2 S31679 Ig heavy chain V r
32 472 36.9 121 2 G36005 Ig heavy chain V r
33 472 36.9 123 2 S38493 Ig heavy chain - h
34 471.5 36.9 118 2 S31116 Ig heavy chain V r
35 471 36.9 125 2 S30531 Ig heavy chain V r
36 470 36.8 100 2 S69896 Ig heavy chain V r
37 470 36.8 121 2 S19666 Ig heavy chain V r
38 470 36.8 140 2 S31686 Ig heavy chain V r
39 469.5 36.7 140 2 S70442 Ig heavy chain pre
40 469 36.7 107 2 S36264 Ig lambda chain V
41 467 36.5 108 2 B49047 Ig kappa chain V r
42 466.5 36.5 128 2 S26790 Ig heavy chain V r
43 466.5 36.5 143 2 S23624 Ig heavy chain V r
44 466 36.5 133 2 A49028 Ig heavy chain V r
45 465.5 36.4 114 2 S46390 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsaenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv anti
A:Reference number: S41374
A:Accession: S41374
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 55.1%; Score 704.5; DB 2; Length 249;

Best Local Similarity 53.7%; Pred. No. 3.4e-44;
Matches 132; Conservative 43; Mismatches 66; Indels 5; Gaps 1;

QY 1 QVRLQSGGGLVQGRSLRLSCAASGFTFDYAMHWVRQAPGKLEWVSGMTWNSGIGY 60
Db 1 QVQLQSGAELVPGASVKLSCTASGENFKDDYIHVKQRPKEGLEWIAPIASGNVKY 60
QY 61 ADSVKGRFTISRDNANKSLYLQMNSLRAEDTAVYYCAREPHNTDAFDINGRGTLVTVSSG 120
Db 61 VPRFQDKATITADTSSNTAYLLLSLTSEDVAVYCARRDITLTSLGYWQGGSTVTVSSR 120
QY 121 GGGPGGGGGGGSDVVMQSPFLSAFYVDITITCRASQGIY----NYLAWYQOKPG 175
Db 121 GGGGGGGGGGGSDLELTQSPSPVVPVIGESVSIQCRSSKSLIYSDGSLYLFWLRPG 180
QY 176 KAPKLIIAASTLQSGVPRFSGSGSGTEFTLTISQLQPEDFGTYCQQLISYPLTFGGG 235
Db 181 QSPQLLIYRMSNLASGVPDFRFGSGSGTFTLRIISRVEADVGYYCMQHREPLTFGAG 240
QY 236 TKVEIK 241
Db 241 TKLELK 246

RESULT 2

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; MUID:95229583

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S31104
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633
A:Accession: S31104
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RA>
A:Cross-references: EMBL:X63080; NID:g32646; PIDN:CAA44802.1; PID:g32647
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.5%; Score 543; DB 2; Length 121;
Best Local Similarity 85.1%; Pred. No. 8.2e-33;
Matches 103; Conservative 9; Mismatches 7; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 1 EVOLVSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGISWNSGSIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCAREPHNTDA--FDIWGRGTLTVTS 118
Db 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTALYYCAKDFVGSWGYYFDLWGRGTLTVTS 120

QY 119 S 119
Db 121 S 121

RESULT 7
S30532
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C:Accession: S30532
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30532
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MA>
A:Cross-references: EMBL:Z18318
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.5%; Score 543; DB 2; Length 123;
Best Local Similarity 82.1%; Pred. No. 8.4e-33;
Matches 101; Conservative 16; Mismatches 2; Indels 4; Gaps 2;

QY 1 QVRLQSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 1 EVOLVSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGISWNSGTLGY 60

QY 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCARE-PHN---TDAFDIWGRGTLTVT 116
Db 61 ADSVKGRFAISRDNKNSLYLOMNSLRAEDTALYYCAKDTPTSSGWSNAPFDIWGQGTMT 120

QY 117 VSS 119
Db 121 VSS 123

RESULT 8
S36273
Ig heavy chain V region (clone alpha-THY-32) - human (fragment)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36273
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty,
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36256; MUID:93178448
A:Accession: S36273
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-120 <GR>
A:Cross-references: EMBL:218834; NID:g33116; PIDN:CAA79286.1; PID:g9339896
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 527; DB 2; Length 120;
Best Local Similarity 86.7%; Pred. No. 1.2e-31;
Matches 104; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVRLQSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 1 QVQLVSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGISWNSGSIGY 60

QY 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCAREPHNTDA--FDIWGRGTLTVTS 118
Db 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTALYYCARGIAVAGAYFYDWGQGTTLTVTS 120

RESULT 9
S11239
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S11239
R:Felgenhauer, M.; Kohl, J.; Rueker, F.
Nucleic Acids Res. 18, 4927, 1990
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains
A:Reference number: S11239; MUID:90370490
A:Accession: S11239
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-145 <FE>
A:Cross-references: EMBL:X53613; NID:g23865; PIDN:CAA37675.1; PID:g762936
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.6%; Score 518.5; DB 2; Length 145;
Best Local Similarity 78.6%; Pred. No. 6e-31;
Matches 99; Conservative 12; Mismatches 8; Indels 7; Gaps 1;

QY 1 QVRLQSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGMTWNSGSIGY 60
Db 20 EVOLVSGGGLVQPGSRSLRSLSCAASGFTFDDYAMHWVROAPGKGLWVSGISWNSGSIGY 79

QY 61 ADSVKGRFTISRDNKNSLYLOMNSLRAEDTAVYYCAR-----EPHNTDAFDIWGRGT 113
Db 80 ADSVKGRFTISRDNKNSLYLOMNSLRAEDMALYYCVKGRDYDVGSGGYTFVAFDIWQGT 139

QY 114 LVTSS 119
Db 140 MVTSS 145

RESULT 10
F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: F36005

R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: GB:M34026
C:Genetics: GDB:IGH4; IGHDY1
A:Gene: GDB:IGH4; OMIM:146910
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 498; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.5e-29;
Matches 93; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 QVRLQSGGGLVQPGSRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
DB 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLWVAVISYDGSNKYY 60

QY 61 ADSVKGRTISRDNKNSLYLQMSLRADTAIVYICAREPHNTDAFDIWRGTLTVSS 119
DB 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYICARDKASDAFDIWRGTLTVSS 119

RESULT 11
S26927
Ig heavy chain V region (DP-31) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26927
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117
A:Accession: S26927
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12333; NID:g32885; PIDN:CAA78203.1; PID:g32886
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 489; DB 2; Length 98;
Best Local Similarity 91.8%; Pred. No. 5.4e-29;
Matches 90; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVRLQSGGGLVQPGSRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
DB 1 EVQLVESGGGLVQPGSRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGISWNSGSIGY 60

QY 61 ADSVKGRTISRDNKNSLYLQMSLRADTAIVYICAR 98
DB 61 ADSVKGRTISRDNKNSLYLQMSLRADTAIVYICAK 98

RESULT 12
PC4281
anti-ss-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C:Accession: PC4281
R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin

A:Reference number: PC4279; MUID:97236289
A:Accession: PC4281
A:Molecule type: protein
A:Residues: 1-123 <SUZ>
C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sj
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 38.1%; Score 487; DB 2; Length 123;
Best Local Similarity 74.6%; Pred. No. 9.7e-29;
Matches 91; Conservative 15; Mismatches 12; Indels 4; Gaps 1;

QY 1 QVRLQSGGGLVQPGSRSLRLSCAASGFTFDDYAMHWVRQAPGKGLWVSGMTWNSGSIGY 60
DB 1 EVQLLESGGGLVQPGSRSLRLSCTVSGFTIGDYAMSVWRQAPGKGLWVSSISWNSGTIGY 60

QY 61 ADSVKGRTISRDNKNSLYLQMSLRADTAIVYICARE---PNTDAFDIWRGTLTVT 116
DB 61 MDSVKGRTISRDNKNSLYLQMSLRPEDTALYICAKDRSDSGYDSRFDIWGGGTAVT 120

QY 117 VS 118
DB 121 VS 122

RESULT 13
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40334
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 38.1%; Score 487; DB 2; Length 132;
Best Local Similarity 82.9%; Pred. No. 1e-28;
Matches 92; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 131 GGGSDVMTQSPSFSAFVGDITTCRASQGIYNYLAWYQKPKAPKLLIYAASLTQS 190
DB 18 GARCIDIQLTQSPSFLSASIGDRVTTTCRASQGIYNYLAWYQKPKAPKLLIYVASTQS 77

QY 191 GVPFSGSGSGTERTLTITSSLPQDFGTYYCOQLISPLTFGGGKTKVEIK 241
DB 78 GVPFSGSGSGTERTLTITSSLPQDFGTYYCOQFNYPFTFGGKTKVEIR 128

RESULT 14
S31107
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31107
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuur
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comp
A:Reference number: S31104; MUID:92111633
A:Accession: S31107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:34:05 ; Search time 410.32 Seconds

(without alignments)
206.735 Million cell updates/sec

Title: US-08-779-457-50

Perfect score: 1278
Sequence: 1 OVRLOSGGGLVQPGRLRL.....COOLISYPLFGGFKVEIK 241

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main: *
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
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14: /cgn2_6/ptodata/2/paa/US090_COMB.pep:*
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US100_COMB.pep:*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1278	100.0	241	11	US-08-779-457-50
2	1086.5	85.0	251	1	PCT-US01-19110-1310
3	1086.5	85.0	251	22	US-09-880-748-1310
4	1070.5	83.8	251	1	PCT-US01-19110-922
5	1070.5	83.8	251	22	US-09-880-748-922
6	1065.5	83.4	251	1	PCT-US01-19110-1320
7	1065.5	83.4	251	22	US-09-880-748-1320

8	1042.5	81.6	253	1	PCT-US01-19110-936	Sequence 936, App
9	1042.5	81.6	253	22	US-09-880-748-936	Sequence 936, App
10	1040	81.4	242	16	US-09-250-056-2	Sequence 2, Appl1
11	1040	81.4	242	16	US-09-250-056B-2	Sequence 2, Appl1
12	1040	81.4	244	1	PCT-US01-19110-82	Sequence 82, Appl1
13	1040	81.4	244	22	US-09-880-748-82	Sequence 82, Appl1
14	1037	81.1	244	1	PCT-US01-19110-261	Sequence 261, App
15	1037	81.1	244	22	US-09-880-748-261	Sequence 261, App
16	1036	81.1	244	1	PCT-US01-19110-164	Sequence 164, App
17	1036	81.1	244	22	US-09-880-748-164	Sequence 164, App
18	1035	81.0	244	1	PCT-US01-19110-280	Sequence 280, App
19	1035	81.0	244	22	US-09-880-748-280	Sequence 280, App
20	1023.5	80.1	239	14	US-09-000-802-15	Sequence 15, Appl
21	1023.5	80.1	248	7	US-08-309-530-6	Sequence 6, Appl1
22	1018.5	79.7	243	1	PCT-US01-19110-1945	Sequence 1945, App
23	1018.5	79.7	243	22	US-09-880-748-1945	Sequence 1945, App
24	1011.5	79.1	247	1	PCT-US01-19110-1177	Sequence 1177, App
25	1011.5	79.1	247	22	US-09-880-748-1177	Sequence 1177, App
26	1008.5	78.9	243	1	PCT-US01-19110-1935	Sequence 1935, App
27	1008.5	78.9	243	22	US-09-880-748-1935	Sequence 1935, App
28	1006.5	78.8	237	1	PCT-US01-19110-2043	Sequence 2043, App
29	1006.5	78.8	237	22	US-09-880-748-2043	Sequence 2043, App
30	1004.5	78.6	237	1	PCT-US01-19110-2019	Sequence 2019, App
31	1004.5	78.6	237	22	US-09-880-748-2019	Sequence 2019, App
32	1004.5	78.6	241	1	PCT-US01-19110-1889	Sequence 1889, App
33	1004.5	78.6	241	22	US-09-880-748-1889	Sequence 1889, App
34	1003.5	78.5	237	1	PCT-US01-19110-2003	Sequence 2003, App
35	1003.5	78.5	237	22	US-09-880-748-2003	Sequence 2003, App
36	1003	78.5	248	1	PCT-US01-19110-1421	Sequence 1421, App
37	1003	78.5	248	22	US-09-880-748-1421	Sequence 1421, App
38	1002.5	78.4	237	1	PCT-US01-19110-2005	Sequence 2005, App
39	1002.5	78.4	237	22	US-09-880-748-2005	Sequence 2005, App
40	1002.5	78.4	239	1	PCT-US01-19110-1922	Sequence 1922, App
41	1002.5	78.4	239	22	US-09-880-748-1922	Sequence 1922, App
42	1001.5	78.4	241	1	PCT-US01-19110-1901	Sequence 1901, App
43	1001.5	78.4	241	22	US-09-880-748-1901	Sequence 1901, App
44	1000.5	78.3	237	1	PCT-US01-19110-2040	Sequence 2040, App
45	1000.5	78.3	237	1	PCT-US01-19110-2114	Sequence 2114, App

ALIGNMENTS

RESULT 1
US-08-779-457-50
Sequence 50, Application US/08779457
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Chiang, Nancy Y.
APPLICANT: Kyung, Jin Kim
APPLICANT: Matthews, William
APPLICANT: Rodrigues, Maria L.
TITLE OF INVENTION: MSX RECEPTOR AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,457
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667197
FILING DATE: 06/20/96

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-779-457-50

Query Match 100.0%; Score 1278; DB 11; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.9e-102;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
DB 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
QY 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
DB 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
QY 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
DB 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
QY 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
DB 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
QY 241 K 241
DB 241 K 241

RESULT 2
PCT-US01-19110-1310
; Sequence 1310, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1310
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1310

Query Match 85.0%; Score 1086.5; DB 1; Length 251;
```

```

Best Local Similarity 84.0%; Pred. No. 1.8e-85;
Matches 210; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
DB 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
QY 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
DB 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
QY 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
DB 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
QY 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
DB 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
QY 241 K 241
DB 241 K 241

RESULT 3
US-09-880-748-1310
; Sequence 1310, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1310
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1310

Query Match 85.0%; Score 1086.5; DB 22; Length 251;
Best Local Similarity 84.0%; Pred. No. 1.8e-85;
Matches 210; Conservative 10; Mismatches 21; Indels 9; Gaps 1;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
DB 1 QVRLQSGGGLVOPGRSLRLSCAASGFTPDYAMHWYRQAPGKGLVWSGTMNNGSIGY 60
QY 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
DB 61 ADSVKGRFTISRDNANKNSLYLQMNLSLRADPTAVYYCARPETHNDADFDINGRTLVTVSSG 120
QY 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
DB 121 GGGPGGGGGGGSDVYMTQSPFSLAFVGDITITTCRASQGIYNYLAWYQQRPKAPKL 180
QY 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
DB 181 LIYAASTLQSGVSPRFSGSGGTEFTLTISLQPEDGTYCCQLLSYPLTFGGGTVEIK 240
QY 241 K 241
DB 241 K 241
```


Db 241 FGGGTKEIK 250

RESULT 4

PCT-US01-19110-922
; Sequence 922, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 922
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-922

Query Match 83.8%; Score 1070.5; DB 1; Length 251;
Best Local Similarity 80.4%; Pred. No. 4.5e-84;
Matches 201; Conservative 21; Mismatches 19; Indels 9; Gaps 1;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60
Db 1 QVQLVQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60
QY 61 ADVKGRFTTISRDAKAKSLYQMNSLRADPTAVYVCARPEHNTD-----AFDIQGR 111
Db 61 AESYKGRFTISRDAKAKSLYQMNSLRADPTAVYVCARVSPYDILGTYLPHAFDVGK 120
QY 112 GTLVTVSSGGGPGGSGGSDVMTQSPSLSAFVGDITTTTCRASQGIYNYLAWYQ 171
Db 121 GTLVTVSSGGGPGGSGGSDVMTQSPSLSAFVGDITTTTCRASQGIYNYLAWYQ 180
QY 172 QKPKAPKLLIYASTQSGVPSRFSGSGTEFTLTISLTQPEDFGYTCQQLISYPLT 231
Db 181 QKPKAPKLLIYKASLSAGAPSRFSGSGTDEFTLTISLTQPDFAFYTCQOYSNPFLT 240
QY 232 FGGGTKEIK 241
Db 241 FGGGTKEIK 250

RESULT 5

US-09-880-748-922
; Sequence 922, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 922
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-922

Query Match 83.8%; Score 1070.5; DB 22; Length 251;
Best Local Similarity 80.4%; Pred. No. 4.5e-84;
Matches 201; Conservative 21; Mismatches 19; Indels 9; Gaps 1;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60
Db 1 QVQLVQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60
QY 61 ADVKGRFTTISRDAKAKSLYQMNSLRADPTAVYVCARPEHNTD-----AFDIQGR 111
Db 61 AESYKGRFTISRDAKAKSLYQMNSLRADPTAVYVCARVSPYDILGTYLPHAFDVGK 120
QY 112 GTLVTVSSGGGPGGSGGSDVMTQSPSLSAFVGDITTTTCRASQGIYNYLAWYQ 171
Db 121 GTLVTVSSGGGPGGSGGSDVMTQSPSLSAFVGDITTTTCRASQGIYNYLAWYQ 180
QY 172 QKPKAPKLLIYASTQSGVPSRFSGSGTEFTLTISLTQPEDFGYTCQQLISYPLT 231
Db 181 QKPKAPKLLIYKASLSAGAPSRFSGSGTDEFTLTISLTQPDFAFYTCQOYSNPFLT 240
QY 232 FGGGTKEIK 241
Db 241 FGGGTKEIK 250

RESULT 6

PCT-US01-19110-1320
; Sequence 1320, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1320
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1320

Query Match 83.4%; Score 1065.5; DB 1; Length 251;
Best Local Similarity 80.0%; Pred. No. 1.2e-83;
Matches 200; Conservative 21; Mismatches 20; Indels 9; Gaps 1;

QY 1 QVRLQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60
Db 1 QVQLVQSGGGLVOPGRSLRLSCAASGFTEDDYAHMWVROAPGKLEWVSGMTWNSGSIQY 60

```
QY 61 ADSVKGRFTISRDNKAKSLYLQMSLSRAEDTAVYYCAREPHNTD-----AFDIWGR 111
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AESVKGKFTISRDNKAKSLYLQMSLSRAEDTAVYYCARVSPSYDILNGYLLPHAFDVGWR 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 112 GTLVTVSSGGGGSGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAWYQ 171
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GTLVTVSSGGGGSGGGGGSDIQTMTQSPSLASIGDVTITTCRASQGIYHMLAWYQ 180
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 QKPKAKRLIYAASLTQSGVPSRFSGSGTEFTLTITSLQPEDFGTYCCQLISTPLT 231
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 QKPKAKRLIYKASSLASGAPSRFSGSGTDTLTITSLQPDPAFYVCOQYSNPFLT 240
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 232 FGGGTKEIK 241
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 FGGGTKEIK 250
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-09-880-748-1320
; Sequence 1320, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1320
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1320

Query Match 83.4%; Score 1065.5; DB 22; Length 251;
Best Local Similarity 80.0%; Pred. No. 1.2e-83;
Matches 200; Conservative 21; Mismatches 20; Indels 9; Gaps 1;
```

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; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 936
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-19110-936

Query Match 81.6%; Score 1042.5; DB 1; Length 253;
Best Local Similarity 81.0%; Pred. No. 1.2e-81;
Matches 204; Conservative 12; Mismatches 25; Indels 11; Gaps 2;

QY 1 QVRLQSGGGGLVQGRSLRLSCAASGFTFDYAMHWYRQAPGKLEWVSGTNTSGSY 58
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGGGGLVQKPKRSRLSCASGFTFDYAMSWRQAPGKLEWYFIRSKAYGTT 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 GYADSVKGRFTISRDNKAKSLYLQMSLSRAEDTAVYYCARPEPHNTD-----AFDIW 109
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EYASVKGKFTISRDNKAKSLYLQMSLSKTEDTAVYYCTRAGGTYDILTGNDYYGMDV 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 110 GRGTLVTVSSGGGGSGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAW 169
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GQGTMTVTVSSGGGGSGGGGGSDVYMTQSPSLAFVGDITITTCRASQGIYNYLAW 180
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 170 YQKPKAKRLIYAASLTQSGVPSRFSGSGTEFTLTITSLQPEDFGTYCCQLISTP 229
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 YQKPKAKRLIYAASLTQSGVPSRFSGSGTEFTLTITSLQPEDFGTYCCQLISTP 240
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 230 LTFGGGTKEIK 241
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 LTFGGGTKEIK 252
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-09-880-748-936
; Sequence 936, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 936
; LENGTH: 253
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; TYPE: prt
; ORGANISM: Homo sapiens
US-09-880-748-936
```

```
Query Match      81.6%; Score 1042.5; DB 22; Length 253;
Best Local Similarity 81.0%; Pred. No. 1.2e-81;
Matches 204; Conservative 12; Mismatches 25; Indels 11; Gaps 2;
```

```
QY 1 QVRLQSGGGVLPGRSLRLSCAASGFTFDYAMHWROAPGKGLMEVSGMTWNS--GSI 58
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGGGLVPGKSLRLSCAASGFTFGDYAMSWRQAPGKGLMEVIRKAAIGTT 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 59 GYADSVKGFPTISRDNKASLYLQNNSLRAEDTAVYYCARPHTD-----AFDIW 109
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EYAAVYKGFPTISRDNKSIAYLQNNSLKTEDTAVYYCTRAGGYDILNGRDYYGMDVW 120
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 110 GGTLTAVSSGGGPGGGGGSDVYMTQSPFLSAFVGDITTCRASGITYNVLAW 169
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GGTMTAVSSGGGSGGGSDVYMTQSPFLSAFVGDITTCRASGITYNVLAW 180
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 170 YQAKPGKAPKLLIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYCCQLISYP 229
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 YQAKPGKAPKLLIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYCCQLISYP 240
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 230 LTFGGGTKEIK 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 LTFGGGTKEIK 252
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 10
US-09-250-056-2
; Sequence 2, Application US/09250056A
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Poul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing Erb2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056A
; EARLIER FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: 60/082,953
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (31)..(35)
; OTHER INFORMATION: VH-CDR1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (50)..(66)
; OTHER INFORMATION: VH-CDR2
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (99)..(108)
; OTHER INFORMATION: VH-CDR3
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (157)..(167)
; OTHER INFORMATION: VL-CDR1
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (184)..(190)
; OTHER INFORMATION: VL-CDR2
; FEATURE:
; NAME/KEY: DOMAIN
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; LOCATION: (223)..(231)
; OTHER INFORMATION: VL-CDR3
US-09-250-056-2
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Query Match      81.4%; Score 1040; DB 16; Length 242;
Best Local Similarity 83.0%; Pred. No. 1.9e-81;
Matches 200; Conservative 15; Mismatches 26; Indels 0; Gaps 0;
```

```
QY 1 QVRLQSGGGVLPGRSLRLSCAASGFTFDYAMHWROAPGKGLMEVSGMTWNSIGY 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVSGGGLVPGGSLRLSCAASGFTSSYAMGWROAPGKGLMEVSSISSSRIYY 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGFPTISRDNKASLYLQNNSLRAEDTAVYYCARPHTDAFDIWRGTLVYSSG 120
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGFPTISRDNKNTLYLQNNSLRAEDTAVYYCAKMDASGSYFNFVGGTLYVSSG 120
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GGGPGGGGGGSDVYMTQSPFLSAFVGDITTCRASGITYNVLAWYQKPGKAPKL 180
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GGGSGGGSGGSEFTLTQSPFLSAFVGDITTCRASGIRNVLAWYQKPGKAPKL 180
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYCCQLISYPLTFGGGTKEIK 240
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDFGTYCCQIYNSYPLTFGGGTKEIK 240
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 K 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 K 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 11
US-09-250-056B-2
; Sequence 2, Application US/09250056B
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Poul, Marie A
; TITLE OF INVENTION: INTERNALIZING ERB2 ANTIBODIES
; FILE REFERENCE: 2500.116US3 Internalizing Erb2 Ab
; CURRENT APPLICATION NUMBER: US/09/250,056B
; PRIOR APPLICATION NUMBER: 60/082,953
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv C1 amino
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (31)..(35)
; OTHER INFORMATION: VH-CDR1
; NAME/KEY: DOMAIN
; LOCATION: (50)..(66)
; OTHER INFORMATION: VH-CDR2
; NAME/KEY: DOMAIN
; LOCATION: (99)..(108)
; OTHER INFORMATION: VH-CDR3
; NAME/KEY: DOMAIN
; LOCATION: (157)..(167)
; OTHER INFORMATION: VL-CDR1
; NAME/KEY: DOMAIN
; LOCATION: (184)..(190)
; OTHER INFORMATION: VL-CDR2
; NAME/KEY: DOMAIN
; LOCATION: (223)..(231)
; OTHER INFORMATION: VL-CDR3
; US-09-250-056B-2
```

```
Query Match      81.4%; Score 1040; DB 16; Length 242;
```

Best Local Similarity 83.0%; Pred. No. 1.9e-81;
Matches 200; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

```
QY 1 QVRLQSGGGLVOPGRLSLRSCAASGFTDDYAMHWROAPGKGLMWSCMTNNSGIGY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSSGGLVOPGRLSLRSCAASGFTSSYAMGVNROAPGKGLMWSSISGSSRIYX 60
QY 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCARREPHNDADINDRGRLVYVSSG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCARREPHNDADINDRGRLVYVSSG 120
QY 121 GGGGCGGSGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 180
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GGGGCGGSGGGGSEFTLTIQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 180
QY 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKVEI 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKVEI 240
QY 241 K 241
Db 241 K 241
```

RESULT 12

PCT-US01-19110-82
; Sequence 82, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-82

Query Match 81.4%; Score 1040; DB 1; Length 244;
Best Local Similarity 81.1%; Pred. No. 1.9e-81;
Matches 197; Conservative 17; Mismatches 27; Indels 2; Gaps 1;

```
QY 1 QVRLQSGGGLVOPGRLSLRSCAASGFTDDYAMHWROAPGKGLMWSCMTNNSGIGY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSSGGLVOPGRLSLRSCAASGFTDDYAMHWROAPGKGLMWSSISGSSRIYX 60
QY 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCARREPH--NTDAFDWGRGTLVTVS 118
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCTKASYLSTSSLDWNGGTLVTVS 120
QY 119 SGGGCGGSGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 178
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SGGGCGGSGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 180
QY 179 KLIIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKTV 238
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KLIIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKTV 240
QY 239 EIK 241
```

Db 241 EIK 243

RESULT 13

US-09-880-748-82
; Sequence 82, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-82

Query Match 81.4%; Score 1040; DB 22; Length 244;
Best Local Similarity 81.1%; Pred. No. 1.9e-81;
Matches 197; Conservative 17; Mismatches 27; Indels 2; Gaps 1;

```
QY 1 QVRLQSGGGLVOPGRLSLRSCAASGFTDDYAMHWROAPGKGLMWSCMTNNSGIGY 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSSGGLVOPGRLSLRSCAASGFTDDYAMHWROAPGKGLMWSSISGSSRIYX 60
QY 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCARREPH--NTDAFDWGRGTLVTVS 118
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKRFTISRDNNAKNSLYLQNSLRADETAVYYCTKASYLSTSSLDWNGGTLVTVS 120
QY 119 SGGGCGGSGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 178
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SGGGCGGSGGGGSDVYMTQSPSFLSAFVGDITITTCRASQGIYNYLAWYQOKPGKAP 180
QY 179 KLIIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKTV 238
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KLIIYAASLTQSGVPSRFSGSGTEFTLTISLQPEDGTYCCOOLISYPLTFGGGKTV 240
QY 239 EIK 241
Db 241 EIK 243
```

? PRIOR FILLING DATE: 2001-03-21
 ? PRIOR APPLICATION NUMBER: 60/293,459
 ? PRIOR FILING DATE: 2001-05-25
 ? NUMBER OF SEQ ID NOS: 3239
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 261
 ? LENGTH: 244
 ? TYPE: PRN
 ? ORGANISM: Homo sapiens
 ? PCT-US01-19110-261

Query Match	81.1%	Score 1037;	DB 1;	Length 244;
Best Local Similarity	80.7%	Pred. NO. 3.4e-81;		
Matches 196; Conservative	17;	Mismatches 28;	Indels 2;	Gaps 1

[illegible]

```

RESULT 15
US-09-880-748-261
: Sequence 261, Application US/09880748
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
: FILE REFERENCE: PF523
: CURRENT APPLICATION NUMBER: 2001-06-15
: PRIOR APPLICATION NUMBER: 60/212,210
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 60/240,816
: PRIOR FILING DATE: 2000-10-17
: PRIOR APPLICATION NUMBER: 60/276,248
: PRIOR FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 60/277,379
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/293,499
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 3239
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 261
: LENGTH: 244
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-880-748-261

```

Query Match	81.1%;	Score 1037;	DB 22;	Length 244;
Best Local Similarity	80.7%;	Pred. No. 3.4e-81;		
Matches 196;	Conservative 17;	Mismatches 28;	Indels 2;	Gaps 1

Oy 1 QVRLOOSGGGLVQPGRSRLSCASGFTFDYAMHWRAQPKGLEWYSGMTWNGSIG 600
||| : ||||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 QVQLAESGGGLVQPGRSRLSCASGFTFDYAMHWRAQPKGLDWSAITWNSGHIDY 600

```

OY 61 AD$VKGRTTISRDNAKNSLYLOMNSLAEPRYAYVYCARREPH--NTDAFIDLNGGTLVTVS 118
    |||:||||:|||||:|||||:|||||:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:~::~:
Db 61 AD$VEGR$R$RDNAKNA$LYLOMNSLRPE$TAVYCTKASTYLSTSS$LDNGG$TLVTVS 120

OY 119 SGGGGPGGGGSGGGGSDVVMVOTSP$PFL$AFVGDITTTTCRASOGIYNYLWAMYQOKPEKAP 178
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 SGGGGSSGGGSGGGGSDIQMTQSP$SLASISGDRVITTTTCRASOGIRNYLWAMYQOKPEKAP 180

OY 179 KLLIYAA$TLO$GVP$SRF$SG$S$TE$ETL$TIS$IQP$EDFCTYTCQQLISTP$LFFGG$TKV 238
    |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 181 KLLIYAA$TLO$GVP$SRF$SG$S$TE$ETL$TIS$LOP$EDVATYTCQKYN$APVAFGQ$TKV 240

OY 239 EIK 241
    |||
Db 241 EIK 243

```

Search completed: August 15, 2002, 16:34:06
Job time: 766 sec

07	1081	GVTSLIKKRESSGVLIDKSNVSCPPAPCLFPTDRIYLODSCSHFVENNTNLGTSKKTPAS	1140
Db	1081	gvtslkkresgvlldkrsvscfpapclfdlrvldgscshfvennnlgtskkttas	1140
07	1141	YMPQFQCTSTGTHKIMENKMDLTV	1165
Db	1141	ympqfqtctstgthkimenkmdltv	1165
RESULT 7			
XX	AAW62544		
XX	AAW62544	standard; protein; 1221 AA.	
AC	AAW62544;		
XX			
DT	12-OCT-1998	(first entry)	
XX			
DE	Human ob-receptor replacement mutant.		
XX			
KW	ob-receptor; hypothalamus; obesity; leptin; diabetes; infertility;		
KW	anorexia; cachexia.		
XX			
OS	Homo sapiens.		
XX			
FN	MO9824881-A1.		
XX			
PD	11-JUN-1998.		
XX			
PF	26-NOV-1997; 97MO-US22165.		
XX			
PR	02-DEC-1996; 96US-0032367.		
XX			
PA	(MERI) MERCK & CO INC.		
XX			
PI	Fong TM, Huang RC, Van Der Ploeg L;		
XX			
DR	WPI; 1998-333304/29.		
XX			
PT	New mutant ob receptor(s) - used to develop products for drug		
PT	screening and for gene therapy for weight control, e.g. obesity or		
PT	anorexia		
XX			
PS	Claim 6; Fig 2; 27pp; English.		
XX			
CC	The ob-receptor (OB-R), a member of the cytokine receptor family is		
CC	transcribed in the hypothalamus and is involved in obesity. The		
CC	replacement mutant has had amino acids 420-496 the second CK-F3		
CC	module in OB-R deleted and replaced by amino acids 500-632. The		
CC	replacement mutant together with mutants lacking a functional first CK-F3		
CC	module or a functional intracellular domain can be used in assays for the		
CC	detection of ligands, agonists, antagonists and ligand mimetics. The		
CC	leptin agonists identified can be used in situations where leptin		
CC	insufficiency causes obesity, diabetes or infertility. The leptin		
CC	antagonists identified can be used in the treatment of anorexia and		
CC	cachexia. The mutant receptor nucleic acids can also be used in gene		
CC	therapy for weight control, e.g. for treating obesity or anorexia.		
XX			
SO	Sequence 1221 AA;		
Query Match 92.9%; Score 5809; DB 19; Length 1221;			
Best Local Similarity 90.6%; Pred. No. 0;			
Matches 1110; Conservative 17; Mismatches 34; Indels 64; Gaps 8			
07	1	MICQFCVLLMEIYVTTAFNLSTPTPMRFKLSCMPNPNSTYDFLLPAGLSKNTSNS	60
Db	1	micqfcvllmefiylvttafnlstptpmrfklscompnpsnydyfllpaglskntsns	60
07	61	NKHVETNVEPKRNSSGTHFSNLKSTTTHRCFCFSESDRNCSLCADNIEGTFVSTVNSLVF	120
Db	61	nkhvetaevpkhnsstgthfnsnlksttthrcfcfseqdrcnslcadniegtfvtvsnslvf	120

QY	121	QOANNNIOQWIKGDKLKTVCVESLFENKLNFRNNYKXHLIYUVEVLEDSPLVPQKS	180
Db	121	qqidannniqgwklgdklilicvyesl fknltfnyukvhllylvprevedsplvpqgs	180
QY	181	FQWYHCMSVHECECELVPPVATKLDNTFLMLCKITSGGVIFQSPMSVQPIINNVKDDP	240
Db	181	fqnwhicmsvhecececlvppvatkldntflmlckitsggvifqspmsvqpiinmvkddp	240
QY	241	LGLHMETDDGNTLKISWSSPPLVPFPLQYQVKSSENSTVJREADKIVSATSLLVDSTLP	300
Db	241	lglhmeitddgnlkliswsppplvpfpplqyqvkssentvtvreadkivsatsllvdstlp	300
QY	301	GSSTVEYQVKRRLDGPGTMSDMSSTPRVFTTQDYIYTPRKILTVSGSNSPHCYTKKEKI	360
Db	301	gsstveyvqrkrlldgpgtmsdmsstprvfttqdyiytprkiltsvgsnshfciytkkenk1	360
QY	361	VPSKEIYWMNMJAEKIPQSOQDYDVSNHSAVYFPFNLEKPKRGXTYQAYVACCNBHECH	420
Db	361	vpskeiywmnmjaekipqsoqdydvsnhsavypfnlekpkrqxtyaayvaccnbhechf	420
QY	421	RYAEL-----YVIDVINISCTDGLY-TKMTCKRMSSTIOSL-----AESLT-----	462
Db	421	qpfllsbgymwlrtnlnsl-----gslsdprctvlpdsyvvprlpssvkaeltlnlgllkls	477
QY	463	-----OLRYHRS-----SLYCSIDPISIHPISEPKCYL	490
Db	478	wkprfvpeennlqfqlrlygskewqkmyevyadakasvslpvpalcavay-qvcrkrl	536
QY	491	QSDGRY-----PCIFQPIFLLSGYTMWRIRHSIGSLDSPPTCVLPDSYVVKRPP	540
Db	537	dglgywmswnpaytvecllqpflllsbgymwlrtnlnsgslsdprctvlpdsyvvkrpp	596
QY	541	SSVAEITINIGLKITSWEKRPVPENNLFOQIRYGLSGKEVQWKMAYEYDASKSVSLPV	600
Db	597	ssvkaeltlnlgllklswekprfvpeennlqfqlrlygskewqkmyevyadakasvslpv	656
QY	601	PDLCAVYAVOYCKRRLDGLGTSMNSMSPAYTVYMDIKYPMRGPERFWRILINGDIYMKKEKV	660
Db	657	pdlcavyavqcrkrlldglgtsmnsmspaytvymdikypmrgrpfwrilngdtmkkekv	716
QY	661	TLWKPLMKNDSCSYORVYINHHGTGNGWSDVGNHKKFELWTBDANVTYVAINSI	720
Db	717	tlwkpmlknhdscsyvryinhhtgngwsvdvgnhkkfelwtbdanvtyvaainsi	776
QY	721	GASVANFELTPEWPMPSKVYNIYOSLSAYPLNSSCVIYSWLLSBDVKLWFIIEWMKLNLED	780
Db	777	gasvanflltswpmksvynlyvqslsayplnsscvyswllsbdvklmfiiekwnlined	836
QY	781	GEIKWLRISSSVKKRYIHDHFPIERKYQFSLYPIFMEVGYGPKIINSEFTODDIEKHOSA	840
Db	837	geikwlrtsssvkryyihdhfpieryqfslypifmegyqpkliinsftgddiekhgda	896
QY	841	GLIYVYVPTISSLLIGTLILSHQKKKILFMEVDVNPKNCSMAOGLNOKRETFEHLFI	900
Db	897	gliyvlypvtisslllgtllilshqkmkklfimedvnpknscswaglnofkretfehlf1	956
QY	901	KHTASVYOCGPLLEPPTISDIDVSDMSMKKDDMMFTYVSLSTLTDIEKSVCSIDPFN	960
Db	957	khtasvtcgppllepeltsedivsdmsmkddmmpctvslstltdieksgvcsidqfn	1016
QY	961	SVNFSSEAGTGVYIEDESQKQFVYKATYILSNSKPSFTEBOGLINSSVYTCFSSKNSPL	1020
Db	1017	svnlfsaeagtevyeaasqfvtkyatylsnshkpsfteeoglinsvtycfssknspl	1076
QY	1021	KDSFNSNSWMELEAOFTILSDQHPNITSPHLTBSGLDELKLBEGNFBENNDDKSITYL	1080
Db	1077	kdsfnsnswmeleagaftilsdqhpnlitshphtfseglidelklegnfbennddksityl1	1136
QY	1081	GWTSIKKRESECVLLTDSRVSCEPFAACETDTRVLYODSCSHFVNNNINLGTSSKKTPAS	1140
Db	1137	gwtsikkrsecvlltdksrvscfpapcftdtrvlyqdcshfvnmninlgtssakktas	1196
QY	1141	YMPQFOTCSTQTHKIMENKMCDDTLV	1165

Db 1197 ymptqfctscqtthkimenkmdltv 1221

RESULT 8

AAW34499 ID AAW34499 standard; protein: 970 AA.

AC AAW34499;

DT 18-MAR-1998 (first entry)

DE Obesity receptor C protein.

KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 959 /label= unknown

FT /note= "encoded by stop codon"

XX WO9725424-A1.

PD 17-JUL-1997.

XX 02-JAN-1997; 97MO-US00128.

XX 31-DEC-1996; 96OS-0774414.

PR 04-JAN-1996; 96OS-0582825.

XX (AMGE-) AMGEN INC.

PI Chang M, Fletcher PA, Welcher AA;

DR WPI: 1997-384981/35.

DR N-PSDB; AAT98530.

PT Obesity protein receptor(s) and related DNA - used to treat weight

PT disorders, e.g. obesity, diabetes and high cholesterol or blood

PT lipid levels

XX Claim 2: Page 72; 151pp; English.

CC This sequence represents the obesity (OB) receptor C protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.

XX Sequence 970 AA;

Query Match 77.3%; Score 4831.5; DB 18; Length 970;

Best Local Similarity 94.4%; Pred. No. 0; Mismatches 24; Indels 25; Gaps 3;

Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

QY 1 MTCQKFCVLLAHMEFYVTYAFNLSTPTPWRKLSLSCMPNPSTYDYFLLPAGLSKMTSNS 60
DB 1 mtcqkfcvllahmefyvtatfnlstptpwrklscompnstydyflllpaglskmtsns 60
QY 61 NGHYTAVBEKFNSSGTHPSNLSKTTFHCCFRSEQDRNCSLCAADNIEGKTFVSVNSLVE 120
DB 61 nghytavebkfnssgthpsnlskttfhccfrseqdrncslcadniegkftvsvnslyve 120
QY 121 GQIDAMWNITQCMWKGLKLFICVYESLFKRLFPNNYNYKVALLYLVLEVLDSPLVQOKGS 180
DB 121 gqidamwnitqcmwkglklficvyeslfkrlfpnnynykvallylvlevl dsplvpqkgs 180

QY 181 FQWYHCNCSVHECCCELVVPYTRAKLNDTLMLCKITSGGVIPOSPLMSYQPIIMKVPDPDP 240
DB 181 fgmwhcnscvheccceelvpytraklndtlmlckitsggvifposplmsyqpiimkvdpdp 240
QY 241 LGLAMEITDDGNLKISWSSPPLVPPPLQYQVYKSENSSTVIRBAXIVASATSLVDSTLP 300
DB 241 lglameitddgnlkiswsspplvpplqyqvysensstvirbaxivatslvdstlvp 300
QY 301 GSSYEVOVGKRLDGPGLMSDSTPRVFTTODVTFPPKILTSVGSNVSFHCYKKENKI 360
DB 301 gssyevovgkrl dgp glmsdstprvftt odvtfppkiltsvgsnvsfchcykkenk 360
QY 361 VPSKETVMMNMLAEKIPQSOYDVSDHVSXVFPFNLETKPRCKFTYDVAVYCCNEHECHH 420
DB 361 vpsketvmmmlaekipqsoydvdsdhvsxvfpfnletkprckfthydvavycnehech 420
QY 421 RYAEIYVIDVYNINISCTDGYLTAKTCRMSSTITQSLAESTDQLRHRSLSYSDIPSTH 480
DB 421 ryaeliyvidvyninisctdgyltktrcwrstlqslaestdqlyhrslsycsdipsh 480
QY 481 PISEPKDCYLOSDGFYECJFOPIFLLSGYTMIRIHSLSGLSDSPPTCVLPDSVVPPLP 540
DB 481 pisepkdcylsdgfyecj fopifllsgytmirihsls glsdspptcvlpdsvvplp 540
QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOFOIRYGLSGREVOMKTEVYDANSKVSLEPV 600
DB 541 ssvkaeitinigllkliswekvpfpennlofoirylsgrevomktevydanskvslypv 600
QY 601 PDLCAVYAAVOYRCRKLDDGLGYMSNNSNPAYTVVMDIKVPMRGEPFRITNGOTMKKEKRV 660
DB 601 pdlcavyaavoyrcrkl d dglgymsnnsnpaytvvmdikvpmrgepfritngotmkkekv 660
QY 661 TLTKRPLMKNDLSQVORYVINHTSCNGWSEDCGNHTKFTPLMEQAHVTVLAINSI 720
DB 661 tltk rplmkndlsqvoryvinhtscngwse dcnhtkftplmeqahv tvla insi 720
QY 721 GASVANFNLTFSWPMKSVNIIVOSLSAYPLNNSCVIVSWILSPSDYKLMFTFEMKLNED 780
DB 721 gasvanfnltfswpmksvniiv oslsayplnns cvivswilspdyklmftfemklned 780
QY 781 GEIKMIRISSVKKYTIHDFRIEYKQFSLYIFMEGKXPRITNSFODIDEKIQSDA 840
DB 781 geikmirissvkkyyti hdfrie ykqfsl yifmegkxpritnsfodidekiqsd 840
QY 841 GLYIVIPVISSSILLGLTLISHQRMKRLFWDVDPNPKNCSWAGLINFQK-----PE 893
DB 841 glyivipvilssillgl tlishqrmkrlfwdvdpnpkn cswaglinfqkmgsmfvk 900
QY 894 TFEHDFIKHT-ASVTCGP-----LLEPETISDVISVDTSKKNKDE 933
DB 901 shhsissstgkhcgprgprlhrtrdcslyllt lprllsypakspsvrncqe 958
RESULT 9
AAW24052 ID AAW24052 standard; protein: 896 AA.
XX AAW24052;
AC AAW24052;
DT 17-MAR-1998 (first entry)
DE Human MSX receptor variant 6.4.
XX Human MSX receptor variant 6.4.
KW Human: MSX receptor; variant 6.4; identification: purification;
KW ligand: activator; antibody; agonist; proliferation: obesity;
KW differential: anæmia; treatment: neoplasia; arteriosclerosis;
KW type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolemia;
KW hypertri glyceridaemia; cancer; cholelithiasis.
XX Homo sapiens.

XX MO9725425-A1.
 PN 17-JUL-1997.
 PD 07-JAN-1997; 97MO-US00325.
 PF 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX (GETH) GENENTECH INC.
 PA Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 XX WPI: 1997-372864/34.
 DR N-PSDB: AAT85576.
 XX MSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Claim 2; Pages 86-89; 219pp; English.
 XX The present sequence is the human MSX receptor variant 6.4,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-MSX receptor antibody can be used as an agonist to activate
 CC the MSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the MSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. MSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid human cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 CC
 CC Sequence 896 AA:
 SQ

Query Match 77.2%; Score 4826; DB 18; Length 896;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 361 VPSKEIVMMNLAEKIPQSOYDVVSDHVSRTVEFNINETKPRGKFTYDAVYCCNEHECH 420
 DB 361 vpskelvwmnlaekipqsgdvsvshvskvtfenlnetkprgkfydayccnehech 420
 OY 421 RYAEIYIDVININSCETDGLTRKMTCRMSTSTQSLAEESTLQRLYRRSSLCSDIPSIH 480
 DB 421 ryaeliyidvininlsctdgltrkmtcrmsststqslaestlqlrlyrrsslycsdipsh 480
 OY 481 PISEPKDCYLOSDFEYCIPOPIFLSGYTMIRINSLSDSPPCVLPDSVVKPLP 540
 DB 481 pisepkdcylsodfeyciopoflsgytmirinslslsdppcvlpdsvvkplp 540
 OY 541 SSYKAEITINIGLIKISWEKRPVENNLQFOIRYGLSGKEVOMKMEVYDAKSKVSLPV 600
 DB 541 ssykaeitiniglikiswekvpvennlqfoirylsglsgkevqmkmyevdakskvslpv 600
 OY 601 PDLCAVAVOVRCKRLDGLGWSKMSNPATYVMDTRVPMRGPEFWRITINGDTMKRKNV 660
 DB 601 pdlcavavyvrckrlldglgwskmsnpatyyvmdtrvpmrgpefwrilingdtmkkeknv 660
 OY 661 TLLMKPLMKNDISCSVORVYINHRTSCNGTWSDEVDGNHRTFTPLMPROAHTVVLAINSI 720
 DB 661 tllwkpimkndiscsvqrvyinhrtscngtwsedvgnhrtfllwteqahvclvainsi 720
 OY 721 GASVANFNLFSPWPMKKNIVQSLASAYPLNSCIVSWILSPSDYKLMYFIENKLNED 780
 DB 721 gasvanfnlfsppwpmkknivqslasayplnscivswilspdyklymyfielklned 780
 OY 781 GEIKWLRMISSVKKYIYHDFIPEKTOFSLYPFMEGVGKPKITNSFTODDTRHOSDA 840
 DB 781 gelkwlrmissvkkyyihdfipektofslypfmegvgkpkitnsftddlekhgsda 840
 OY 841 GLXYIVPVITSSITLGLTILISHQRKRLFWEDVPMPKNCNMAQGLNFOK 891
 DB 841 glxyivpvitssitlgltilishqrmklfwevdpmpkncnmaqglntfo 891

RESULT 10
 AAM24053
 ID AAM24053 standard; Protein; 923 AA.
 XX
 AC AAM24053;
 XX
 DT 17-MAR-1998 (first entry)
 XX
 DE Human MSX receptor variant 12.1.
 XX
 KW Human; MSX receptor; variant 12.1; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 XX
 OS Homo sapiens.
 XX
 PN MO9725425-A1.
 PD 17-JUL-1997.
 XX
 PF 07-JAN-1997; 97MO-US00325.
 XX
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 XX
 DR WPI: 1997-372864/34.

DR N-PSDB; AAT85577.
 XX MSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT hematopoiesis or for treating tumors
 XX
 XX Claim 2; Pages 89-93; 219pp; English.
 XX
 CC The present sequence is the human MSX receptor variant 12.1,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-MSX receptor antibody can be used as an agonist to activate
 CC the MSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the MSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. MSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 CC
 XX
 XX Sequence 923 AA:

Query Match 77.2%; Score 4826; DB 18; Length 923;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIOCKECVLLHMEFIVITAFNLSYPTPMRFKLSGMPNNTYDYLPLAGISKNTNS 60
 DB 1 MIOCKECVLLHMEFIVITAFNLSYPTPMRFKLSGMPNNTYDYLPLAGISKNTNS 60
 QY 61 NGHYETAVEBFKNSGTHFSNLSKTFHCFRSEODRNCSCADNTEGKFVSTVNSL 120
 DB 61 NGHYETAVEBFKNSGTHFSNLSKTFHCFRSEODRNCSCADNTEGKFVSTVNSL 120
 QY 121 QQIDAMNITOCMLKGLDLFTCYVESLFKNLFRNTYKVVHLLYLVLEDSPLVPOKGS 180
 DB 121 QQIDAMNITOCMLKGLDLFTCYVESLFKNLFRNTYKVVHLLYLVLEDSPLVPOKGS 180
 QY 181 FQWHCHCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMNVKXDP 240
 DB 181 FQWHCHCSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMNVKXDP 240
 QY 241 LGLHMEITDGNLKSNSPPLVFPLOYOVKYSNSTYIRREADKIVSATSLVDSILP 300
 DB 241 LGLHMEITDGNLKSNSPPLVFPLOYOVKYSNSTYIRREADKIVSATSLVDSILP 300
 QY 301 GSSEYVQVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSTHCITYKKNKI 360
 DB 301 GSSEYVQVRGKRLDGPGLSDWSTPRVFTTQDVYIFPPKILTSVGSNVSTHCITYKKNKI 360
 QY 361 VPKETIYMMNLAEKIRQSGDYVSDHVSKVTFPNLNETPRGFTYDAYCCNEHCCH 420
 DB 361 VPKETIYMMNLAEKIRQSGDYVSDHVSKVTFPNLNETPRGFTYDAYCCNEHCCH 420
 QY 421 RYAEIYVIVNINISCTDGYLTKMTCRWGSTSTIOSLAESTLQRYHRSSTYCSIDPSIH 480
 DB 421 RYAEIYVIVNINISCTDGYLTKMTCRWGSTSTIOSLAESTLQRYHRSSTYCSIDPSIH 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLP 540
 DB 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMIRINHSLSLSDSPPTCVLPDSVYKPLP 540
 QY 541 SSVKAETITIGILKTSWKEPVPENNLQFIKIGLSGKVEQKMTYVYAKSKSVSLPV 600
 DB 541 SSVKAETITIGILKTSWKEPVPENNLQFIKIGLSGKVEQKMTYVYAKSKSVSLPV 600

QY 601 PDICAVYAVOVRCKRLDGLGYSMNSNPATYVMDIKVPRGPEFWRINIGDTMKKEKNV 660
 DB 601 PDICAVYAVOVRCKRLDGLGYSMNSNPATYVMDIKVPRGPEFWRINIGDTMKKEKNV 660
 QY 661 TLMLKPLMKNDSCSVORYINHHSTSCGTSWSEDDVGNHTKFTPLMTBOAHTVYLAINST 720
 DB 661 TLMLKPLMKNDSCSVORYINHHSTSCGTSWSEDDVGNHTKFTPLMTBOAHTVYLAINST 720
 QY 721 GASVANFNLFSPWMSKVNVIVOSLAVPLNLSGCVYMWISPSDYKMYRTIEKMNED 780
 DB 721 GASVANFNLFSPWMSKVNVIVOSLAVPLNLSGCVYMWISPSDYKMYRTIEKMNED 780
 QY 781 GEIKWLRISSSVKKYIYHDFIRPLEKYQFSLYPIFMEGVGKPKIINSFTQDIEKHQSDA 840
 DB 781 GEIKWLRISSSVKKYIYHDFIRPLEKYQFSLYPIFMEGVGKPKIINSFTQDIEKHQSDA 840
 QY 841 GLYIVYVYIISSLLIGTLLISHQRRKKLFMEVVPKPKCSMAQGINPQK 891
 DB 841 GLYIVYVYIISSLLIGTLLISHQRRKKLFMEVVPKPKCSMAQGINPQK 891

RESULT 11

AAW34497 standard; protein: 972 AA.

AAW34497:

18-MAR-1998 (first entry)

Obesity receptor A protein.

Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

high blood lipid level; obesity; diabetes; high cholesterol level;

weight loss; therapy; weight maintenance.

Homo sapiens.

Location/Qualifiers

Misc-difference 897 /label= unknown

Misc-difference 919 /note= "encoded by stop codon"

Misc-difference 925 /label= unknown

Misc-difference 939 /note= "encoded by stop codon"

Misc-difference 948 /label= unknown

Misc-difference 952 /label= unknown

Misc-difference 971 /note= "encoded by stop codon"

Misc-difference 971 /label= unknown

Misc-difference 971 /note= "encoded by stop codon"

MO9725424-A1.

17-JUL-1997.

02-JAN-1997; 97MO-US00128.

31-DEC-1996; 96US-0774414.

04-JAN-1996; 96US-0582825.

(AMGE-) AMGEN INC.

Chang M, Fletcher FA, Welcher AA;

XX WP1: 1997-384981/35.
 DR N-PSDB: AAT98528.
 XX
 PT Obesity protein receptor(s) and related DNA - used to treat weight
 PT disorders, e.g. obesity, diabetes and high cholesterol or blood
 PT lipid levels
 XX
 PS Claim 1; Page 64; 151pp; English.
 CC
 CC This sequence represents the obesity (OB) receptor A protein. This
 CC sequence has one or more of the biological properties of naturally
 CC occurring OB receptor protein. The OB receptor proteins and OB
 CC receptor/OB protein complexes are used for the treatment of obesity,
 CC diabetes, high blood lipid levels and high cholesterol levels. The
 CC proteins may also be used to treat an individual for weight loss or
 CC weight maintenance required for purely cosmetic purposes.
 XX
 SQ Sequence 972 AA;

Query Match 77.2%; Score 4826; DB 18; Length 972;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MICQKFCVLLHMERLYITAFNLSTPTPMRFKLSCMPNSTYDFLLPAGLSKNTS 60
 DB 1 micqkfcvllhmerlyitafnlstptpmrfklscompnstydfllpaglskntns 60
 OY 61 NGHYEAVPEKNSGTHFSNLSKTFHCCFSEODRNSCLADNTECKTFSTVNSLVP 120
 DB 61 nghyeavpeknsgthfnsnlsktfhccfseodrnscldadntecktfstvnslvp 120
 OY 121 QOIDANMNIOCLWKDCLKFICVESLFEKNLFNNYKHLHYLPEVEDSEPLVPQKS 180
 DB 121 qoidanmnioclwkdklfciveslfeknlfnnynkhlhylopevedseplvpqks 180
 OY 121 qgidanmnioclwkdklfciveslfeknlfnnynkhlhylopevedseplvpqks 180
 DB 121 qgidanmnioclwkdklfciveslfeknlfnnynkhlhylopevedseplvpqks 180
 OY 181 FQMVHNCNSVHECCCELVPPPAKLNDTLMLCKITSGGVIFQSPILMSVQPINMVKPDP 240
 DB 181 fgmvhncnsvhccceclvpplaklndtlmlckitsggvifqspilmsvqpinmvkdpdp 240
 OY 241 IGLHMEITDDGLKISMSSPILVPPLOYQVYKSESTVIREADKIVSATSLINDSTIP 300
 DB 241 iglhmeitddglnklsmsspilvpployqvkysestvlreadkivsatslindstip 300
 OY 241 iglhmeitddglnklsmsspilvpployqvkysestvlreadkivsatslindstip 300
 DB 241 iglhmeitddglnklsmsspilvpployqvkysestvlreadkivsatslindstip 300
 OY 301 GSSYEVOYGRKLDGPGIWSMSTPRVFTTQDVIFPPKILTVSGSNVSFHCITKKENKI 360
 DB 301 gssyevoyrkldgpgiwsmsstprvfttqdvifppkiltvsgsnvsfhcittkknki 360
 OY 301 gssyevoyrkldgpgiwsmsstprvfttqdvifppkiltvsgsnvsfhcittkknki 360
 DB 301 gssyevoyrkldgpgiwsmsstprvfttqdvifppkiltvsgsnvsfhcittkknki 360
 OY 361 VPSKETVMMNLAERIKPOSQYDVSDHVSQVTFPNNINETKPRGKFTYDAVYCCNEHECH 420
 DB 361 vpsketvmmnlaekipqsqydvsvdhvskvtfnninetrkprgkftydavycnehech 420
 OY 421 RYAEIYVIDVININISCEFTGYLTAKMTCRMSTSTIOSIAESTOLRKHRSLSKSPSIH 480
 DB 421 ryaeliyvidvininisceftgyltakmtcrmststiosiaestolrkhrrslskspsih 480
 OY 421 ryaeliyvidvininisceftgyltakmtcrmststiosiaestolrkhrrslskspsih 480
 DB 421 ryaeliyvidvininisceftgyltakmtcrmststiosiaestolrkhrrslskspsih 480
 OY 481 PISEPKDCYLQSDGFYEICTFPIFLLSGYTMMIRINHSLSLSDSPETCYLPDSVYKPLP 540
 DB 481 pisepkdcylqsdgfyecifpifllsgytmmirinhslslsdspetcylpdsvykplp 540
 OY 481 pisepkdcylqsdgfyecifpifllsgytmmirinhslslsdspetcylpdsvykplp 540
 DB 481 pisepkdcylqsdgfyecifpifllsgytmmirinhslslsdspetcylpdsvykplp 540
 OY 541 SSVKAEITINIGLLKISWKRPYFPENNIOFOIRYGLSGEVOVMKMEVVDASKSVSLV 600
 DB 541 ssvkaeitinigllkismkryfpenniofoiryglsggevomkmevvdasksvslv 600
 OY 541 ssvkaeitinigllkismkryfpenniofoiryglsggevomkmevvdasksvslv 600
 DB 541 ssvkaeitinigllkismkryfpenniofoiryglsggevomkmevvdasksvslv 600
 OY 601 PDLCAVYAVOVCKRLDGLGYSNNSNPAYTVMDIKVPMRPREPFRITNGDMKKEKNV 660
 DB 601 pdlcavyavovckrldglgysnnsnpaytvmdikvpmrprepfritngdmkkekny 660
 OY 601 pdlcavyavovckrldglgysnnsnpaytvmdikvpmrprepfritngdmkkekny 660
 DB 601 pdlcavyavovckrldglgysnnsnpaytvmdikvpmrprepfritngdmkkekny 660
 OY 661 TLLMKPLMKNDLSGVQRYVINHHSTSCNGSTMSDVGNNHKTFFLWTEQAHVTVIAINSI 720
 DB 661 tllmkplmkndlscvqrvyvinhstscngstmsdvgnnhktfflwt eqahv tviainsi 720

OY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNNSCVIVSWILSPSDYKLMYFIEMKNLND 780
 DB 721 gasvanfnltfswpmkknivqslaysayplnnsccvsvswilspdyklymfiiemknlned 780
 OY 781 GELKWLRISSSVKRYIHHFTPIEKYQSFYPIFMEGKGRKIINSFPODDIEKHQSA 840
 DB 781 gelkwlrlsssvkryihhftpiekyqsfyplfmevgkgrkiinsftqddlekhsda 840
 OY 841 GUYIVPVISSSILLGTLLISHORMKLFEWEDVPNPKNSWAOGLNFPK 891
 DB 841 gylivpviissillgtllishormklfewedvpnpknswaoglnfpk 891

RESULT 12

AAW34498

ID AAW34498 standard; protein: 999 AA.

AC AAW34498;

DT 18-MAR-1998 (first entry)

DE Obesity receptor B protein.

KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
 KW high blood lipid level; obesity; diabetes; high cholesterol level;
 KW weight loss; therapy; weight maintenance.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 905 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 933 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 971 /label= unknown

FT /note= "encoded by stop codon"

FT Misc-difference 988 /label= unknown

FT /note= "encoded by stop codon"

PD WO9725424-A1.

PD 17-JUL-1997.

PF 02-JAN-1997; 97WO-US00128.

PR 31-DEC-1996; 96US-0774414.

PR 04-JAN-1996; 96US-0582825.

PA (AMGE-) AMGEN INC.

PI Chang M, Fletcher FA, Welcher AA;

DR WP1: 1997-384981/35.

DR N-PSDB: AAT98529.

PT Obesity protein receptor(s) and related DNA - used to treat weight

PT disorders, e.g. obesity, diabetes and high cholesterol or blood

PT lipid levels

PS Claim 2; Page 68; 151pp; English.

CC This sequence represents the obesity (OB) receptor B protein. This
 CC sequence has one or more of the biological properties of naturally
 CC occurring OB receptor protein. The OB receptor proteins and OB
 CC receptor/OB protein complexes are used for the treatment of obesity,
 CC diabetes, high blood lipid levels and high cholesterol levels. The
 CC proteins may also be used to treat an individual for weight loss or
 CC weight maintenance required for purely cosmetic purposes.

SQ Sequence 999 AA:

Query Match 77.2%: Score 4826; DB 18; Length 999;

Best Local Similarity 100.0%: Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCOKFCVYLLHMEFYVITAFNLSPYTPWPKLSKMPNSNYDYFLPAGLSKNTSNS 60
 DB 1 mtcokfcvylhweifyltafnlsyplwprklskmpnsnydyfllpaglskntns 60
 QY 61 NGHYETAVERKFNSSGTHFSNLSKTFPHCCFRSEODRNSLCADNTEGKTFVTSVLV 120
 DB 61 nghyetavepkrfnssgthfnslnsktfphccfrseqdncslcadnlegkrfvatsvls 120
 QY 121 QOITDAMNIOCMKLGDKLFCYVESLFRKLFNNYKVVLLVLEVEDSPLVQKGS 180
 DB 121 qoitdamniqcmklgdklfcyveslfrklnfnynkvhllyvlevedsplvpqkgs 180
 QY 181 FQWVHNCNSVHECCCECLVPYPTAKLNDTLMLCKITSGVIFQSPPLMSVOPIMNVKPD 240
 DB 181 fqmwhncnsvehccceclvpyptaklndtlmlckitsgvifqspplmsvopimnvkpd 240
 QY 241 LGLHMETDDGNLKISWSSPPLVFPLOYKYSNSTVYIRADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkiswsspplvpfplokyksnstvireadkivsatsllvdsilp 300
 QY 301 GGSYEVOVRGKRLDGPFGIMSDMSTPRVETQDVIYFPFKITLTVSGSNVSPHCYKKE 360
 DB 301 ggsyevovrgkrlidgpfgiwsdmsctprvfttqdvlyfpkltlsvgsnsvshcykkek 360
 QY 361 VPSKETIVMMNLAEKIPQSOYDVSDVSHSVKTFEFLNETPRGKTFYDAVYCCNEHC 420
 DB 361 vpsketivmmnlakelpsqdydvshsvkftfelnepgkrfydayvccnehech 420
 QY 421 RYAEIYVIDVNNISCEYDGLFKMTCRMSTSTQSLAESTLDRHRSSLVYSDIPSTR 480
 DB 421 ryaeliyvidvnniscedyglfkmtcrwststqslaestlqtrhrsslycsdipstr 480
 QY 481 PIPEPKDCYQSDGFECIFQPIFELLSGYTMMIRINHSGLSDSPPCVLPDSVVKPLP 540
 DB 481 pipekdcyqsdgfyecifqpfllsgytmairinhsiglsdpspcvlpdsvvpkrlp 540
 QY 541 SSVKAEITINIGLLKISMEKVPENNLFOIRYGLSGKEVQKMEVYDAKSKSVSLP 600
 DB 541 ssvkaeitinigllkiswekvpennlfoirylsgkevyqkmyevyadaksksvslp 600
 QY 601 PDLCAVYAVQVRCKRLDGLCYNSMSPATVYMDIKVPRGPEFMRITNGDTMKKEKN 660
 DB 601 pdlcavayavqvrckrlidglcywnsmpatvymdikvprgpefmrtingdtmkkek 660
 QY 661 TLLMKRPLMKNDLSQVORYVINHTSCNGTSEDVGNHTKFTFLMTLQATVVLAINST 720
 DB 661 tllmkrlmkndlsqvoryvinhtscngtseavgntkftflmtlqatvvlainst 720
 QY 721 GASVANFNLTSPMKSQVNIQSLAVPLNNSCVIVSWILSPSDYKILMFTIEMKNLND 780
 DB 721 gaavanfnltspmksvniqslavplnnsccvsvswilspdykilmftiemknlnd 780
 QY 781 GELKMLRISSVKRYIHHFIRLEKYQFSLYPIFMGCVKPKRTINSFTODDLEKHQSD 840
 DB 781 gelkmlrissvkrxyihhfrlekyqfslypifmgcvkpkrtinsftoddlekhsda 840
 QY 841 GLVYIPVIVISSSILGLTLLISHQRKRLFWEDVPRPKCSWAQGLNFOK 891
 DB 841 glvyipvivissilgltllishqrkrlfwedvprpkcswagqlnfo 891

RESULT 13

AAW38214
 ID AAW38214 standard; Protein; 958 AA.
 XX
 AC AAW38214;

XX 11-JUN-1998 (first entry)
 XX
 DE Human OB-R variant Form 1.
 XX
 KW Detection; defective obese protein receptor; defective OB-R; human;
 KW defective leptin receptor; variant Form 1; infertility.
 XX
 XX Homo sapiens.
 XX
 XX MO9741263-A1.
 XX
 XX 06-NOV-1997.
 XX
 PD 28-APR-1997: 97WO-US07676.
 PF
 XX 29-APR-1996: 96US-0640389.
 XX
 PA (PROG-) PROGENITOR INC.
 XX
 PI Clotfi J, Shafer AW, Snodgrass RH, Zupancic TJ;
 XX
 DR WPI: 1997-549757/50.
 DR N-PSDB; AAT95779.
 XX
 PT
 PS
 XX
 PS Disclosure; Fig 3; 40pp; English.

The present sequence was used in the development of a novel method for detecting a defective obese protein or leptin receptor (OB-R) in cells. Them method comprises contacting RNA extracted from a cell population (preferably an ovary, prostate, testis, sperm, ova, ovarian follicular or blood cell population) with an oligonucleotide derived from a portion of the human OB-R variant Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are associated with infertility, as they are unable to correctly transduce signals from leptin binding. The detection method can be used to diagnose infertility, or predisposition to infertility, while treatments that inhibit or down regulate the variants, gene therapy to replace them in homozygotes or direct activation of downstream signal transduction can be used to improve fertility. CC Also described is the use of labelled DNA probes based on the OB-R sequence to screen for other variants.

SQ Sequence 958 AA:

Query Match 77.1%: Score 4819.5; DB 18; Length 958;
 Best Local Similarity 94.1%: Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

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 DB 181 fqmwhncnsvehccceclvpyptaklndtlmlckitsgvifqspplmsvopimnvkpd 240
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QY 421 RYAEIYVIDVNNISCTEDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480
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Db 421 ryaeiyvidvnniscetdgyltkmtcrwststlqslaeestlqlryhrrslsycsidpsih 480
QY 481 PISPEKDCYIQSGDFYECITFPIILISGYTMWIRINSLGSLDSPPCVLPDSVVKRLPP 540
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QY 541 SSVAEETINIGLTKISMEKVPPENNLOFQIRYGLSGKEQWQMYEYDAKSKSVSLPV 600
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DT 02-FEB-1998 (first entry)
XX
DE Human OB-R Leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
KW diagnosis; human.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT MISC-difference 85 /note= "variation from published sequence"
FT MISC-difference 109 /note= "variation from published sequence"
FT MISC-difference 223 /note= "variation from published sequence"
FT MISC-difference 845.862 /note= "variation from published sequence"
FT Domain /label= "Transmembrane_domain"
FT MISC-difference 892..958 /note= "divergence from published sequence"
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PN MO9726370-A1.

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XX 24-JUL-1997.
PD
XX 17-JAN-1997; - 97MO-US00570.
PF
XX 18-JAN-1996; 96US-0588190.
PA (PROG-) PROGENITOR INC.
PI Clotfif J, Shafer AM, Snodgrass HR, Zupancic TJ;
PI N-PSDB; AAT89193.
DR WPI: 1997-385353/35.
DR N-PSDB; AAT89193.
XX
XX Detecting defective leptin receptor by hybridisation assay - and
PT treatment of obesity with agent that inhibits the defective
PT receptor, also screening for compounds that supplement leptin
PT activity
PS Claim 12; Fig 1A-E; 26pp; English.
PS
XX This polypeptide comprises a variant of the human leptin receptor
CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
CC derived from overlapping clones isolated from a human foetal liver
CC library. The sequence shows near identity to a published OB-R
CC sequence in the extracellular domain, with the exception of 3 amino
CC acids, but there is extensive diversity in the intracellular
CC cytoplasmic domain at the C-terminal end. A claimed method for
CC detection of OB-R in cells comprises extraction of RNA and testing
CC this for hybridisation to an oligonucleotide (1) derived from the
CC OB-R variant gene, especially from the region beyond nucleotide
CC 2770. Also claimed are methods of: (1) treating obesity by
CC administration of an agent that inhibits expression of the OB-R
CC variant gene; and (2) identification of a compound that can
CC supplement activity of leptin by: (1) incubating cells expressing
CC OB-R variant first with leptin and then with a test compound, and
CC (11) comparing activation signals between cells treated and not
CC treated with the test compound. Inhibition/down-regulation of the
CC variant OB-R (found in obese people) improves response of cells to
CC weight regulation by leptin. Replacing variant OB-R by gene therapy
CC (in homozygous individuals) can be used to treat obesity. Labelled
CC probes based on the gene can be used to isolate other variant forms
CC of the receptor gene or to detect the variant gene (e.g. for
CC determining predisposition to obesity), while the OB-R gene can be
CC used to express recombinant OB-R (optionally as fusion protein) and
CC in standard hybridisation assays. The OB-R gene can also be used
CC therapeutically in cases of overexpression of functional OB-R
CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.
XX
SQ Sequence 958 AA;

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Query Match 77.1%; Score 4819.5; DB 18; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

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Db 301 gssyevgrkrlidgplwdsstprvfttqdvlyfppklltsgsnvshfciykkenk 360
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Db 841 glyivvyvYiISstllglTllishqrmkklfMedvprpkcsnawglnfqklegssfvk 900
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Db 901 shhsllstsqghchcgrpgplhrtktrdicslvyltlrpllsydpakapsvtnq 958

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RESULT 15
AAW19535
ID AAW19535 standard; Protein; 958 AA.
XX
AC AAW19535;
XX
DT 02-FEB-1998 (first entry)
XX
DE Human OB-R leptin receptor variant.
XX
KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
KW diagnosis; human.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT MISC-difference 85 /note= "variation from published sequence"
FT MISC-difference 109 /note= "variation from published sequence"
FT MISC-difference 223 /note= "variation from published sequence"

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FT FT /note= "variation from published sequence"
FT Domain 845..862
FT /label= Transmembrane_domain
FT MISC-difference 892..958
FT /note= "divergence from published sequence"
PN WO9726272-A1.
PD 24-JUL-1997.
PF 17-JAN-1997: 97MO-US00880.
PR 18-JAN-1996: 96US-0588189.
PA (PROG-) PROGENITOR INC.
XX Cioffi J, Shafer AM, Snodgrass HR, Zupancic TJ;
XX P-PSDB; AAT72649.
XX WPI: 1997-385291/35.
XX
XX This polypeptide comprises a variant of the human leptin receptor
XX (OB-R). Its sequence was deduced from a contiguous cDNA (AA72649)
XX derived from overlapping clones isolated from a human foetal liver
XX library. The sequence shows near identity to a published OB-R
XX sequence in the extracellular domain, with the exception of 3 amino
XX acids, but there is extensive diversity in the intracellular
XX cytoplasmic domain at the C-terminal end, suggesting alternative
XX splicing of a common precursor mRNA. A claimed method for
XX detection of OB-R in cells comprises extraction of RNA and testing
XX this for hybridisation to an oligonucleotide (1) derived from the
XX OB-R variant gene, especially from the region beyond nucleotide
XX CC 2770. Also claimed are methods of: (1) treating obesity by
XX administration of an agent that inhibits expression of the OB-R
XX variant gene; and (2) identification of a compound that can
XX supplement activity of leptin by: (1) incubating cells expressing
XX OB-R variant first with leptin and then with a test compound, and
XX (1) comparing activation signals between cells treated and not
XX treated with the test compound. Inhibition/down-regulation of the
XX variant OB-R (found in obese people) improves response of cells to
XX weight regulation by leptin. Replacing variant OB-R by gene therapy
XX (in homozygous individuals) can be used to treat obesity. Labelled
XX probes based on the gene can be used to isolate other variant forms
XX of the receptor gene or to detect the variant gene (e.g. for
XX determining predisposition to obesity), while the OB-R gene can be
XX used to express recombinant OB-R (optionally as fusion protein) and
XX in standard hybridisation assays. The OB-R gene can also be used
XX therapeutically in cases of overexpression of functional OB-R
XX (causing loss of appetite and hypermetabolic activity). Cells
XX engineered to express variant receptor are used in method (2) to
XX screen for (ant)agonists of leptin/OB-R interaction, also to generate
XX antibodies that competitively inhibit, neutralise or enhance activity
XX of the variant receptor.
XX
SQ Sequence 958 AA:

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Query Match 77.1%; Score 4819.5; DB 18; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

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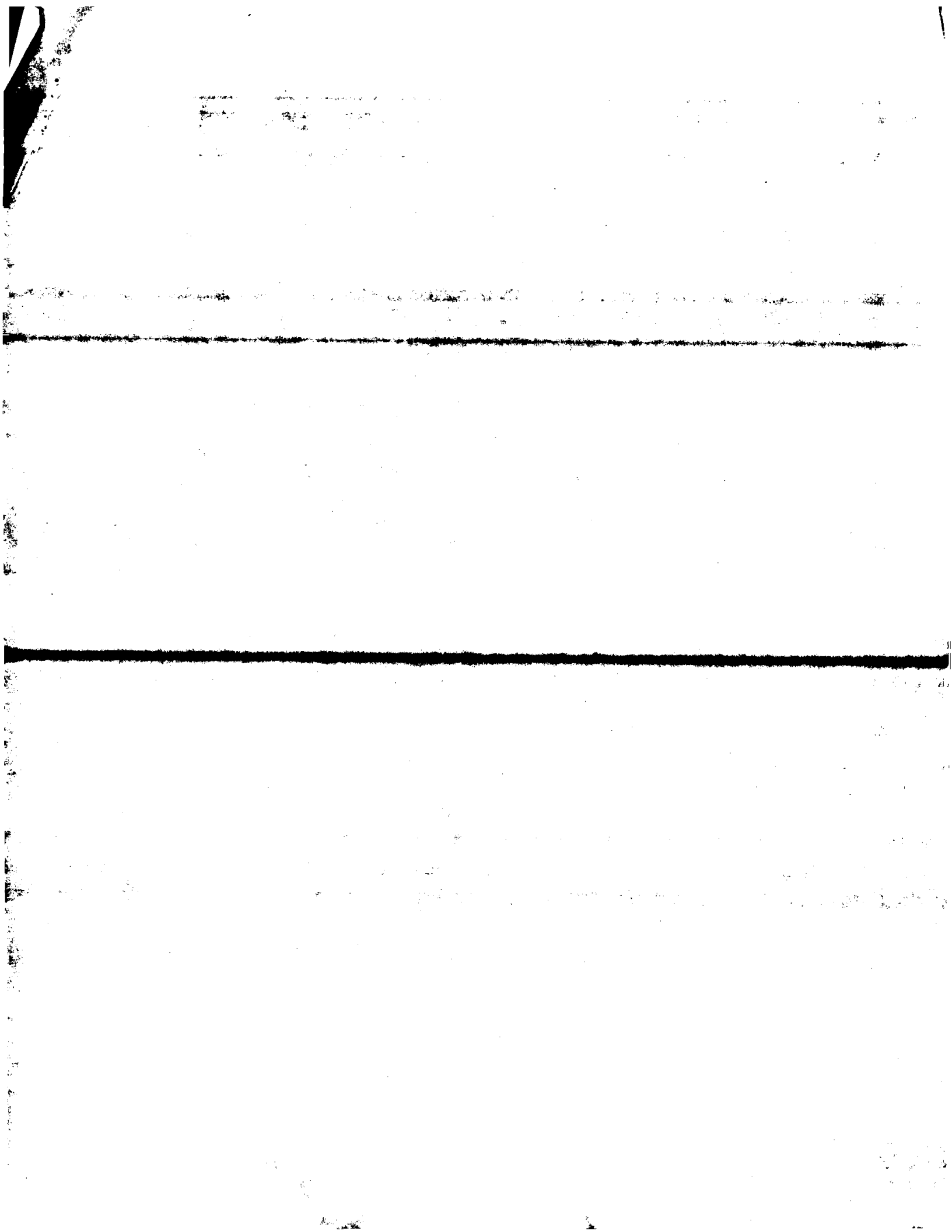
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Db 901 shhslisstcqhkhcgrpgqplnrktrdicslylltlppllsydpakspsvnrtpqe 958
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Job time: 313 sec



Thu Aug 15 16:32:48 2002

us-08-779-457-2.ra1

Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

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(without alignments)
718.400 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	6246	99.9	1165	US-08-618-957A-11	Sequence 11, Appl1
5	6172	98.7	1165	US-08-640-389A-11	Sequence 11, Appl1
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7	4819.5	77.1	960	US-08-355-888A-8	Sequence 8, Appl1
8	4819.5	77.1	960	US-08-693-657-8	Sequence 8, Appl1
9	4819.5	77.1	960	US-08-640-389A-3	Sequence 3, Appl1
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11	4816	77.0	908	US-08-693-657-8	Sequence 8, Appl1
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18	4791.5	76.6	958	US-08-640-389A-8	Sequence 8, Appl1
19	4788	76.6	906	US-08-640-389A-9	Sequence 9, Appl1
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ALIGNMENTS

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36	370	5.9	77	4	US-08-803-346-63	Sequence 63, Appl1
37	345.5	5.5	918	2	US-08-825-558-6	Sequence 6, Appl1
38	316	5.1	708	1	US-07-797-556-2	Sequence 2, Appl1
39	316	5.1	708	1	US-08-308-881-2	Sequence 2, Appl1
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45	309.5	4.9	75	4	US-08-803-346-60	Sequence 60, Appl1

RESULT 1

US-08-599-455B-4
Sequence 4, Application US/08599455B
Patent No. 5972621

GENERAL INFORMATION:

APPLICANT: Tarragilla, Louis A.
APPLICANT: Tepper, Robert J.
APPLICANT: Calpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkiojohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-4

Query Match 100.0%; Score 6254; DB 2; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIOKFCVLLHMEFIVITAFNLSYPIFPMRKLSCMPNSTYDFLLPAGLSKNTS 60
DB 1 MIOKFCVLLHMEFIVITAFNLSYPIFPMRKLSCMPNSTYDFLLPAGLSKNTS 60
QY 61 NGHETAVEPKFNSGTHSNLSKTTFHCCFRSEODRNCSLADNIEGKTFVTSVLV 120
DB 61 NGHETAVEPKFNSGTHSNLSKTTFHCCFRSEODRNCSLADNIEGKTFVTSVLV 120
QY 121 QOQDAMNIOCMKGLDKLFCVSESLFKLFRNNYKVVLLVLEPLVEDSLPVOKS 180
DB 121 QOQDAMNIOCMKGLDKLFCVSESLFKLFRNNYKVVLLVLEPLVEDSLPVOKS 180
QY 181 FQVHNCNSVHECCCLVPPVPAKNDTLMLCKITSGVIFQSPILMSVQPIKMKRDP 240
DB 181 FQVHNCNSVHECCCLVPPVPAKNDTLMLCKITSGVIFQSPILMSVQPIKMKRDP 240
QY 241 LGIHMETTDGDKLKISWSPPLVPPLOVOYKTSNSTTVIRADKIVSATSLVDSILP 300
DB 241 LGIHMETTDGDKLKISWSPPLVPPLOVOYKTSNSTTVIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRGKRLDGPFGMSDMSTPRVFTTODVIFPPKLTISVGSNVSPHCYKKEK 360
DB 301 GSSYEVOVRGKRLDGPFGMSDMSTPRVFTTODVIFPPKLTISVGSNVSPHCYKKEK 360
QY 361 VPSKEIWMNMNLAEKIPQSOYDVSDVSKVTFPNLNETPKRGKFTYDAVCCNECHH 420
DB 361 VPSKEIWMNMNLAEKIPQSOYDVSDVSKVTFPNLNETPKRGKFTYDAVCCNECHH 420
QY 421 RVAEIYVIDVNIINISCTEDGYLTAKMCRNSTSTYQSLAESTLOLRHRSLSYCDIPSH 480
DB 421 RVAEIYVIDVNIINISCTEDGYLTAKMCRNSTSTYQSLAESTLOLRHRSLSYCDIPSH 480
QY 481 PISEPKDYQSDGFECEJFOPFELLSGYTMMIRINHSIGSLDPSPTCYLPDSVPLRP 540
DB 481 PISEPKDYQSDGFECEJFOPFELLSGYTMMIRINHSIGSLDPSPTCYLPDSVPLRP 540
QY 541 SSYKAEITINIGLKIISWEKPVPENNLOFOIRYGLSGKEVQKMYEYDAKSKSYL 600
DB 541 SSYKAEITINIGLKIISWEKPVPENNLOFOIRYGLSGKEVQKMYEYDAKSKSYL 600
QY 601 PDLCAVYAVOVRKRLDGLGYMSNPNPAYVMDIKVPRGPEFRRIINGDPMKKEKNV 660
DB 601 PDLCAVYAVOVRKRLDGLGYMSNPNPAYVMDIKVPRGPEFRRIINGDPMKKEKNV 660
QY 661 TLAKMPLMKNDLSQVORYINHTSCNGTWSGSDVGNHRTFTFLMEQOAHVTVLAINSI 720
DB 661 TLAKMPLMKNDLSQVORYINHTSCNGTWSGSDVGNHRTFTFLMEQOAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSVNIYVSLAYPLNSCVIYSWILSPSDYKLMFIEEMKLNED 780
DB 721 GASVANFNLTFSWPMKSVNIYVSLAYPLNSCVIYSWILSPSDYKLMFIEEMKLNED 780
QY 781 GEIKMLRISSSVAKYIHHFPIEIKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKMLRISSSVAKYIHHFPIEIKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLVYIPIVLISSIIILGLTLLSHORMKLFMEDVNPKNCSAOGNLNOKPTEFHLPT 900
DB 841 GLVYIPIVLISSIIILGLTLLSHORMKLFMEDVNPKNCSAOGNLNOKPTEFHLPT 900
QY 901 KHTASVTCGPLLEPTEI SEDISVDTSMKNDKEMPTTVVSLSTDLKSGVCIQDQFN 960
DB 901 KHTASVTCGPLLEPTEI SEDISVDTSMKNDKEMPTTVVSLSTDLKSGVCIQDQFN 960

QY 961 SYNSEAECTEYTYEDESOROPFVKYATLISNSKPSGTGEQGLINSVTKCFSSKN SPL 1020
DB 961 SYNSEAECTEYTYEDESOROPFVKYATLISNSKPSGTGEQGLINSVTKCFSSKN SPL 1020
QY 1021 KOSFSSSWETFAQAFIISDQHPNIIISPHLTFSEGLDELKLEGNFPPENNDKKSIYLL 1080
DB 1021 KOSFSSSWETFAQAFIISDQHPNIIISPHLTFSEGLDELKLEGNFPPENNDKKSIYLL 1080
QY 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 GYTSIKKRESGVLLTDKSRVSCFPAPCFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFOTCSTQHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQHKIMENKMDLTV 1165

RESULT 2

US-09-069-781B-4
Sequence 4, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-069-781B-4

Query Match 100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MICOKFCVLLHMEFIYITAFNLSTPTTPWRFKLSGMPNSTYDYELPLAGLSKNTSNS 60
DB 1 MICOKFCVLLHMEFIYITAFNLSTPTTPWRFKLSGMPNSTYDYELPLAGLSKNTSNS 60
QY 61 NGHETAVEPEKFNSSGTHFSNLSTPHCCFRSDQDRNCSLCAQNIHGKTFVSVNSLVF 120
DB 61 NGHETAVEPEKFNSSGTHFSNLSTPHCCFRSDQDRNCSLCAQNIHGKTFVSVNSLVF 120
QY 121 QOIDANNIQCWLKGDILKFLTCYVESLFKNLFRNRYNKHLLVLPVLEDSPLVPQGS 180
DB 121 QOIDANNIQCWLKGDILKFLTCYVESLFKNLFRNRYNKHLLVLPVLEDSPLVPQGS 180
QY 181 FOMVHCNSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMWKDPDP 240
DB 181 FOMVHCNSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMWKDPDP 240
QY 241 LGHMEITDDGNLKISWSSPLVPPLQYQVKSSENSTTVIRADKIVSATSLVDSILP 300
DB 241 LGHMEITDDGNLKISWSSPLVPPLQYQVKSSENSTTVIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGGIWSDMSTPRVFTQDYIYFPFKILTVGSVNSFHCITYKKEKNT 360
DB 301 GSSYEVOVGRKRLDGGIWSDMSTPRVFTQDYIYFPFKILTVGSVNSFHCITYKKEKNT 360
QY 361 VPSKEIYVMNNLAEKIPQSQDYDVSDHVSQVTFENLNETPRGKFTYDAYCCNEHECHH 420
DB 361 VPSKEIYVMNNLAEKIPQSQDYDVSDHVSQVTFENLNETPRGKFTYDAYCCNEHECHH 420
QY 421 RYVELVIVDNNINISCTDGYLTKMTCRMSSTSTQSLAESTLQLRHRSLSYCSDDIPSIH 480
DB 421 RYVELVIVDNNINISCTDGYLTKMTCRMSSTSTQSLAESTLQLRHRSLSYCSDDIPSIH 480
QY 481 PISEPRDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGSDSPPTCVLPDSVNAPLPP 540
DB 481 PISEPRDCYLOSDFEYECIFQPIFILSGYTMIRINHSLSGSDSPPTCVLPDSVNAPLPP 540
QY 541 SSKVKEITINIGLKISWEKPVFPENNLOFQIRYGLSGREYQMKATEVYDAKSQSVSLPV 600
DB 541 SSKVKEITINIGLKISWEKPVFPENNLOFQIRYGLSGREYQMKATEVYDAKSQSVSLPV 600
QY 601 PDLCAVYAVOVCKRLDGGIWSMNSNPAYVYVMDIKVPMRGPETVRILINGDTMKKEKAV 660
DB 601 PDLCAVYAVOVCKRLDGGIWSMNSNPAYVYVMDIKVPMRGPETVRILINGDTMKKEKAV 660
QY 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWSDEDVGNHTKFFLMTQAHYTVLAINSI 720
DB 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWSDEDVGNHTKFFLMTQAHYTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNNSCVIVSWILSPSDYKLMFLIEMKNLMD 780
DB 721 GASVANFNLTFSWPMKSNIVQSLAYPLNNSCVIVSWILSPSDYKLMFLIEMKNLMD 780
QY 781 GEIKMLRISSSVKRYIHDFPIPKYQFSLYPIRMEGVGPKIINSTODDIEKHQSDA 840
DB 781 GEIKMLRISSSVKRYIHDFPIPKYQFSLYPIRMEGVGPKIINSTODDIEKHQSDA 840
QY 841 GLYIVAVPIISSLILGLTLLSHQRMKLLFWEDEVNPNKNSWAGLNFQRPETFEHFLI 900
DB 841 GLYIVAVPIISSLILGLTLLSHQRMKLLFWEDEVNPNKNSWAGLNFQRPETFEHFLI 900
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QY 901 KHTASVTCGPLLEPETISEDITSYTSKKNKDEMPPTVVSLSSTDLKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPETISEDITSYTSKKNKDEMPPTVVSLSSTDLKSGVCSIDQFN 960
QY 961 SVNFSEAGTEVTEYEDESQOPFVKYATLISNSKPSSTGEQGLINSVTKCFSSKNSPL 1020
DB 961 SVNFSEAGTEVTEYEDESQOPFVKYATLISNSKPSSTGEQGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNWEIEAOFILSDQHPNIIISPHJFSEGLDELLKLEGFPEPNNDKSIYYL 1080
DB 1021 KDSFNSNWEIEAOFILSDQHPNIIISPHJFSEGLDELLKLEGFPEPNNDKSIYYL 1080
QY 1081 GVSISIKKREGSVLLTQKSRVSCFPAPCLFTDRIVLQDSCSHVYENNINIGTSKTFPAS 1140
DB 1081 GVSISIKKREGSVLLTQKSRVSCFPAPCLFTDRIVLQDSCSHVYENNINIGTSKTFPAS 1140
QY 1141 YMFQFQCTSTQTHKIMENKMDLTV 1165
DB 1141 YMFQFQCTSTQTHKIMENKMDLTV 1165
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RESULT 3

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US-09-093-814-1
; Sequence 1, Application US/09093814
; Patent No. 6270981
; GENERAL INFORMATION:
; APPLICANT: Carpenter et al.
; TITLE OF INVENTION: ASSAY SYSTEMS FOR LEPTIN-ENHANCING AGENTS
; FILE REFERENCE: REG 580-A
; CURRENT APPLICATION NUMBER: US/09/093,814
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/049,108
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-093-814-1
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Query Match 99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICOKFCVLLHMEFIYITAFNLSTPTTPWRFKLSGMPNSTYDYELPLAGLSKNTSNS 60
DB 1 MICOKFCVLLHMEFIYITAFNLSTPTTPWRFKLSGMPNSTYDYELPLAGLSKNTSNS 60
QY 61 NGHETAVEPEKFNSSGTHFSNLSTPHCCFRSDQDRNCSLCAQNIHGKTFVSVNSLVF 120
DB 61 NGHETAVEPEKFNSSGTHFSNLSTPHCCFRSDQDRNCSLCAQNIHGKTFVSVNSLVF 120
QY 121 QOIDANNIQCWLKGDILKFLTCYVESLFKNLFRNRYNKHLLVLPVLEDSPLVPQGS 180
DB 121 QOIDANNIQCWLKGDILKFLTCYVESLFKNLFRNRYNKHLLVLPVLEDSPLVPQGS 180
QY 181 FOMVHCNSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMWKDPDP 240
DB 181 FOMVHCNSVHECCCECLVPPTAKLNDTLMLCKITSGVIFQSPILMSVOPIMWKDPDP 240
QY 241 LGHMEITDDGNLKISWSSPLVPPLQYQVKSSENSTTVIRADKIVSATSLVDSILP 300
DB 241 LGHMEITDDGNLKISWSSPLVPPLQYQVKSSENSTTVIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGGIWSDMSTPRVFTQDYIYFPFKILTVGSVNSFHCITYKKEKNT 360
DB 301 GSSYEVOVGRKRLDGGIWSDMSTPRVFTQDYIYFPFKILTVGSVNSFHCITYKKEKNT 360
QY 361 VPSKEIYVMNNLAEKIPQSQDYDVSDHVSQVTFENLNETPRGKFTYDAYCCNEHECHH 420
DB 361 VPSKEIYVMNNLAEKIPQSQDYDVSDHVSQVTFENLNETPRGKFTYDAYCCNEHECHH 420
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QY 421 RYAEIYVIDVININISCEITDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIPSIH 480
DB 421 RYAEIYVIDVININISCEITDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIPSIH 480
QY 481 PISEKDCYLOSDFEYECIFOPIFLLSGTYTWMIRINHSLGSDSPPTCYLPDSVYKPLPP 540
DB 481 PISEKDCYLOSDFEYECIFOPIFLLSGTYTWMIRINHSLGSDSPPTCYLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKPVFEPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
DB 541 SSVKAEITINIGLTKISWEKPVFEPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
QY 601 POLCAVYAVQVBCRLDGLGYWSNMSNPAYTVVMDIKYMRGPFEWRJINGDTMKENNV 660
DB 601 POLCAVYAVQVBCRLDGLGYWSNMSNPAYTVVMDIKYMRGPFEWRJINGDTMKENNV 660
QY 661 TLKMPRLKNDLSQVORVYVNHHTSCNGTMSDYGNTKFTFLTEQAHTVYVLAINSI 720
DB 661 TLKMPRLKNDLSQVORVYVNHHTSCNGTMSDYGNTKFTFLTEQAHTVYVLAINSI 720
QY 721 GASVANFNLTFSMPKSVYVOSLSAYPLNSSCVYVSWILSPDKIMVFIEMKNLND 780
DB 721 GASVANFNLTFSMPKSVYVOSLSAYPLNSSCVYVSWILSPDKIMVFIEMKNLND 780
QY 781 GEIKMLRISSSVKYYIHDFPIPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
DB 781 GEIKMLRISSSVKYYIHDFPIPIEKYOFSLYPIFMEGVGKPKIINSFTODDIEKHOSDA 840
QY 841 GUYIVPYVYISSILLGLTLLSHOBKMLFEDVPRNRCNSWAGOLNOKRETEHLEFI 900
DB 841 GUYIVPYVYISSILLGLTLLSHOBKMLFEDVPRNRCNSWAGOLNOKRETEHLEFI 900
QY 901 KKTASVTCGPLLEPTEISEDIVDTSMKNKDEMMPTVYVSLSTTDLKSGVCSIDQFN 960
DB 901 KKTASVTCGPLLEPTEISEDIVDTSMKNKDEMMPTVYVSLSTTDLKSGVCSIDQFN 960
QY 961 SYNFSBAECTEYTYEDESOROPFVKYATLISNSKPSGTEGEOGLINSSVTKCFSSKNPDL 1020
DB 961 SYNFSBAECTEYTYEDESOROPFVKYATLISNSKPSGTEGEOGLINSSVTKCFSSKNPDL 1020
QY 1021 KQSFNSMSMEIEAOAFILISDQHPNITSPHLTFESGLDELKLEGNPEENNDRKSIYVL 1080
DB 1021 KQSFNSMSMEIEAOAFILISDQHPNITSPHLTFESGLDELKLEGNPEENNDRKSIYVL 1080
QY 1081 GVTSIKKRESGYLLTDKSRVSCPPAPCLFTDIRVLODSCSHFVENNINILGTSKKTFFAS 1140
DB 1081 GVTSIKKRESGYLLTDKSRVSCPPAPCLFTDIRVLODSCSHFVENNINILGTSKKTFFAS 1140
QY 1141 YAPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YAPQFOTCSTQTHKIMENKMDLTV 1165

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RESULT 4
US-08-618-957A-11
Sequence 11, Application US/08618957A
Patent No. 6355237

GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
APPLICANT: Snider, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA

```

ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-11

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Query Match 99.9%; Score 6246; DB 4; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICQFCVLLHMERITYTAFNLSPYTPWRFKSCMPNSTYVFLPGLSKNTNS 60
DB 1 MICQFCVLLHMERITYTAFNLSPYTPWRFKSCMPNSTYVFLPGLSKNTNS 60
QY 61 NGHYTEAPEKNSSGTFHSNLSKTFHCQFSEBDRNCSLCADIIEGKTFTVSNLSVF 120
DB 61 NGHYTEAPEKNSSGTFHSNLSKTFHCQFSEBDRNCSLCADIIEGKTFTVSNLSVF 120
QY 121 QOIDANMNIOCKADKLFTCYVESLFKNLFRNRYVHLLYVPEVLDSPLVPQGS 180
DB 121 QOIDANMNIOCKADKLFTCYVESLFKNLFRNRYVHLLYVPEVLDSPLVPQGS 180
QY 181 FQMVHCNCSVHECCCLVVPYPAKLNDTLMLCKITSGVIFQSPLMGVSOPINMYKPPDP 240
DB 181 FQMVHCNCSVHECCCLVVPYPAKLNDTLMLCKITSGVIFQSPLMGVSOPINMYKPPDP 240
QY 241 LGLHMEITDDGNLKISWSSPLVPPLOQYKYSNSTTVIREADKIYSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKISWSSPLVPPLOQYKYSNSTTVIREADKIYSATSLVDSILP 300
QY 301 GSSYEYQVGRKLDGPGIWSDMSTRVFTTQDVITPPKILTSVGSNVSFHCITYKKEKI 360
DB 301 GSSYEYQVGRKLDGPGIWSDMSTRVFTTQDVITPPKILTSVGSNVSFHCITYKKEKI 360
QY 361 VPSKEIYMMNLAEKIIPQSOYVDVSDHYSKYVFFNLNFKPGKRTYAVVCCNHECHH 420
DB 361 VPSKEIYMMNLAEKIIPQSOYVDVSDHYSKYVFFNLNFKPGKRTYAVVCCNHECHH 420
QY 421 RYAEIYVIDVININISCEITDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIPSIH 480
DB 421 RYAEIYVIDVININISCEITDGYLTAKMTCRMSTSTIOSLAESTLOLRHRSLSYCSIPSIH 480
QY 481 PISEKDCYLOSDFEYECIFOPIFLLSGTYTWMIRINHSLGSDSPPTCYLPDSVYKPLPP 540
DB 481 PISEKDCYLOSDFEYECIFOPIFLLSGTYTWMIRINHSLGSDSPPTCYLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKPVFEPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600
DB 541 SSVKAEITINIGLTKISWEKPVFEPENNLOFOIRYGLSGKEVOMKMEYVDASKSVSLPV 600

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Db 541 SSVKAEITINIGLILKISWEKPVPENNLOFQIRYGLSGKEVQKMEYVDAKSVSILPV 600
QY 601 PDLCAVYAVOVCKRLDGLGYWMSNPNPATYVMDIKVPMRGPEFRIRIINGDTMKKKNV 660
Db 601 PDLCAVYAVOVCKRLDGLGYWMSNPNPATYVMDIKVPMRGPEFRIRIINGDTMKKKNV 660
QY 661 TLMLKPLMKNDLSGVQRYVINHHHTSCNGTWSBDVGNHRTKFTPLMTEQAHVTVLAINSI 720
Db 661 TLMLKPLMKNDLSGVQRYVINHHHTSCNGTWSBDVGNHRTKFTPLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSCIVYISWILSPDYLKLMFTIEMKMLNED 780
Db 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSCIVYISWILSPDYLKLMFTIEMKMLNED 780
QY 781 GEIKMLRISSVKKYIHHFPIEIKYQSLPIFMEGKPKIINSFTQDDIEKHOSDA 840
Db 781 GEIKMLRISSVKKYIHHFPIEIKYQSLPIFMEGKPKIINSFTQDDIEKHOSDA 840
QY 841 GLYVYVPIVLISSILGLTLISHOAKMLFEDVNPKNCSMAOGLNFOKEBTEFHEI 900
Db 841 GLYVYVPIVLISSILGLTLISHOAKMLFEDVNPKNCSMAOGLNFOKEBTEFHEI 900
QY 901 KHTASTCGPLLEPTISSEDISVDTSMKNKDEMPETVVSILSTDLEKGSVCISDQFN 960
Db 901 KHTASTCGPLLEPTISSEDISVDTSMKNKDEMPETVVSILSTDLEKGSVCISDQFN 960
QY 961 SVNFEAEGETEYVDESOQOPFVKYATLISNSKPSSETGEQGLINSVTKCFSSKNPL 1020
Db 961 SVNFEAEGETEYVDESOQOPFVKYATLISNSKPSSETGEQGLINSVTKCFSSKNPL 1020
QY 1021 KQSFSSSMEIEQAFFILSDQHPNITSPHITSEGLDELKLEGFPENNNKKSIYYL 1080
Db 1021 KQSFSSSMEIEQAFFILSDQHPNITSPHITSEGLDELKLEGFPENNNKKSIYYL 1080
QY 1081 GVSIRKREGVLLTQKSRVSCFPAPCLFTDIRVLQDSCHFVENNINLGTSKKTFFAS 1140
Db 1081 GVSIRKREGVLLTQKSRVSCFPAPCLFTDIRVLQDSCHFVENNINLGTSKKTFFAS 1140
QY 1141 YMFQOTCSTQTHKIMENKCDLTV 1165
Db 1141 YMFQOTCSTQTHKIMENKCDLTV 1165

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RESULT 5
US-08-640-389A-11
Sequence 11, Application US/08640389A
Patent No. 5912123
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clofifi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEPTIN
TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

```

; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-640-389A-11

```

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Query Match          98.7% Score 6172; DB 2; Length 1165;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1155; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

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QY 1 MICOKECVLLHMEFIYVTAENLSYPIPNRFRKLSCEPNSYDYFLPAGLSKNTS 60
Db 1 MICOKECVLLHMEFIYVTAENLSYPIPNRFRKLSCEPNSYDYFLPAGLSKNTS 60
QY 61 NGHETAVPEKINSSTGTHPSNLSTKTHFCCFSSBDQDRNCLADNIEGTFVYSNLSVF 120
Db 61 NGHETAVPEKINSSTGTHPSNLSTKTHFCCFSSBDQDRNCLADNIEGTFVYSNLSVF 120
QY 121 OQIDANMNIOCMKGLDKLFICYVESLFRNLFRNRYKVKHLLVYLPEVLEDSPLVPQKS 180
Db 121 OQIDANMNIOCMKGLDKLFICYVESLFRNLFRNRYKVKHLLVYLPEVLEDSPLVPQKS 180
QY 181 FQVHNCVSHHECECLVVPYPAKLDNLLMCLITSGGVIFQSPPLMSYQPTNMYKPDPP 240
Db 181 FQVHNCVSHHECECLVVPYPAKLDNLLMCLITSGGVIFQSPPLMSYQPTNMYKPDPP 240
QY 241 LGIHMETTDGNIKISMSPLVPPLOYOVKSENSTVIREADKIVATSLSYDSTLP 300
Db 241 LGIHMETTDGNIKISMSPLVPPLOYOVKSENSTVIREADKIVATSLSYDSTLP 300
QY 301 GSSYEVOVGKRLDGPISMDMSTPRVFTQDIYPPKILTVSGSNVSHCIYKKNKT 360
Db 301 GSSYEVOVGKRLDGPISMDMSTPRVFTQDIYPPKILTVSGSNVSHCIYKKNKT 360
QY 361 VPSKEIYVMMNLAETIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
Db 361 VPSKEIYVMMNLAETIPQSOYDVSDHVSQVTFENLNETKPRGKFTYDAVYCCNEHECH 420
QY 421 RVAKELVIDVNIINISQETDGYLTKMCRWSTSTIOSLAESTTOLRYHRSLSYCSDIPIH 480
Db 421 RVAKELVIDVNIINISQETDGYLTKMCRWSTSTIOSLAESTTOLRYHRSLSYCSDIPIH 480
QY 481 PISEPKDYLOSDFEETIFQPIFLLSGYTMIRINHSLSLSDSPPTCVLPDSVAPLPP 540
Db 481 PISEPKDYLOSDFEETIFQPIFLLSGYTMIRINHSLSLSDSPPTCVLPDSVAPLPP 540
QY 541 SSVKAEITINIGLILKISWEKPVPENNLOFQIRYGLSGKEVQKMEYVDAKSVSILPV 600
Db 541 SSVKAEITINIGLILKISWEKPVPENNLOFQIRYGLSGKEVQKMEYVDAKSVSILPV 600
QY 601 PDLCAVYAVOVCKRLDGLGYWMSNPNPATYVMDIKVPMRGPEFRIRIINGDTMKKKNV 660
Db 601 PDLCAVYAVOVCKRLDGLGYWMSNPNPATYVMDIKVPMRGPEFRIRIINGDTMKKKNV 660
QY 661 TLMLKPLMKNDLSGVQRYVINHHHTSCNGTWSBDVGNHRTKFTPLMTEQAHVTVLAINSI 720
Db 661 TLMLKPLMKNDLSGVQRYVINHHHTSCNGTWSBDVGNHRTKFTPLMTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSCIVYISWILSPDYLKLMFTIEMKMLNED 780
Db 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSCIVYISWILSPDYLKLMFTIEMKMLNED 780

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QY 781 GEIKMLRISSVKKYYIHDFIPIEKYQSLYIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSVKKYYIHDFIPIEKYQSLYIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVYIISILLGLTLLSHQRMKLFMEDVNPKNCSMAOGLNFOKPEFHEHFI 900
DB 841 GLYIVPVYIISILLGLTLLSHQRMKLFMEDVNPKNCSMAOGLNFOKPEFHEHFI 900
QY 901 KHNASTCGPILLEPETHISDIDSVTSMKNKDEMPITVYSLSTDLKSGVCIQSDQEN 960
DB 901 KHNASTCGPILLEPETHISDIDSVTSMKNKDEMPITVYSLSTDLKSGVCIQSDQEN 960
QY 961 SVNFSAEGETVYEDDESORQPEVYKATILINSKPSGTGEQGLINSVYTKPSKNSPL 1020
DB 961 SVNFSAEGETVYEDDESORQPEVYKATILINSKPSGTGEQGLINSVYTKPSKNSPL 1020
QY 1021 KQFSNMSWEIEQAFFILSDOHNIISPHLTSEGLDELKLEGNFPEENNDKKSIIYL 1080
DB 1021 KQFSNMSWEIEQAFFILSDOHNIISPHLTSEGLDELKLEGNFPEENNDKKSIIYL 1080
QY 1081 GYTSIKRRSGVLLTDKSRVSCPAPCLFTDIRVQDSCSHFVENNINLGTSSKTFAS 1140
DB 1081 GYTSIKRRSGVLLTDKSRVSCPAPCLFTDIRVQDSCSHFVENNINLGTSSKTFAS 1140
QY 1141 YMPQFQTCSTQ-THKIMENKMDLV 1165
DB 1141 YMPQFQTCSTQTHKIME-KMCDLV 1165

RESULT 6

US-08-618-957A-8
Sequence 8, Application US/08618957A
Patent No. 6355237

GENERAL INFORMATION:

APPLICANT: Shodgrass, H. Ralph
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas Joel
TITLE OF INVENTION: METHODS FOR USING THE OBESSE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 008907-0033-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 958 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-618-957A-8

Query Match 77.1%; Score 4819.5; DB 4; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MLCQKCVVLLMEFYITTAENLSIPTPMKPKLSCMPNSTYDFLLPAGLSKRTS 60
DB 1 MLCQKCVVLLMEFYITTAENLSIPTPMKPKLSCMPNSTYDFLLPAGLSKRTS 60
QY 61 NGHETAVPEPKNSSGTTHSNLSKTFHCCCFSEODRNCSLCADNIEGTFVTVSLVF 120
DB 61 NGHETAVPEPKNSSGTTHSNLSKTFHCCCFSEODRNCSLCADNIEGTFVTVSLVF 120
QY 121 QOIDANMNIQCMKGDJLFCYVESLEKRLFRNRYKVHLLVLEVEDSPVLPQKS 180
DB 121 QOIDANMNIQCMKGDJLFCYVESLEKRLFRNRYKVHLLVLEVEDSPVLPQKS 180
QY 181 FQWVHCNCSVHCECECLVVPYPAKINDTLLMCLKITSGGVITQSPIMSVQPIIMVAPDP 240
DB 181 FQWVHCNCSVHCECECLVVPYPAKINDTLLMCLKITSGGVITQSPIMSVQPIIMVAPDP 240
QY 241 LGLHMEITDGNLKLISMSSPPLVPFPLOQVYSENSTVIREADKIVATSILVDSILP 300
DB 241 LGLHMEITDGNLKLISMSSPPLVPFPLOQVYSENSTVIREADKIVATSILVDSILP 300
QY 301 GSSYEYQVGRKRLDGPGLMSDMSSTPRVFTTODVYIFPRKILTSVGSNVSFHCITKKENKI 360
DB 301 GSSYEYQVGRKRLDGPGLMSDMSSTPRVFTTODVYIFPRKILTSVGSNVSFHCITKKENKI 360
QY 361 VSKKEIVMMNLAEKIPQSOYDVSDHVSQVTFENLNEKPRGKFTYDAVYCNEHECH 420
DB 361 VSKKEIVMMNLAEKIPQSOYDVSDHVSQVTFENLNEKPRGKFTYDAVYCNEHECH 420
QY 421 RYAEIVYDVNINISCEVDGYLTKMTGRWSTSTIOSLASTQRLRYHNSLSYCSIDPSIH 480
DB 421 RYAEIVYDVNINISCEVDGYLTKMTGRWSTSTIOSLASTQRLRYHNSLSYCSIDPSIH 480
QY 481 PISEPRDCYLOSDGFECELFQPIFLLSGTWMTIRHNSIGSLDSPCTCLPDSVYKPLP 540
DB 481 PISEPRDCYLOSDGFECELFQPIFLLSGTWMTIRHNSIGSLDSPCTCLPDSVYKPLP 540
QY 541 SSVKAEITINIGLKLISWEKPVPEENLOFOIRYGLSGKEVOMKMEVDASKSVSLPV 600
DB 541 SSVKAEITINIGLKLISWEKPVPEENLOFOIRYGLSGKEVOMKMEVDASKSVSLPV 600
QY 601 PDLCAVYAVQVRCRRLDGLGYSNMSNPAYTVVMDIKVPMRGPPEMRTIINGDTMKKEKV 660
DB 601 PDLCAVYAVQVRCRRLDGLGYSNMSNPAYTVVMDIKVPMRGPPEMRTIINGDTMKKEKV 660
QY 661 TLLMKPLMKNDLSQVQRYVINHHNHSNGTWSGDNHKKFFLMEQAHVTVLAINSI 720
DB 661 TLLMKPLMKNDLSQVQRYVINHHNHSNGTWSGDNHKKFFLMEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVINVOISLAVPLNSSCVIYSWLTSDDYKLMFIEMKNLND 780
DB 721 GASVANFNLTFSMPMSKVINVOISLAVPLNSSCVIYSWLTSDDYKLMFIEMKNLND 780
QY 781 GEIKMLRISSVKKYYIHDFIPIEKYQSLYIFMEGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKMLRISSVKKYYIHDFIPIEKYQSLYIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYIVPVYIISILLGLTLLSHQRMKLFMEDVNPKNCSMAOGLNFOKPEFHEHFI 900
DB 841 GLYIVPVYIISILLGLTLLSHQRMKLFMEDVNPKNCSMAOGLNFOKPEFHEHFI 900
QY 894 TFEHLFIKHT-ASYVCGP-----LLEPETISDIDVTSMKNKDE 933
DB 901 SHHSLISSTQGHKHCGRQGPLHKKTRDLCGLVYLLTLPILSLDPAKSPSVKRTQ 958

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RESULT 7
US-08-355-888A-8
; Sequence 8, Application US/08355888A
; Patent No. 5763211
;
GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8884
;
TELEX: 66141 PENNIE
;
INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
US-08-355-888A-8

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Query Match          77.1% Score 4819.5; DB 1; Length 960;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

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QY 1 MICOKECVLLHMEFIYVTAANLSYPIPWPKLSKMPNSTYDFLLPAGLSKMTSNS 60
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QY 121 QOQIDANMNQCKLKGDKLFICYVESLFKNLFNNYKYLHLLVLEVELEDSPLVQKGS 180
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DB 123 QOQIDANMNQCKLKGDKLFICYVESLFKNLFNNYKYLHLLVLEVELEDSPLVQKGS 182
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DB 243 LGLHMEITDGNLKLISWSSPPLVPPLOYOVKXSENSSTVIREADKIVATSLSLVD 302
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QY 301 GSSYEVOVGKRLDGPGLMSDMSSTPRVFTTQVYIYPPKILTSVGSNVSFHCILYK 360
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DB 303 GSSYEVOVGKRLDGPGLMSDMSSTPRVFTTQVYIYPPKILTSVGSNVSFHCILYK 362
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DB 363 VPSKEIVMMNNIAEKIPQSOQDVYSDHVSQVTFPNLNETKPRCKFTYDAVYCCNEHECH 422
   |||||
QY 421 RAELVIVIDVNNISCEPQGYLTKMCRWSTSTIQLAESTLQLRHRSLSYSDIPSTH 480
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QY 541 SSVKABITINIGLKLISWEKPVFPENNLOFQIRYGLSGKEVOKMYEYVDAKSKSVSLPV 600
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DB 543 SSVKABITINIGLKLISWEKPVFPENNLOFQIRYGLSGKEVOKMYEYVDAKSKSVSLPV 602
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QY 601 PDLCAVYAVOVRCKRLDGLGYMSNMSPAYTYVMDIKVPRGEPFRITINGDTMKREKV 660
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QY 661 TLMLKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTPLMTEQAHVYVLAINSI 720
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DB 663 TLMLKPLMKNDLSQVQRYVINHTSCNGTWSSEVGNHTKFTPLMTEQAHVYVLAINSI 722
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QY 721 GASVANENLTFSPWPMKSVNIYQSLASVPLNSSCVIYSWILSPSDYKLMFTIEKMNMD 780
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DB 723 GASVANENLTFSPWPMKSVNIYQSLASVPLNSSCVIYSWILSPSDYKLMFTIEKMNMD 782
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QY 781 GEIKMLRISSVKKYIYHDFITEKYOSLPIFMEGKPKIINSFQODDIEKHQSDA 840
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DB 783 GEIKMLRISSVKKYIYHDFITEKYOSLPIFMEGKPKIINSFQODDIEKHQSDA 842
   |||||
QY 841 GLYIVPVIISSIIILGTLILSHQMKLIFMEDVNPKNCSAOGINTOK-----PE 893
   |||||
DB 843 GLYIVPVIISSIIILGTLILSHQMKLIFMEDVNPKNCSAOGINTOK-----PE 902
   |||||
QY 894 TFEHLFIKHT-ASVTGP-----LLLEPITISEDIVDTSKNDE 933
   |||||
DB 903 SHHSLISSQGHKHCGRPGPLHRKTRDCLSLVLTLPPLISYDPAKSPSVRNQ 960
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```

```

RESULT 8
US-08-693-697-8
; Sequence 8, Application US/08693697
; Patent No. 5869610
;
GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0b
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.

```

REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-0037-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-693-697-8

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIYITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTSNS 60
 DB 3 MICQKFCVLLHMEFIYITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTSNS 62
 QY 61 NGHYTEAEPKNSSGTHFSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVE 120
 DB 63 NGHYTEAEPKNSSGTHFSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVE 122
 QY 121 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180
 DB 123 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 182
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 DB 183 PQMHVHCNSVHECCCECLVPPPAKLNDTLMLCLKITSQGVITQSPPLMSVQPINMKKDPDP 242
 QY 241 LGLHMEITPDGKLTSMSSPPLVPLOYQVYSENSTVIREADKIYATSLDVSILP 300
 DB 243 LGLHMEITPDGKLTSMSSPPLVPLOYQVYSENSTVIREADKIYATSLDVSILP 302
 QY 301 GSSYEVOVGRKRLDGPGLMSDSTPRVFTTQDVLYFPFKILT SVGSNVSFHCITKKENKI 360
 DB 303 GSSYEVOVGRKRLDGPGLMSDSTPRVFTTQDVLYFPFKILT SVGSNVSFHCITKKENKI 362
 QY 361 VSKETLYMMANLAETIPQSQDYVSDHYSKVTFENLNKPRGKFTYDAVYCCNEHECHH 420
 DB 363 VSKETLYMMANLAETIPQSQDYVSDHYSKVTFENLNKPRGKFTYDAVYCCNEHECHH 422
 QY 421 RAELIYVIDVNNINISCEITGTYLTKMCRMSTSTIOSLAESTQLRHRSLVCSIDPSIH 480
 DB 423 RAELIYVIDVNNINISCEITGTYLTKMCRMSTSTIOSLAESTQLRHRSLVCSIDPSIH 482
 QY 481 PISEPKDYLQSDGFECIFQPIFLLSGYTMMIRINHSIGLSDSPPTCVLPDSVVKPLRP 540
 DB 483 PISEPKDYLQSDGFECIFQPIFLLSGYTMMIRINHSIGLSDSPPTCVLPDSVVKPLRP 542
 QY 541 SSVKAEITINILKLTSMKRPVPENNDLOFQIRGLSGEVOVMKRYEVDASKSVSLPV 600
 DB 543 SSVKAEITINILKLTSMKRPVPENNDLOFQIRGLSGEVOVMKRYEVDASKSVSLPV 602
 QY 601 PULCAVYAQVQCKRLDGLGYTWSNNSNPAYTVVMDIKVPMRQPEFRRIINGCTMKKEKRV 660
 DB 603 PULCAVYAQVQCKRLDGLGYTWSNNSNPAYTVVMDIKVPMRQPEFRRIINGCTMKKEKRV 662
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 DB 663 TLIMKPLKNDLSQVQRYVYINHTSCNGTWSQEDVGNHTKFTFLMTEQAHYTVVLAINSI 722
 QY 721 GASVANFNLTFSMPKSVIIVOSLSATPLNNSCVIYSLSLSDVKLKLFIIEKMLNLD 780
 DB 723 GASVANFNLTFSMPKSVIIVOSLSATPLNNSCVIYSLSLSDVKLKLFIIEKMLNLD 782
 QY 781 GEIKWLRISSVKKYIYIHDFPIEKYQSLYPIFMEGVGKKIINSTFQODDIEKHQSDA 840

DB 783 GEIKWLRISSVKKYIYIHDFPIEKYQSLYPIFMEGVGKKIINSTFQODDIEKHQSDA 842
 QY 841 GLYVIVPVISSSILLGLTLISHQRMKLFWEVDYPNPKNSWAGLNFOR-----PE 893
 DB 843 GLYVIVPVISSSILLGLTLISHQRMKLFWEVDYPNPKNSWAGLNFORKLESMFYK 902
 QY 894 TFEHLFIKHT-ASVTCGP-----LLLEPETISDIDVDSWKAKDE 933
 DB 903 SHNHSLISTQGHKKGCRPGQGLHRRKTRDLSYLVLTLPLLSYDPAKSPSVNRTOE 960

RESULT 9
 US-08-640-389A-3
 Sequence 3, Application US/08640389A
 Patent No. 5912123

GENERAL INFORMATION:
 APPLICANT: Snodgrass, H. R.
 APPLICANT: Cioffi, Joseph
 APPLICANT: Zupancic, Thomas J.
 APPLICANT: Shater, Alan W.
 TITLE OF INVENTION: DETECTION OF THE LEPTIN
 TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
 TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/640,389A
 FILING DATE: 29-APR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M.
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-032

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-640-389A-3

Query Match 77.1%; Score 4819.5; DB 2; Length 960;
 Best Local Similarity 94.1%; Pred. No. 0;
 Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

QY 1 MICQKFCVLLHMEFIYITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTSNS 60
 DB 3 MICQKFCVLLHMEFIYITAFNLSTPTPMRFKLSCMPNSTYDYFLLPAGLSKNTSNS 62
 QY 61 NGHYTEAEPKNSSGTHFSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVE 120
 DB 63 NGHYTEAEPKNSSGTHFSNLSKATFHCCFRSEODRNCSLCADNIEGTFVSTVNSLVE 122
 QY 121 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 180
 DB 123 QOIDANMNIOCKLKGDKLFICYVESLFKNLFRNRYKVVHLLVLPVLEDSPLVPQKGS 182


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OY 181 FQWVHCNCSVHECCCLVVPVPAKINDTLLMCLKITSGGVITFQSPPLMSVQPINMKVDPDP 240
DB 183 FQWVHCNCSVHECCCLVVPVPAKINDTLLMCLKITSGGVITFQSPPLMSVQPINMKVDPDP 242
OY 241 LGLHMETDGNLKITSMSSPPLVPPLQYQVYSENSTVIRADKIVATSILVDSILP 300
DB 243 LGLHMETDGNLKITSMSSPPLVPPLQYQVYSENSTVIRADKIVATSILVDSILP 302
OY 301 GSSYEVOVGRKLDGPGISDMSTPRVFTTQDYIYPPKILTVSGSNVSFHCYKKENKI 360
DB 303 GSSYEVOVGRKLDGPGISDMSTPRVFTTQDYIYPPKILTVSGSNVSFHCYKKENKI 362
OY 361 VPSKEIYVMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFYYDAVYCNEHECHH 420
DB 363 VPSKEIYVMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFYYDAVYCNEHECHH 422
OY 421 RYAEIYVIDVNNISCEOTGYLTKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
DB 423 RYAEIYVIDVNNISCEOTGYLTKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 482
OY 481 PISEPRDCYLOSDFEYECIFOPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 540
DB 483 PISEPRDCYLOSDFEYECIFOPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 542
OY 541 SSVKAEITINIGLKITSMKRPVPPENNLOPQIRYGLSGKEVOQMKAEVYDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLKITSMKRPVPPENNLOPQIRYGLSGKEVOQMKAEVYDAKSKSVSLPV 602
OY 601 PDLCAVAVOVRCKRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFRIINGDTMKREKNV 660
DB 603 PDLCAVAVOVRCKRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFRIINGDTMKREKNV 662
OY 661 TLLMRPLMKNDLSGVQYRVYINHHSTSCNGTWSDEDVGNHRTKFFLMTQAHVTVLAINSI 720
DB 663 TLLMRPLMKNDLSGVQYRVYINHHSTSCNGTWSDEDVGNHRTKFFLMTQAHVTVLAINSI 722
OY 721 GASVANENLTFEPMPSKVNIQSLSAVPLNSSCVIYSLISDSYDLAMFLIEMKMLND 780
DB 723 GASVANENLTFEPMPSKVNIQSLSAVPLNSSCVIYSLISDSYDLAMFLIEMKMLND 782
OY 781 GEIKMLRISSSVKYYIHDFPIEYQFSLYPIFMEGVGKPKIINSFYODDIEKQSDA 840
DB 783 GEIKMLRISSSVKYYIHDFPIEYQFSLYPIFMEGVGKPKIINSFYODDIEKQSDA 842
OY 841 GLYIVYPIVSISSILLGLTLLISHQMKLEFEDVYVNPKNCSWAQGLNFQKMLEGSMFYK 893
DB 843 GLYIVYPIVSISSILLGLTLLISHQMKLEFEDVYVNPKNCSWAQGLNFQKMLEGSMFYK 902
OY 894 TFEHLFIKHT-ASVTCGP-----LLEPTEISEDSVDTSKNKDE 933
DB 903 SHHSLISTQGHKMGKRGPOGPLHKKTRDCLSLVYLLTLPPLSLDPAKSPSVKNTQE 960

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; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,888
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-696-8

Query Match 77.1%; Score 4819.5; DB 3; Length 960;
Best Local Similarity 94.1%; Pred No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

OY 1 MICQKFCVYLLHMEFIYVTAENLSYPIPPWRKFLSCMPNNTYDYFLLPAGLSKMTSNS 60
DB 3 MICQKFCVYLLHMEFIYVTAENLSYPIPPWRKFLSCMPNNTYDYFLLPAGLSKMTSNS 62
OY 61 NGHYETAVERKPRSSSTHNSLSKTFHCCFRSEODRNCSLCADNIEGTFVSTVSLVF 120
DB 63 NGHYETAVERKPRSSSTHNSLSKTFHCCFRSEODRNCSLCADNIEGTFVSTVSLVF 122
OY 121 QQDAMNNIOCMKGLKLFICVSESLFKMLFRNYKYKVLVYLPEVLEDSPLVPOKGS 180
DB 123 QQDAMNNIOCMKGLKLFICVSESLFKMLFRNYKYKVLVYLPEVLEDSPLVPOKGS 182
OY 181 FQWVHCNCSVHECCCLVVPVPAKINDTLLMCLKITSGGVITFQSPPLMSVQPINMKVDPDP 240
DB 183 FQWVHCNCSVHECCCLVVPVPAKINDTLLMCLKITSGGVITFQSPPLMSVQPINMKVDPDP 242
OY 241 LGLHMETDGNLKITSMSSPPLVPPLQYQVYSENSTVIRADKIVATSILVDSILP 300
DB 243 LGLHMETDGNLKITSMSSPPLVPPLQYQVYSENSTVIRADKIVATSILVDSILP 302
OY 301 GSSYEVOVGRKLDGPGISDMSTPRVFTTQDYIYPPKILTVSGSNVSFHCYKKENKI 360
DB 303 GSSYEVOVGRKLDGPGISDMSTPRVFTTQDYIYPPKILTVSGSNVSFHCYKKENKI 362
OY 361 VPSKEIYVMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFYYDAVYCNEHECHH 420
DB 363 VPSKEIYVMNNIAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFYYDAVYCNEHECHH 422
OY 421 RYAEIYVIDVNNISCEOTGYLTKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 480
DB 423 RYAEIYVIDVNNISCEOTGYLTKMCRWSTSTIOSLAESTIOLRHRSSLYCSDIPSIH 482
OY 481 PISEPRDCYLOSDFEYECIFOPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 540
DB 483 PISEPRDCYLOSDFEYECIFOPIFLLSGYTMIRINHSIGSLDSPPTCVLPDSVVKPLP 542
OY 541 SSVKAEITINIGLKITSMKRPVPPENNLOPQIRYGLSGKEVOQMKAEVYDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLKITSMKRPVPPENNLOPQIRYGLSGKEVOQMKAEVYDAKSKSVSLPV 602
OY 601 PDLCAVAVOVRCKRLDGLGYWMSNMSNPAYTVVMDIKVPMRGPEFRIINGDTMKREKNV 660

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|||||
Db 603 PDLCAVYAVQVCKRLDGLGYSNNSNPAYTYVMDIKYMRGPFRRIINGDTMKKEKV 662
QY 661 TLLMPLKNDLSCVQRYVNHHTSCNGTSEDVGNHKTFTLMTBOAHVTYLAINSI 720
Db 663 TLLMPLKNDLSCVQRYVNHHTSCNGTSEDVGNHKTFTLMTBOAHVTYLAINSI 722
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFYIEMKNLND 780
Db 723 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFYIEMKNLND 782
QY 781 GEIKMLRISSVKKYYIHDFPIEKYQSLPIFMEYGKRIINSFQODIEKHQSDA 840
Db 783 GEIKMLRISSVKKYYIHDFPIEKYQSLPIFMEYGKRIINSFQODIEKHQSDA 842
QY 841 GLYIVIPVISSILLGLTLISHQRMKLFMEDVNPNCNCSMAOGLNFK-----PE 893
Db 843 GLYIVIPVISSILLGLTLISHQRMKLFMEDVNPNCNCSMAOGLNFKMLGSGMFK 902
QY 894 TEHLFIKHT-ASVTCGP-----LLEPETISEDIVDTSMKNKE 933
Db 903 SHHSLISTQGHKKGRCQGPLHRTKRDLCSLVYLTLPLLSYDPAKSPSVRNTOE 960
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RESULT 11
US-08-693-697-33
; Sequence 33, Application US/08693697
; Patent No. 5869610
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; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Clotfelter, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-693-697-33
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Query Match 77.0%; Score 4816; DB 2; Length 908;
Best Local Similarity 99.1%; Pred. No. 0;
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Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
QY 1 MICQKFCVLLHMERIYTTAFNLSPYIPMRFKLSCMPNSTDYDFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHMERIYTTAFNLSPYIPMRFKLSCMPNSTDYDFLLPAGLSKNTSNS 62
QY 61 NGHYETAVEPKFNSSGTHESNLKSTTFHCCFRSEODRNCCLCADNIEGTFVSTVNSLVF 120
Db 63 NGHYETAVEPKFNSSGTHESNLKSTTFHCCFRSEODRNCCLCADNIEGTFVSTVNSLVF 122
QY 121 QOIDANMNTOCMLKGDIKLFTCYVESLFRNNYKHLHYLPEVLEDSPLVPQKS 180
Db 123 QOIDANMNTOCMLKGDIKLFTCYVESLFRNNYKHLHYLPEVLEDSPLVPQKS 182
QY 181 FQMVHNCNSVHCCBCLVVPPTAKLNDTLMLCKITSGVIRQSPPLMSVQPIINMYKPPDP 240
Db 183 FQMVHNCNSVHCCBCLVVPPTAKLNDTLMLCKITSGVIRQSPPLMSVQPIINMYKPPDP 242
QY 241 LGLHMEITDDGMLKTSWSSPLVPPLOYQVYKSENSSTVIREADKIYASATSLVDSILP 300
Db 243 LGLHMEITDDGMLKTSWSSPLVPPLOYQVYKSENSSTVIREADKIYASATSLVDSILP 302
QY 301 GSSYEYQVGRKRLDGPGLTMDKSTPRVFTTODVITFPFKILTSVGSNVSFHCITYKKNKI 360
Db 303 GSSYEYQVGRKRLDGPGLTMDKSTPRVFTTODVITFPFKILTSVGSNVSFHCITYKKNKI 362
QY 361 VSKETIWMNMLAEKIPQSYDVSDHVKYTFEFLNLTETKPRGKFTYDAVYCNEHECHH 420
Db 363 VSKETIWMNMLAEKIPQSYDVSDHVKYTFEFLNLTETKPRGKFTYDAVYCNEHECHH 422
QY 421 RYAEIYVDVININICETDGYITKMTCKWSTSTIOSLABSTLOLRYHNSLYCSIDPSIH 480
Db 423 RYAEIYVDVININICETDGYITKMTCKWSTSTIOSLABSTLOLRYHNSLYCSIDPSIH 482
QY 481 PISEPRDCTLOSDFYECIFOPILFISGYTMIIRINHSIGSLDSPPTCYLPDSYKPLPP 540
Db 483 PISEPRDCTLOSDFYECIFOPILFISGYTMIIRINHSIGSLDSPPTCYLPDSYKPLPP 542
QY 541 SSVKAEITINILDLKISWEKPYFPENNLOFOIRYGLSGREYQMKYEVYDAKSYSILPV 600
Db 543 SSVKAEITINILDLKISWEKPYFPENNLOFOIRYGLSGREYQMKYEVYDAKSYSILPV 602
QY 601 PDLCAVYAVQVCKRLDGLGYSNNSNPAYTYVMDIKYMRGPFRRIINGDTMKKEKV 660
Db 603 PDLCAVYAVQVCKRLDGLGYSNNSNPAYTYVMDIKYMRGPFRRIINGDTMKKEKV 662
QY 661 TLLMPLKNDLSCVQRYVNHHTSCNGTSEDVGNHKTFTLMTBOAHVTYLAINSI 720
Db 663 TLLMPLKNDLSCVQRYVNHHTSCNGTSEDVGNHKTFTLMTBOAHVTYLAINSI 722
QY 721 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFYIEMKNLND 780
Db 723 GASVANFNLTFSMPMSKVINIYOSLSAYPLNSSCVIYSWILSPSDYKLMFYIEMKNLND 782
QY 781 GEIKMLRISSVKKYYIHDFPIEKYQSLPIFMEYGKRIINSFQODIEKHQSDA 840
Db 783 GEIKMLRISSVKKYYIHDFPIEKYQSLPIFMEYGKRIINSFQODIEKHQSDA 842
QY 841 GLYIVIPVISSILLGLTLISHQRMKLFMEDVNPNCNCSMAOGLNFK-----PETFEHL 898
Db 843 GLYIVIPVISSILLGLTLISHQRMKLFMEDVNPNCNCSMAOGLNFKMLGSGMFK 902
```

```
RESULT 12
US-08-588-190-3
; Sequence 3, Application US/08588190
; Patent No. 5856098
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Clotfelter, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
```

TITLE OF INVENTION: VARIANT AND METHODS FOR REGULATING OBESITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0029-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-190-3

Query Match 77.0%; Score 4814.5; DB 2; Length 960;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

QY 1 MCGQFCVYLLMEFYITVTAENLSPTTPMRPKLSGMPNNTYDFLLPAGISKTSTNS 60
DB 3 MCGQFCVYLLMEFYITVTAENLSPTTPMRPKLSGMPNNTYDFLLPAGISKTSTNS 62
QY 61 NCHYEFAVEPKFNSSGTHFSNLSKTFHCCFSEODRNCSLCADNTEGKTFVSTNSLVF 120
DB 63 NCHYEFAVEPKFNSSGTHFSNLSKTFHCCFSEODRNCSLCADNTEGKTFVSTNSLVF 122
QY 121 QOIDANWNIQCMILKGDILKFCYVESLFFKNLFRNRYKYVHLVYLPEVLDESPLYBQKGS 180
DB 123 QOIDANWNIQCMILKGDILKFCYVESLFFKNLFRNRYKYVHLVYLPEVLDESPLYBQKGS 182
QY 181 FQWVHCNCSVHCCCELVVPTAKLNDTLMLCLKITSGSVTFQSPILMSQPIINMVRPDP 240
DB 183 FQWVHCNCSVHCCCELVVPTAKLNDTLMLCLKITSGSVTFQSPILMSQPIINMVRPDP 242
QY 241 LGLHHEITDGMILKISWSPPPLVPFLOVQVYSENSTVIREADIVATSLLVDSILP 300
DB 243 LGLHHEITDGMILKISWSPPPLVPFLOVQVYSENSTVIREADIVATSLLVDSILP 302
QY 301 GSSYEYQVGRKLDGPGILSDWSTPRVFTTQDVLYEPFKILTSVGSNSVHFCIYKKENKI 360
DB 303 GSSYEYQVGRKLDGPGILSDWSTPRVFTTQDVLYEPFKILTSVGSNSVHFCIYKKENKI 362
QY 361 VSKKEIYVMMNLAEKIPQSQDYVSDVSKVTFENLNEFKPKRGKFTYDAVYCCNEHECHH 420
DB 363 VSKKEIYVMMNLAEKIPQSQDYVSDVSKVTFENLNEFKPKRGKFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVIVDNVINSCTDGYLTAKMCRWSTSTIOSLASTIQLARHRSLSVCSIDIPSIH 480
DB 423 RYAEIYVIVDNVINSCTDGYLTAKMCRWSTSTIOSLASTIQLARHRSLSVCSIDIPSIH 482

QY 481 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMIRINHSGLSDSPPTCYLPDSVYVPLPP 540
DB 483 PISEPKDCYLOSDFEYECIFOPIFLLSGYTMIRINHSGLSDSPPTCYLPDSVYVPLPP 542
QY 541 SSVKAEITTNIGLKITSMKPVFPENNLOPIRNYGLSGKEVQKMYEYDANKSVSLPV 600
DB 543 SSVKAEITTNIGLKITSMKPVFPENNLOPIRNYGLSGKEVQKMYEYDANKSVSLPV 602
QY 601 PDLCAVAYAVQVGRKLDGPGILSDWSTPRVFTTQDVLYEPFKILTSVGSNSVHFCIYKKENKI 660
DB 603 PDLCAVAYAVQVGRKLDGPGILSDWSTPRVFTTQDVLYEPFKILTSVGSNSVHFCIYKKENKI 662
QY 661 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQATVTLAINSI 720
DB 663 TLLMKPLMKNDLSQVQRYVINHTSCNGTSEDVGNHTKFTFLMTEQATVTLAINSI 722
QY 721 GASVANFNLTFSWPKNVINQSLAVPLNNSCVIYISWILSPSDYKLMFIIEMKMLND 780
DB 723 GASVANFNLTFSWPKNVINQSLAVPLNNSCVIYISWILSPSDYKLMFIIEMKMLND 782
QY 781 GEIKMLRISSVKKYIYHDFIPIEYQPSLYPIFMEGGRKPIINSFTQODIEKHQSDA 840
DB 783 GEIKMLRISSVKKYIYHDFIPIEYQPSLYPIFMEGGRKPIINSFTQODIEKHQSDA 842
QY 841 GLVYIVPVIISSILGLTLLISHQPMKLLFMEVDPNPKNSMAOGLNFQK-----PE 893
DB 843 GLVYIVPVIISSILGLTLLISHQPMKLLFMEVDPNPKNSMAOGLNFQKLEGSMPFK 902
QY 894 TPEHLEIKHT-ASVTCGP-----LLEPETISEIISVDTSKKNDE 933
DB 903 SHHSLISSTQGHKRGROGPLHRRTRDCLSLVLLTLPILLSTYDPAKSPVRNTOE 960

RESULT 13
US-08-618-957A-3
Sequence 3, Application US/08618957A
Patent No. 6355237
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. Ralph
APPLICANT: Clifton, Joseph
APPLICANT: Zupancic, Thomas Joel
TITLE OF INVENTION: METHODS FOR USING THE OBESITY
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,957A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 960 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-618-957A-3

Query Match 77.0%; Score 4814.5; DB 4; Length 960;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 900; Conservative 7; Mismatches 26; Indels 25; Gaps 3;

QY 1 MTCQKCVVLLHMEFYVTAENLSPITPWPRKLSKMPNSTYDYFLLPAGLSKNTSNS 60
 DB 3 MTCQKCVVLLHMEFYVTAENLSPITPWPRKLSKMPNSTYDYFLLPAGLSKNTSNS 62
 QY 61 NGHYEAVPEPKRSSGTHSNLSKTFHCCFSEODRNSCLADNIEGRTFVSTVNSLVF 120
 DB 63 NGHYEAVPEPKRSSGTHSNLSKTFHCCFSEODRNSCLADNIEGRTFVSTVNSLVF 122
 QY 121 QOIDANMNIOQWLKGDLEFICVESLFRNLFERNYKVALLYLVEVLEDSPLVPQKGS 180
 DB 123 QOIDANMNIOQWLKGDLEFICVESLFRNLFERNYKVALLYLVEVLEDSPLVPQKGS 182
 QY 181 FQWVHONGSVHECCCELVVPAKLDLMLCKITSGVIFQSPPLMSVQPTMMVPRDP 240
 DB 183 FQWVHONGSVHECCCELVVPAKLDLMLCKITSGVIFQSPPLMSVQPTMMVPRDP 242
 QY 241 LGLHMEITDDGNLKTSMSSPPLVPPLOQVKSSENSTVIREADKIVSATSLVDSILP 300
 DB 243 LGLHMEITDDGNLKTSMSSPPLVPPLOQVKSSENSTVIREADKIVSATSLVDSILP 302
 QY 301 GSSEYQVQVGRKLDGPGIISDMSTPRVFTTODVYIFPPKILTSVGSVNSFHCITYKENKI 360
 DB 303 GSSEYQVQVGRKLDGPGIISDMSTPRVFTTODVYIFPPKILTSVGSVNSFHCITYKENKI 362
 QY 361 VPSKETVMMNLAEKIPQSOYDVSDHVSQVPPENLNENKPRCKFYDDAVCCNEHCCH 420
 DB 363 VPSKETVMMNLAEKIPQSOYDVSDHVSQVPPENLNENKPRCKFYDDAVCCNEHCCH 422
 QY 421 RAELVVIDVNNINISCEITDGYLTAKMCRWSTSTIQSLASTIQLRYHRSLSYCSIDIPSIH 480
 DB 423 RAELVVIDVNNINISCEITDGYLTAKMCRWSTSTIQSLASTIQLRYHRSLSYCSIDIPSIH 482
 QY 481 PISEPRDCLQSDGFECEIFQPIFLLSGYTMWIRINHSIGSDSPCTCVLPDSVVRPLRP 540
 DB 483 PISEPRDCLQSDGFECEIFQPIFLLSGYTMWIRINHSIGSDSPCTCVLPDSVVRPLRP 542
 QY 541 SSYKAEITINIGLKTSMKRPVPPENNLOFOLRYGSLGKEVQMKVEYDAKSKSYSLVP 600
 DB 543 SSYKAEITINIGLKTSMKRPVPPENNLOFOLRYGSLGKEVQMKVEYDAKSKSYSLVP 602
 QY 601 PDLCAVAYAVQVGRKLDGLGYWSNMSNPAYTYVMIDIKVPMRGEPEFRRIINGDTMKKEKNV 660
 DB 603 PDLCAVAYAVQVGRKLDGLGYWSNMSNPAYTYVMIDIKVPMRGEPEFRRIINGDTMKKEKNV 662
 QY 661 TLLMRPLMNDSLCSQVQVRIINHHTSCNGTWSEDVGNHKKFFLLMEQAHYTVVLAINSI 720
 DB 663 TLLMRPLMNDSLCSQVQVRIINHHTSCNGTWSEDVGNHKKFFLLMEQAHYTVVLAINSI 722
 QY 721 GASVANFNLTFSWPMKSVIIVOSLSAYPLNSSCVIWSLTPSDYKLMFTIEMKMLNED 780
 DB 723 GASVANFNLTFSWPMKSVIIVOSLSAYPLNSSCVIWSLTPSDYKLMFTIEMKMLNED 782
 QY 781 GEIKWLRISSSVKYYIHDFIPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
 DB 783 GEIKWLRISSSVKYYIHDFIPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
 QY 841 GLYVIVPVISSISLLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFOK-----PE 893

DB 843 GLYVIVPVISSISLLGLTLLISHQRMKLFMEDVNPKNCSWAQGLNFOKMGSMFYK 902
 QY 894 TFEHLFIKHT-ASVTCG-----LLLEPETSEISVDTSKKNDE 933
 DB 903 SHHSLISTQGHKHCGRPOGPLHRTKIDLSLYITLPLSLDPKSPSVKNTQE 960

RESULT 14
 US-08-618-957A-10

; Sequence 10, Application US/08618957A

; Patent No. 6355237

; GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. Ralph

; APPLICANT: Clotfi, Joseph

; APPLICANT: Zupancic, Thomas Joel

; APPLICANT: Shafer, Alan Wayne

; TITLE OF INVENTION: METHODS FOR USING THE OBES

; TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIA TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/618,957A

; FILING DATE: 20-MAR-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Poissant, Brian M.

; REGISTRATION NUMBER: 28,462

; REFERENCE/DOCKET NUMBER: 008907-0033-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 896 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-618-957A-10

Query Match 77.0%; Score 4814; DB 4; Length 896;
 Best Local Similarity 99.7%; Pred. No. 0;

Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTCQKCVVLLHMEFYVTAENLSPITPWPRKLSKMPNSTYDYFLLPAGLSKNTSNS 60
 DB 1 MTCQKCVVLLHMEFYVTAENLSPITPWPRKLSKMPNSTYDYFLLPAGLSKNTSNS 60
 QY 61 NGHYEAVPEPKRSSGTHSNLSKTFHCCFSEODRNSCLADNIEGRTFVSTVNSLVF 120
 DB 63 NGHYEAVPEPKRSSGTHSNLSKTFHCCFSEODRNSCLADNIEGRTFVSTVNSLVF 120
 QY 121 QOIDANMNIOQWLKGDLEFICVESLFRNLFERNYKVALLYLVEVLEDSPLVPQKGS 180
 DB 123 QOIDANMNIOQWLKGDLEFICVESLFRNLFERNYKVALLYLVEVLEDSPLVPQKGS 180

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QY 181 FOMVHNCNSVHECCBCLVVPVPAKLNITLLMCLKITSGVIFQSPPLMSVOPINMWKPDPP 240
DB 181 FOMVHNCNSVHECCBCLVVPVPAKLNITLLMCLKITSGVIFRSPPLMSVOPINMWKPDPP 240
QY 241 LGLHMEITDDGNLKTSMSSPPLVPPLOQYKXSENSSTTVIREAKIYSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKTSMSSPPLVPPLOQYKXSENSSTTVIREAKIYSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPGLMSDMSSTPRVFTTODVIFPPKILTVSGNSVFNHCYKKEKNT 360
DB 301 GSSYEVOVGRKRLDGPGLMSDMSSTPRVFTTODVIFPPKILTVSGNSVFNHCYKKEKNT 360
QY 361 VPSKELIVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKTTYDAVYCNEHECHH 420
DB 361 VPSKELIVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKTTYDAVYCNEHECHH 420
QY 421 RYAEIYDIVNINISCEIDGYLTMTCKRMSTSTIOSLAESTIQLRYHRSLSYCSIDPSIH 480
DB 421 RYAEIYDIVNINISCEIDGYLTMTCKRMSTSTIOSLAESTIQLRYHRSLSYCSIDPSIH 480
QY 481 PISEPKDCYLQSDGFYECLFOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540
DB 481 PISEPKDCYLQSDGFYECLFOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540
QY 541 SSVKAEITINIGLKTSMKEKVPFPENNLOFOIRYGLSGKEVOVMKMEVYDAKSKSYSLPV 600
DB 541 SSVKAEITINIGLKTSMKEKVPFPENNLOFOIRYGLSGKEVOVMKMEVYDAKSKSYSLPV 600
QY 601 PDLCAVYAVOVACKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFMRITNGDTMKREKNV 660
DB 601 PDLCAVYAVOVACKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFMRITNGDTMKREKNV 660
QY 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTSEEDVGNHTKFTFLMTQAHYTVVLAINSI 720
DB 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTSEEDVGNHTKFTFLMTQAHYTVVLAINSI 720
QY 721 CASVANPMLTSPMSKVNIVQSLSATYPLNSCVIYSLTSDYKLMFTIEKKNLND 780
DB 721 CASVANPMLTSPMSKVNIVQSLSATYPLNSCVIYSLTSDYKLMFTIEKKNLND 780
QY 781 GEIKMLRITSSSVKYYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFODDIEKHQSDA 840
DB 781 GEIKMLRITSSSVKYYIHDHFIPIEKYOPSLYPIFMEGVGKPKIINSFODDIEKHQSDA 840
QY 841 GLYIVAVPIISSILLGLTLLISHORMKRLFWEDVYPNPKNCMAOGLNFQX 891
DB 841 GLYIVAVPIISSILLGLTLLISHORMKRLFWEDVYPNPKNCMAOGLNFQX 891

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RESULT 15
US-08-693-697-36
: Sequence 36, Application US/08693697
: Patent No. 5869610
: GENERAL INFORMATION:
: APPLICANT: Snodgrass, H. R.
: APPLICANT: Clotfi, Joseph
: APPLICANT: Zupancic, Thomas J.
: APPLICANT: Shafer, Alan W.
: TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
: TITLE OF INVENTION: RECEPTOR
: NUMBER OF SEQUENCES: 38
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

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: SOFTWARE: FASTSEQ for Windows Version 2.0b
: :
: : CURRENT APPLICATION DATA:
: : APPLICATION NUMBER: US/08/693,697
: : FILING DATE: 05-AUG-1996
: : CLASSIFICATION: 435
: : ATTORNEY/AGENT INFORMATION:
: : NAME: Polsant, Brian M.
: : REGISTRATION NUMBER: 28,462
: : REFERENCE/DOCKET NUMBER: 8907-0037-999
: : TELECOMMUNICATION INFORMATION:
: : TELEPHONE: 650-493-4935
: : TELEFAX: 650-493-5556
: :
: : TELEX: 66141 PENNIE
: : INFORMATION FOR SEQ ID NO: 36:
: : SEQUENCE CHARACTERISTICS:
: : LENGTH: 898 amino acids
: : TYPE: amino acid
: : STRANDEDNESS: single
: : TOPOLOGY: linear
: : MOLECULE TYPE: protein
: : FRAGMENT TYPE: internal
: :
: : US-08-693-697-36

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Query Match 77.0%; Score 4814; DB 2; Length 898;
Best local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MICOKFCVLLHMEFIYVTAANLSYPIPMRFKLSGMPNSYDVFLLPAGLSKNTS 60
DB 3 MICOKFCVLLHMEFIYVTAANLSYPIPMRFKLSGMPNSYDVFLLPAGLSKNTS 62
QY 61 NGHYETAVERPKENSQTHRSNLKTTFHCCFSESDRNCSLCADNIEGTFTVSNVSLVF 120
DB 63 NGHYETAVERPKENSQTHRSNLKATFHCCFSESDRNCSLCADNIEGTFTVSNVSLVF 122
QY 121 QQIDANWNIQCKLKGDKLFCYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKS 180
DB 123 QQIDANWNIQCKLKGDKLFCYVESLFKNLFRNRYKVHLLVLPVLEDSPLVPQKS 182
QY 181 FOMVHNCNSVHECCBCLVVPVPAKLNITLLMCLKITSGVIFQSPPLMSVOPINMWKPDPP 240
DB 183 FOMVHNCNSVHECCBCLVVPVPAKLNITLLMCLKITSGVIFRSPPLMSVOPINMWKPDPP 242
QY 241 LGLHMEITDDGNLKTSMSSPPLVPPLOQYKXSENSSTTVIREAKIYSATSLVDSILP 300
DB 243 LGLHMEITDDGNLKTSMSSPPLVPPLOQYKXSENSSTTVIREAKIYSATSLVDSILP 302
QY 301 GSSYEVOVGRKRLDGPGLMSDMSSTPRVFTTODVIFPPKILTVSGNSVFNHCYKKEKNT 360
DB 303 GSSYEVOVGRKRLDGPGLMSDMSSTPRVFTTODVIFPPKILTVSGNSVFNHCYKKEKNT 362
QY 361 VPSKELIVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKTTYDAVYCNEHECHH 420
DB 363 VPSKELIVMMNLAEKIPQSOQYDVSDHVSKEYTFENLNETKPRGKTTYDAVYCNEHECHH 422
QY 421 RYAEIYDIVNINISCEIDGYLTMTCKRMSTSTIOSLAESTIQLRYHRSLSYCSIDPSIH 480
DB 423 RYAEIYDIVNINISCEIDGYLTMTCKRMSTSTIOSLAESTIQLRYHRSLSYCSIDPSIH 482
QY 481 PISEPKDCYLQSDGFYECLFOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 540
DB 483 PISEPKDCYLQSDGFYECLFOPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVYKPLPP 542
QY 541 SSVKAEITINIGLKTSMKEKVPFPENNLOFOIRYGLSGKEVOVMKMEVYDAKSKSYSLPV 600
DB 543 SSVKAEITINIGLKTSMKEKVPFPENNLOFOIRYGLSGKEVOVMKMEVYDAKSKSYSLPV 602
QY 601 PDLCAVYAVOVACKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFMRITNGDTMKREKNV 660
DB 603 PDLCAVYAVOVACKRLDGLGYWSNMSNPAYTYVMDIKVPMRGPEFMRITNGDTMKREKNV 662
QY 661 TLLMKPLKNDSLCSVQRYVINHHTSCNGTSEEDVGNHTKFTFLMTQAHYTVVLAINSI 720

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Db	663	TLIMKPLMKNDISICVQRYVINHHHTSCNGTMSDEDYGNHHTKFTFLMTEQAHTVTLAINSI	722
Qy	721	GASVANENITFSWPMKSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLND	780
Db	723	GASVANENITFSWPMKSKVNIYOSLSAYPLNSSCVIYSWILSPSDYKLMYFIEMKNLND	782
Qy	781	GEIKMLRISSSVKYYIHDHFTPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHQSDA	840
Db	783	GEIKMLRISSSVKYYIHDHFTPIEKYQSLYPIFMEGVGKPKIINSFTODDIEKHQSDA	842
Qy	841	GLYIVPVIISSSILLGFTLLISHQRMKLLFWEDEVNPNRNCSSWAOGLNFOK	891
Db	843	GLYIVPVIISSSILLGFTLLISHQRMKLLFWEDEVNPNRNCSSWAOGLNFOK	893

Search completed: August 15, 2002, 16:22:13
 Job time: 423 sec

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QY 421 RYAEIYVDVNIINISCEYDGLTKMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVDVNIINISCEYDGLTKMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PTSEPKDCYLOSAGDYECIFQPIFLLSGYTMWIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PTSEPKDCYLOSAGDYECIFQPIFLLSGYTMWIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRDLGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHSTSCNGTSEDVGNHTKFTFLATEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHSTSCNGTSEDVGNHTKFTFLATEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLPIFMEGVGKPKIINSETQDDIERKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLPIFMEGVGKPKIINSETQDDIERKHQSDA 840
QY 841 GLYVIVPVISSIIILLGTLISHORMKFLWEDVPNPKNCSWAOGNLFQK-----PE 893
Db 841 GLYVIVPVISSIIILLGTLISHORMKFLWEDVPNPKNCSWAOGNLFQK-----PE 893
QY 894 TFEHLFIKHT-ASVTCGP-----LLLEPETISEDISVDTSWKNKDE 933
Db 901 SHHSLISSTQGHKCGRPQGLHRTKTRDCLSLVYLLTLPPLLSYDPAKSPSVRNTQE 958

RESULT 8
QI3593 ID QI3593 PRELIMINARY; PRT; 906 AA.
AC QI3593;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL; U52913; AAC50510.1; -.
DR HSP; p16471; lBP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.
FT SEQUENCE 906 AA; 103487 MW; 6D51126F33076626 CRC64;

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Query Match 77.0%; Score 4816; DB 4; Length 906;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 MICQKFCVLLHWBIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWBIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYTEAVPEKFNSSGTHFSNLKSTTFHCCFRSEODRNCCLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVPEKFNSSGTHFSNLKSTTFHCCFRSEODRNCCLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIQWLKGLDLKLFICYVESLFKNLFRNYKVHLLYVLPVELEDSPVPQKGS 180
Db 121 QOIDANWNIQWLKGLDLKLFICYVESLFKNLFRNYKVHLLYVLPVELEDSPVPQKGS 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFOSPLMSVQPINVKPDP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFOSPLMSVQPINVKPDP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIYSATSLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIYSATSLVDSILP 300
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTTQDVYFPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIIVWNNLAEKIPOSQYDVSDHVSKVTFPNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIIVWNNLAEKIPOSQYDVSDHVSKVTFPNNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVDVNIINISCEYDGLTKMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVDVNIINISCEYDGLTKMTCRWSTSTIOSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PTSEPKDCYLOSAGDYECIFQPIFLLSGYTMWIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
Db 481 PTSEPKDCYLOSAGDYECIFQPIFLLSGYTMWIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCRDLGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHSTSCNGTSEDVGNHTKFTFLATEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDSLCSVQRYVINHHSTSCNGTSEDVGNHTKFTFLATEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIIWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLPIFMEGVGKPKIINSETQDDIERKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLPIFMEGVGKPKIINSETQDDIERKHQSDA 840
QY 841 GLYVIVPVISSIIILLGTLISHORMKFLWEDVPNPKNCSWAOGNLFQK--PETFEHL 898
Db 841 GLYVIVPVISSIIILLGTLISHORMKFLWEDVPNPKNCSWAOGNLFQK--PETFEHL 898

RESULT 9
QI3594 ID QI3594 PRELIMINARY; PRT; 896 AA.
AC QI3594;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52914; AAC50511.1; -.
DR HSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
SQ SEQUENCE 896 AA; 102516 MW; 73c431f8c578cd07 CRC64;

Query Match 77.0%; Score 4814; DB 4; Length 896;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTCQFCVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
DB 1 MTCQFCVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHETAVEPKFNSGTHFNSLTKTTHCCFRSEDRNCSLCADNIEGRTFTVSTNSLVF 120
DB 61 NGHETAVEPKFNSGTHFNSLTKTTHCCFRSEDRNCSLCADNIEGRTFTVSTNSLVF 120
QY 121 QQIDANNWNIQCKLGDLCFYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWNIQCKLGDLCFYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHCCCECLVPVPTAKLNDLLMCLKITSGGVIFQSPILMSVQPINMVKPDPP 240
DB 181 FQWVHCNCSVHCCCECLVPVPTAKLNDLLMCLKITSGGVIFQSPILMSVQPINMVKPDPP 240
QY 241 LGLHWEITDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHWEITDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRLDGPFGIWSDMSTPRVFTQDVIYFPKILTSVGSNSFHCYKKNKI 360
DB 301 GSSYEVQVRGKRLDGPFGIWSDMSTPRVFTQDVIYFPKILTSVGSNSFHCYKKNKI 360
QY 361 VPSKEIVWMMNLAEKIPOSQYDVVSDHYSKVTFNFLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVWMMNLAEKIPOSQYDVVSDHYSKVTFNFLNETKPRGKFTYDAVYCCNEHECHH 420
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DB 421 RYAEILYVIDVNIINISCTDGYLTWKTCRWSTSTIOSLAESTLQLRYHRSLSYCSIDPSTH 480
QY 481 PTSEPKDCYQSDGFYECIFQIFILLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
DB 481 PTSEPKDCYQSDGFYECIFQIFILLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSYSVLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSYSVLPV 600
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DB 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSYSVLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYSNNSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRCKRLDGLGYSNNSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQARTVTVLAINSI 720
DB 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKYNIVQSLNAYPLNSSCVLVSILSPDYKLYAFIIEWKNLND 780
DB 721 GASVANFNLTFSWPMKYNIVQSLNAYPLNSSCVLVSILSPDYKLYAFIIEWKNLND 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYIVIVPVISSSILLGLTLLSHORMKKLFWEDVPNPKNCNSWAQGLNFQK 891
DB 841 GLYIVIVPVISSSILLGLTLLSHORMKKLFWEDVPNPKNCNSWAQGLNFQK 891

RESULT 10
Q9QWG3 PRELIMINARY; PRT: 1162 AA.
AC Q9QWG3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LEPTIN RECEPTOR B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KK OBSE; TISSUE=BRAIN, HYPOTHALAMUS;
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joost H.G.;
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
RT hyperinsulinemic KK mouse strain.";
RL J. Endocrinol. 21:337-345(1998).
DR EMBL: Y10296; CAA71342.1; -.
DR HSSP: P16471; 1BP3.
DR MGD: MGI-104993; Lepr.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 3.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
FT VARIANT 600 600 N -> D.
SQ SEQUENCE 1162 AA; 130787 MW; 541E77CBB46EC00D CRC64;

Query Match 76.1%; Score 4761.5; DB 11; Length 1162;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 878; Conservative 116; Mismatches 167; Indels 5; Gaps 5;

QY 1 MTCQFCVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
DB 1 MTCQFCVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHETAVEPKFNSGTHFNSLTKTTHCCFRSEDRNCSLCADNIEGRTFTVSTNSLVF 120
DB 61 NGHETAVEPKFNSGTHFNSLTKTTHCCFRSEDRNCSLCADNIEGRTFTVSTNSLVF 120
QY 61 KGASEAIVEAKFNSSGIVPELSKTVFHCFCGNEQGNCSALTDTNTEGKTLASVVKASVF 120
DB 61 KGASEAIVEAKFNSSGIVPELSKTVFHCFCGNEQGNCSALTDTNTEGKTLASVVKASVF 120
QY 121 QQIDANNWNIQCKLGDLCFYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWNIQCKLGDLCFYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
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Db 419 RYAEIYVIDVNIINISCTDGLTKMTCRWNSTNTIQSLAGSTLQRLYRRSLYCFDIPSIH 478
QY 481 PISEPKDCYLOSDFGFEYCFQPIFLLSGYTMWIRINHSGLSGLSDSPPTCVLPDSDVWKPLPP 540
Db 479 PISKPKDCYLOSDFGFEYCFQPIFLLSGYTMWIRINHPGLSGLSDSPPTCVLPDSDVWKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGREVOVMKYEYVDAKSYSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGREVOVMKYEYVDAKSYSVSLPV 598
QY 601 PDLCAVAVQVRCKRDLGLGYSNWNPNAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
Db 599 PDFCAVAVQVRCKRDLGLGYSNWNPNAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 658
QY 661 TLLWKKPLMKNDLSLCSVQRYVINHTSCNGTWSGVEDVGNHTKFTFLWTEQAHVTVVLAINSI 720
Db 659 TLLWKKPLMKNESLCSVQRYVINHTSCNGTWSGVEDVGNHTKFTFLWTEQAHVTVVLAINSI 718
QY 721 GASVANFLTFSWPMKSNVIVQSLAYSPLNSSCVIYSWILSPSDYKLMYPIIEWKNLNE 780
Db 659 TLLWKKPLMKNESLCSVQRYVINHTSCNGTWSGVEDVGNHTKFTFLWTEQAHVTVVLAINSI 718
QY 721 GASVANFLTFSWPMKSNVIVQSLAYSPLNSSCVIYSWILSPSDYKLMYPIIEWKNLNE 780
Db 719 GASVANFLTFSWPMKSNVIVQSLAYSPLNSSCVIYSWILSPSDYKLMYPIIEWKNLNE 778
QY 781 GEIKWLRISSSVKYYIHDHFIPRIEYQPSLYPIFMEGVGKPKKIINSFTODDTEKHQSDA 840
Db 779 GEIKWLRISSSVKYYIHDHFIPRIEYQPSLYPIFMEGVGKPKKIINSFAODNTEKHQSDA 838
QY 841 GLYVIVPVISSSILLGLTLLSHQRMKKLFWEDVNPKNCSWAQGLNFQKPEF 895
Db 839 GLYVIVPVISSSILLGLTLLSHQRMKKLFWEDVNPKNCSWAQGLNFQKRGF 893

RESULT 12
Q9MVL1 PRELIMINARY; PRT; 894 AA.
AC Q9MVL1;
AC Q9MVL1;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-DEC-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
expression in the adipose tissue of normal, hyperinsulinemic, and type
2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225873; AAF35387.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopoietic_receptor_L_F2.
DR InterPro; IPR003531; Hematopoietic_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAFO32238AFB9 CRC64;
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Query Match 73.4%; Score 4590; DB 6; Length 894;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 849; Conservative 15; Mismatches 25; Indels 2; Gaps 1;

QY 1 MICOKECVVLLHKEFYIVITAFNLSPYIPWRFKLSMPPNSYDYFLLPAGLSKNTNS 60
Db 1 MICOKECVVLLHKEFYIVITAFNLSPYIPWRFKLSMPPNSYDYFLLPAGLSKNTNSL 60
QY 61 NGHYETAPEKPFNSSTHFSNLSTKTFHCFRSEQDRNCSLCADNIEGKTFVTSVNSLV 120
Db 61 NGHYETAPEKPFNSSTHFSNLSTKTFHCFRSEQDRNCSLCADNIEGKTFVTSVNSLV 118
QY 121 QQIDANNITQCVLKGDLKLFICYVESLFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKS 180
Db 119 QQGANNNITQCVLKGDLKLFICYVESLFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKS 178
QY 181 FQMVHCNCSVHECCGCLVPVPTAKLNDTLLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 179 FQMVHCNCSVHECCGCLVPVPTAKLNDTLLMLCKITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSNSPPLVPFPLOQYKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKIWSNSPPLVPFPLOQYKYSNSTTVIREADKIVSATSLLVDSILP 298
QY 301 GSSYEVOVRCKRDLGPGIWSDMSTPRVFTTQDVIYPPPKILTSGVSNVSPHFCIYKKNKI 360
Db 299 GSSYEVOVRCKRDLGPGIWSDMSTPRVFTTQDVIYPPPKILTSGVSNVSPHFCIYKKNKI 358
QY 361 VPSKEIYVWNNLAETKIPQSOYDVVSDHVSQVTFNLFNETKPRCKFTYDAVYCNEHECHH 420
Db 359 VSSKKIYVWNNLAETKIPQSOYDVVSDHVSQVTFNLFNETKPRCKFTYDAVYCNEHECHH 418
QY 421 RYAEIYVIDVNIINISCTDGLTKMTCRWNSTNTIQSLAESTLQRLYRRSLYCFDIPSIH 480
Db 419 RYAEIYVIDVNIINISCTDGLTKMTCRWNSTNTIQSLAESTLQRLYRRSLYCFDIPSIH 478
QY 481 PISEPKDCYLOSDFGFEYCFQPIFLLSGYTMWIRINHSGLSGLSDSPPTCVLPDSDVWKPLPP 540
Db 479 PISKPKDCYLOSDFGFEYCFQPIFLLSGYTMWIRINHPGLSGLSDSPPTCVLPDSDVWKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGREVOVMKYEYVDAKSYSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPENNLOQIRYGLSGREVOVMKYEYVDAKSYSVSLPV 598
QY 601 PDLCAVAVQVRCKRDLGLGYSNWNPNAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
Db 599 PDFCAVAVQVRCKRDLGLGYSNWNPNAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 658
QY 661 TLLWKKPLMKNDLSLCSVQRYVINHTSCNGTWSGVEDVGNHTKFTFLWTEQAHVTVVLAINSI 720
Db 659 TLLWKKPLMKNESLCSVQRYVINHTSCNGTWSGVEDVGNHTKFTFLWTEQAHVTVVLAINSI 718
QY 721 GASVANFLTFSWPMKSNVIVQSLAYSPLNSSCVIYSWILSPSDYKLMYPIIEWKNLNE 780
Db 719 GASVANFLTFSWPMKSNVIVQSLAYSPLNSSCVIYSWILSPSDYKLMYPIIEWKNLNE 778
QY 781 GEIKWLRISSSVKYYIHDHFIPRIEYQPSLYPIFMEGVGKPKKIINSFTODDTEKHQSDA 840
Db 779 GEIKWLRISSSVKYYIHDHFIPRIEYQPSLYPIFMEGVGKPKKIINSFAODNTEKHQSDA 838
QY 841 GLYVIVPVISSSILLGLTLLSHQRMKKLFWEDVNPKNCSWAQGLNFQK 891
Db 839 GLYVIVPVISSSILLGLTLLSHQRMKKLFWEDVNPKNCSWAQGLNFQK 889

RESULT 13
Q9MVS2 PRELIMINARY; PRT; 848 AA.
ID Q9MVS2;
AC Q9MVS2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).
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GN OBR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Hu X., Dai R., Li N., Wu C.;
RT "Expression, Detection, and Partial Cloning of Porcine Leptin Receptor
(OBR) Gene.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF167719; AAF89633.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
FT NON_TER 848
FT NON_TER 848
SQ SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;

Query Match 63.5%; Score 3970.5; DB 6; Length 848;
Best Local Similarity 86.5%; Pred. No. 6.9e-285;
Matches 735; Conservative 43; Mismatches 69; Indels 3; Gaps 3;

QY 7 CVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLPAGLSKNTSNNGHYET 66
Db 1 CVVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLPAGLSKNTSTLNGHDEA 59
QY 67 AVEPFNSSGTHFSL-SKTTPHCCFRSEBDRNCISLCADNIEGKTFVSNLSLVFQQIDA 125
Db 60 VVEMELNSSGTYLNLSSKTFTHCCFWEEDKNCVSHADNIAKAFVSNVSLVFQQTCA 119
QY 126 NNNICWLKGDGLKLFICYVESLFKNLFNRYNYKVLHLLYVLPVLEDSPLVPQKGSFQMVH 185
Db 120 NNNICWKKEDLKFICYMESLFKNPFKNYDLKVLHLLYVLEVLGSPLLPQKGSFQVQ 179
QY 186 CNCVHECECLVPVPTAKLNDTLMLKITSGGVIFQSPLMVOPINMKVDPDPLGLHM 245
Db 180 CNCVHECECHVPVSAKLANLTLLMYKITSGGAVFHSPLMSVQPINVKPDPLGLHM 239
QY 246 EITDGNLKISWSPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLVDSILPGSSYE 305
Db 240 EITDGNLKISWSSPLVFPFLOQYQVYKSENSTTNRRADEIVSDTSLVDSVLPSSYE 299
QY 306 VQVRKRLDGPGLGSDWSTPRVFTTQDVIYPPPKILTSVGSNVSFHCYKKNKIVPSKE 365
Db 300 VQVRKRLDGPGLGSDWSTPFTTQDVIYPPPKILTSVGSNLSLHCYKKNKIVPSKE 359
QY 366 IYWNANLAKIPQSQYDVVSDVSVKTFPNLNETPRGKFTDYAVCCNEHCHRYAEL 425
Db 360 IYWNANLAKIPQSQYDVVSDVSVKTFPNMNAKPRGKFTDYAVCCNEHCHRYAEL 419
QY 426 YVIDVNIINISCTDGLYLNKMTCRWSTSTQSLAESTLQLRVHRSSLYCSDIPSIHPISPP 485
Db 420 YVIDVNIINISCTDGLYLNKMTCRWSTNAQSLVSTLQLRVHRSSLYCSDVPSVHPISPP 479
QY 486 KDCYLQSDGFYECIFQPIPLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPPSSVKA 545
Db 480 KDCQLQRQGFYECIFQPIPLLSGYTMWIRINHPPLGSLSDSPPTCVLPDSVVKPLPPSSVKA 539
QY 546 EITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKNMEVYDAKSKSVSLVPDLCA 605
Db 540 EITAKIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKNMEVYDVKLSTSLVPDLCA 599
QY 606 VTAVQVRCKRLDGLGWSNWSNPATVTVMDIKVPMRGPFEWIRINGDTMKKEKNTVLLWK 665
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Db 600 VTAVQVRCKRLDGLGWSNWSNPATVTVTDVVKVIRGPFEWIRINEDATKKERNITLLWK 659
QY 666 PLMKNDLSQVQRYVYINHHHTSCNGTWSEDVGNHRTFTFLWTQAHVTVVLAINSIGASVA 725
Db 660 PLMKNDLSQVRSYVYVVKHHTSRHGTSWSEDVGNHRTKLTFLWTQAHSVTVVLAINSIGASSA 719
QY 726 NFNLTFSWPMKVNIVQSLSAYSPLNSSCVIVSWILSPDYKLMYFIEMKKNLNEGEIKW 785
Db 720 NFNLTFSWPMKVNIVQSLSAYSPLNSSCVGLSWILSPDYNLMLYFIEMKKNLNEDEIKW 779
QY 786 LRAISSVKKYYIHDHFPIETKYQFSLYPIFMGVGKPKIINFTODDIEKHOSDAGLYVI 845
Db 780 LRAIPSVKKYYIHDHFPIETKYQFSLYPIFMGVGKPKIINFTQDG-EKRRNDAGLYVI 838
QY 846 VPIIISSSIL 855
Db 839 VPIIISSSIL 848

RESULT 14
Q62960
ID Q62960 PRELIMINARY; PRT: 895 AA.
AC Q62960;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
GN ROB-R.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA Wang M.-Y., Unger R.H.;
RT "Characterization of leptin receptors in normal and Zucker diabetic fatty rats.";
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U53144; AAB03088.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;

Query Match 59.6%; Score 3729; DB 11; Length 895;
Best Local Similarity 76.5%; Pred. No. 5.4e-267;
Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;

QY 1 MTCQKFCVYVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLPAGLSKNTSN 60
Db 1 MTCQKFCVYVLLHWEFIYVITAFNLSPYTPWRFKLSCHMPNSTYDYFLPAGLSKNTSSL 60
QY 61 NGHYETAPEPKFNSNGSTHFSNLKTKTFHCCFRSEQRNCSLCADNIEGKTFVTVNSLVF 120
Db 61 KGASEALVEAKENSTGIYVSELSKTFHCCFGNCGNCSALTGNTGKTLASVVKPLVF 120
QY 121 QQIDANWNLQCHLKGDLKLFICYVESLFLNLPFNRYKVLHLLYVLPVLEDSPLVPQKGS 180
Db 121 RGLGVNWDIECHWKMGDLTLFICHMEPLLNPKNYDKSVHLLYDLPVDDLPPLPKDS 180
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLKITSGGVIFQSPLMVOPINMKVDPDP 240
Db 181 FQTVQCNCVRE-CECHVVPVPRAKVNYALLMYLEITSAGVSFQSPLMVOPINMKVDPDP 239
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Qy	241	LGLHMETDGNLKIASHSSPPLVPFPLOQYKVKSYSENSTTVIRREADKIVSATSLLVDSILP	300
Db	240	LGLRMEVTDGNNLKISWSDSGTKAPFLLQYQVKYLNS-TIVREAAEIVSDTSLLVDSILP	298
Qy	301	GSSVEVOVRCKRLDGPGIGWSDMSTPRVFETDDVIYPPPKLLTSVGSNVSFHCIYKKENKI	360
Db	299	GSSVEVOVRCKRLDGSGVSWDSLSLPQLFTTQDVNYIPPKLLTSVGSNASFCIIYKNENGT	358
Qy	361	VPSKEIYVMNMLAEKIPQSQYDVVSDHVSKSVTFPNLNNETKPRGKFTFYDAVYCNEHECHH	420
Db	359	ISSKOIYVMNMLAEKIPETQYNTVSHDKSVTESNLKATRPGRKFTFYDAVYCNEEQCQH	418
Qy	421	RYAELYYVDVYNINSCETDGYLRKMTCRWSTSIQSLASTOLRLYHRHSRLVCSDIPSHT	480
Db	419	RYADLYYVDVYNINSCETDGYLRKMTCRWSPSTIQSLVGSTVOLRLYHRHSRLVCSDNPISR	478
Qy	481	PISEPKCYLQSDGCFYECIFQPIFFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP	540
Db	479	PTSELKNCVLQTDGLYECVQSOPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP	538
Qy	541	SSVAEITINTGLLKISWEKPVPENNLOFIQIRYGUSGEVQMKVEYVDAKSVSLSLPV	600
Db	539	SNVKAETINTGLLKISWEKPVPENNLOFIQIRYGLNGEKIEQWKTHEVDFDAKSASLPV	598
Qy	601	PDLCAVAVOVRCKRLDGLCYWNASNPAVTVMYDIKPMRGPEFWRIINGDTMKKEKNV	660
Db	599	SDLCAVAVOVRCKRLDGLCYWNASSPATLYMVDKVPMRGPFRWIMDGDITTKERNV	658
Qy	661	TLLWKPLMKNDSLCSQORYVINIHSTSCNGTWSEDEVGNHRTKFTFLPWFEQAHTVTVLAINSI	720
Db	659	TLLWKPLMKNDSLCSQRRYVVVKHRTAHNGTWQDVCNQTNLTFLSCESAHTVTVLIDINSI	718
Qy	721	GASVANENLFSTPMSKVNTVQSLSAYPNLNSSCVIVSWILSPSDYKLMTFIIEWKNLND	780
Db	719	GASLVNFNLFTSPMSKVNGWQSLSAYPNLSSCVILSWTLSPNDYSLLYLVIEWKNLND	778
Qy	781	GEIKWLAISSSVKXYIYTHDFIPIEKYQFSLYPIEWEGVGKPKIINSFTQDDIDEKHOSDA	840
Db	779	DGMKWLAIIPNVNKXYIYHDNFIEPIEKYQFSLYPVFVEGVGKPKIINGFTKDDIAKQNDA	838
Qy	841	GLXVIVPVLISSSTLLGLTLLISHQRMKLFWEDVPNPKNCSSWAQGLNFQK	891
Db	839	GLXVIVPILISSCVLLGLTLLISHQRMKLFWDDVPNPKNCSSWAQGLNFQK	889
RESULT	15		
ID	Q9DDK1	PRELIMINARY; PRT; 1147 AA.	
AC	Q9DDK1;		
DC	01-MAR-2001 (TtEMBLrel. 16, Created)		
DT	01-MAR-2001 (TtEMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TtEMBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR.		
OB	OB-R.		
OS	Melagris gallopavo (Common turkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Achoseauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
OX	NGBL_TaxID=9103;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN;		
RA	Richards M.P., Poch S.M., Ashwell C.M.;		
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AF321362; AAC40323.1; -.		
DR	HSSP; P40189; IBQU.		
DR	InterPro; IPR002996; CRA.		
DR	InterPro; IPR003961; FN.III.		
DR	Pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 4.		
KW	Receptor.		
FT	SEQUENCE 1133 1133 Q -> R.		
SQ	SEQUENCE 1147 AA; 129131 MW; 34197B7908F734F4 CRC64;		

Qy	1022	DSFSNSWELEAQAFILSDQ---HP----	NIISPLHTFSEGLDELKLEGNPFENNDK	1074
		::: : :	::: : :	
Db	1011	GVCSGSWEIGSEFULLPQDGRPKTSLIS----	SEGFSEPSDQDDAFTDGSPE	1065
		::: : :	::: : :	
Qy	1075	KSIYYIGVTSIKKRESEGVLLTDKSRVCSPPFAPCLFTDIRVLQDSCSHFVENNIN-IGTS	1133	
		::: ::: : :	::: ::: : :	
Db	1066	RGLCYLGITSLOKRENAIFLTSRLMCHFTADLLRGVGLQNT-----PPNLNAPLQS	1120	
		::: : :	::: : :	
Qy	1134	SKYTFASYMPQFQTCSTQTHKIMEN	1158	
		: : : : : : : :	: : : : : : : :	
Db	1121	SIKAIYVPYVPQFQNTAAKQVQETEN	1145	
		::: : :	::: : :	

Search completed: August 15, 2002, 16:35:36
Job time: 796 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:10 ; Search time 28.14 Seconds
(without alignments)
1602.995 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICQKFCVLLHWEFYIVP.....QTCSTQTHKIMENKMDLT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6246	99.9	1165	1 LEPR_HUMAN	P48357 homo sapien
2	4784.5	76.5	1162	1 LEPR_RAT	O62959 rattus norv
3	4766.5	76.2	1162	1 LEPR_MOUSE	P48356 mus musculus
4	366	5.9	917	1 IL6B_MOUSE	Q00560 mus musculus
5	345.5	5.5	918	1 IL6B_HUMAN	P40189 homo sapien
6	339.5	5.4	918	1 IL6B_RAT	P40190 rattus norv
7	313	5.0	837	1 GCSR_MOUSE	P40223 mus musculus
8	294.5	4.7	1097	1 LIFR_HUMAN	P42702 homo sapien
9	284	4.5	836	1 GCSR_HUMAN	O99062 homo sapien
10	281.5	4.5	1092	1 LIFR_MOUSE	P42703 mus musculus
11	220.5	3.5	862	1 IL2S_HUMAN	O99665 homo sapien
12	220	3.5	830	1 PRLR_COLLI	Q90374 columba liv
13	220	3.5	874	1 IL2S_MOUSE	P97378 mus musculus
14	209.5	3.3	831	1 PRLR_CHICK	Q04594 gallus gall
15	190	3.0	831	1 PRLR_MELGA	Q91094 meleagris q
16	184	2.9	2481	1 LIFR_XENLA	O91740 xenopus lae
17	173.5	2.8	1493	1 NEOL_MOUSE	P97798 mus musculus
18	172	2.8	2012	1 DSCA_HUMAN	O60469 homo sapien
19	170.5	2.7	1461	1 NEOL_HUMAN	Q92859 homo sapien
20	169.5	2.7	1443	1 NEOL_CHICK	Q90610 gallus gall
21	166.5	2.7	2029	1 LAR_DROME	P16621 drosophila
22	165	2.6	630	1 PRLR_ORENI	O91513 oreochromis
23	162	2.6	1447	1 DCC_MOUSE	P70211 mus musculus
24	158.5	2.5	462	1 IL6A_RAT	P22273 rattus norv
25	154.5	2.5	2386	1 FINC_HUMAN	P02751 homo sapien
26	153.5	2.5	460	1 IL6A_MOUSE	P22272 mus musculus
27	151	2.4	1377	1 NEOL_RAT	P97603 rattus norv
28	150.5	2.4	610	1 PRLR_RAT	P05710 rattus norv
29	147.5	2.4	638	1 GHR_MACMU	P79194 macaca mula
30	146	2.3	3063	1 CAIC_HUMAN	O99715 homo sapien
31	145.5	2.3	2477	1 FINC_RAT	P04937 rattus norv
32	144.5	2.3	1302	1 NRG_DROME	P20241 drosophila
33	144	2.3	581	1 PRLR_CEREL	Q28235 cervus elap

RESULT 1

ID	LEPR_HUMAN	STANDARD;	PRT;	1165 AA.
AC	P48357;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).			
GN	LEPR OR OBR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=96128129; PubMed=8548812;			
RA	Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,			
RA	Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,			
RA	Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,			
RA	Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;			
RT	*Identification and expression cloning of a leptin receptor, OB-R.;			
RL	Cell 83:1263-1271(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Thompson D.B., Ossowski V., Sutherland J., Apel W.,			
RA	Bierstfeldt J.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	VARIANT ARG-223.			
RX	MEDLINE=96270489; PubMed=8666155;			
RA	Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;			
RT	*The hypothalamic leptin receptor in humans: identification of			
RT	incidental sequence polymorphisms and absence of the db/db mouse and			
RL	fa/fa rat mutations.;			
RL	Diabetes 45:992-994(1996).			
RN	[4]			
RP	VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.			
RX	MEDLINE=97289327; PubMed=9144432;			
RA	Echwald S.N., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,			
RA	Andersen T., Chung W.K., Leibel R.L., Pedersen O.;			
RT	*Amino acid variants in the human leptin receptor: lack of association			
RT	to juvenile onset obesity.;			
RL	Biochem. Biophys. Res. Commun. 233:248-252(1997).			
RN	[5]			
RP	VARIANTS ARG-109; ARG-223 AND ASN-656.			
RX	MEDLINE=97431549; PubMed=9287054;			
RA	Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,			
RA	Sothorn M., Udall J.N., Kahle B., Leibel R.L.;			
RT	*Exonic and intronic sequence variation in the human leptin receptor			
RT	gene (LEPR).;			
RL	Diabetes 46:1509-1511(1997).			
RN	[6]			
RP	VARIANTS ARG-109 AND ARG-223.			
RP	MEDLINE=97301763; PubMed=9158141;			
RX	Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;			

34 143.5 2.3 1447 1 DCC_HUMAN P43146 homo sapien
35 143 2.3 638 1 GHR_HUMAN P10912 homo sapien
36 142.5 2.3 3135 1 S230_PLAFO Q08372 plasmodium
37 141 2.3 581 1 PRLR_BOVIN Q28172 bos taurus
38 141 2.3 878 1 IL3B_MOUSE P26954 mus musculus
39 140.5 2.2 638 1 GHR_PIG P19756 sus scrofa
40 140.5 2.2 638 1 GHR_RABIT P19941 oryctolagus
41 139 2.2 635 1 TPOR_HUMAN P10586 homo sapien
42 138 2.2 1897 1 PTPF_HUMAN P07589 bos taurus
43 138 2.2 2265 1 FINC_HUMAN Q92398 chlamydia p
44 136 2.2 928 1 PMP9_CHLPN P54755 gallus gall
45 135.5 2.2 1013 1 EPA5_CHICK

ALIGNMENTS

"Structure and sequence variation at the human leptin receptor gene in lean and obese Pima Indians."
Hum. Mol. Genet. 6:675-679(1997).
[7]
VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
MEDLINE=99075638; PubMed=9806295;
Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J., Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;
RA "transmission disequilibrium and sequence variants at the leptin
RT receptor gene in extremely obese German children and adolescents.";
RL Hum. Genet. 103:540-546(1998).
RN [8]
VARIANTS ARG-109; ARG-223 AND ASN-656.
RP MEDLINE=97318795; PubMed=9175732;
RX Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L., Strosberg A.D., McKeigue P.M., Scott J., Aitman T.J.;
RA "Leptin receptor gene variation and obesity: lack of association in a
RT white British male population.";
RL Hum. Mol. Genet. 6:869-876(1997).
RN CC -I- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC CC -I- SUBCELLULAR LOCATION: Type I fibronectin protein.
CC CC -I- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC EMBL: U43168; AAA93015.1; --
DR EMBL: U59263; AAB09673.1; --
DR EMBL: U59248; AAB09673.1; JOINED.
DR EMBL: U59249; AAB09673.1; JOINED.
DR EMBL: U59250; AAB09673.1; JOINED.
DR EMBL: U59251; AAB09673.1; JOINED.
DR EMBL: U59252; AAB09673.1; JOINED.
DR EMBL: U59253; AAB09673.1; JOINED.
DR EMBL: U59254; AAB09673.1; JOINED.
DR EMBL: U59255; AAB09673.1; JOINED.
DR EMBL: U59256; AAB09673.1; JOINED.
DR EMBL: U59257; AAB09673.1; JOINED.
DR EMBL: U59258; AAB09673.1; JOINED.
DR EMBL: U59259; AAB09673.1; JOINED.
DR EMBL: U59260; AAB09673.1; JOINED.
DR EMBL: U59261; AAB09673.1; JOINED.
DR EMBL: U59262; AAB09673.1; JOINED.
DR HSP: P40189; 1BQU.
DR MIM: 601007; --
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003529; Hematopo_receptor_L_F2.
DR Pfam: PF00041; fn3; 2.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Polymorphism.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1165 LEPTIN RECEPTOR.
FT DOMAIN 22 841 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 842 862 POTENTIAL.
FT DOMAIN 863 1165 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 237 320 FIBRONECTIN TYPE-III 1.
FT DOMAIN 537 623 FIBRONECTIN TYPE-III 2.
FT DOMAIN 738 823 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).

FT	CARBOHYD	206	206	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	347	347	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	433	433	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	516	516	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	659	659	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	670	670	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	688	688	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	697	697	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	728	728	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. .)	{POTENTIAL}. .
FT	VARIANT	109	109	K -> R.	/FTid=VAR_002703.
FT	VARIANT	204	204	K -> R.	/FTid=VAR_002704.
FT	VARIANT	223	223	Q -> R.	/FTid=VAR_002705.
FT	VARIANT	656	656	K -> N.	/FTid=VAR_002706.
FT	VARIANT	675	675	S -> T.	/FTid=VAR_002707.
FT	SEQUENCE	1165 AA;	132449 MW;	8FF21D9AF5125808	CRC64;
Query Match					
Best Local Similarity 99.9%; Score 6246; DB 1; Length 1165;					
Matches 1164; Conservative 0; Mismatches 1; Indels 0; Gaps					
Qy	1	MICOKFCVLLHWEFIVYITAFNLSPYIPWPRFKLSMCPNPSTDYDFLLPAGLSKNTSNS	60		
Dd	1	MICOKFCVLLHWEFIVYITAFNLSPYIPWPRFKLSMCPNPSTDYDFLLPAGLSKNTSNS	60		
Qy	61	NGHYETAPEPKFNSSGTHPHNLSKTTFHCCFRSEQDRNCSLCADNTEGTGFVSTVNSLVF	120		
Dd	61	NGHYETAPEPKFNSSGTHPHNLSKTTFHCCFRSEQDRNCSLCADNTEGTGFVSTVNSLVF	120		
Qy	121	OQIDANNIOCWLGDKDLFCVCVESLFRKNLFNRYNKVHLVLVLPVELEDSPVPQKS	180		
Dd	121	OQIDANNIOCWLGDKDLFCVCVESLFRKNLFNRYNKVHLVLVLPVELEDSPVPQKS	180		
Qy	181	FQMWHCNSVHECECLVPVPTAKLANDTLMLCKLKITSGGVIFQSPLMSVQPINMKVPDP	240		
Dd	181	FQMWHCNSVHECECLVPVPTAKLANDTLMLCKLKITSGGVIFQSPLMSVQPINMKVPDP	240		
Qy	241	LGLHMETDGNLKISWSSPPLVPFPLOQVKYSSENSTTVIREADKIVSATSLLDVSILP	300		
Dd	241	LGLHMETDGNLKISWSSPPLVPFPLOQVKYSSENSTTVIREADKIVSATSLLDVSILP	300		
Qy	301	GSSYEVOVRKRLDGPGIWSDWSTPRVFETQDVLYPPKKLTTSVGNSVGHCIYKENKI	360		
Dd	301	GSSYEVOVRKRLDGPGIWSDWSTPRVFETQDVLYPPKKLTTSVGNSVGHCIYKENKI	360		
Qy	361	VPSKEIYWMNLAEKIQSOYQVDVVSDHVSKVTFFENLNETHKRGKFITYDAVYCNEHCCH	420		
Dd	361	VPSKEIYWMNLAEKIQSOYQVDVVSDHVSKVTFFENLNETHKRGKFITYDAVYCNEHCCH	420		
Qy	421	RYAELYVIDVINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPTSH	480		
Dd	421	RYAELYVIDVINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRVHRSSLYCSDIPTSH	480		
Qy	481	PISEPKDCYLQSDGFECIFQPFIPLLSGYTWTWIRIHNSLGLSDSPPTCVLPDSVVKPLPP	540		
Dd	481	PISEPKDCYLQSDGFECIFQPFIPLLSGYTWTWIRIHNSLGLSDSPPTCVLPDSVVKPLPP	540		
Qy	541	SSVKAETIINGILLKTSWEKPVPENNLOQIRYGLSGKEVOMKYEVYDAKSKSVSLVP	600		
Dd	541	SSVKAETIINGILLKTSWEKPVPENNLOQIRYGLSGKEVOMKYEVYDAKSKSVSLVP	600		
Qy	601	PDLCAVAVOVRKRLDGLGIYWSNNSNPAYTVVMYDIKVPMRGPFEFWRIINGDTMKKEKNV	660		
Dd	601	PDLCAVAVOVRKRLDGLGIYWSNNSNPAYTVVMYDIKVPMRGPFEFWRIINGDTMKKEKNV	660		


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QY 661 TLLWKPLMKNDLSQVRYVINHHSTSCNGTWSGVNHTKFTFLMTEQAHVTYVLAINSI 720
DB 661 TLLWKPLMKNDLSQVRYVINHHSTSCNGTWSGVNHTKFTFLMTEQAHVTYVLAINSI 720
QY 721 GASVANFNLTFSWPKSNKVINQVLSAYPLNSSCVIVSILSPSDYKLMVFIIEKNLNE 780
DB 721 GASVANFNLTFSWPKSNKVINQVLSAYPLNSSCVIVSILSPSDYKLMVFIIEKNLNE 780
QY 781 GEIKWLRISSSVKYYIHDFIPIEKYQSLYPIFMGVGPKKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDFIPIEKYQSLYPIFMGVGPKKIINSFTODDIEKHQSDA 840
QY 841 GUYVIVPVISSILLGLTLLISHORMKLFWEQVNPKNCSWAGLNFQRPPEFHLFI 900
DB 841 GUYVIVPVISSILLGLTLLISHORMKLFWEQVNPKNCSWAGLNFQRPPEFHLFI 900
QY 901 KHTASVTCGLPILPETISEDISVDTSMKNKDEMPTTVVSLSTDLKSGVCLSDQFN 960
DB 901 KHTASVTCGLPILPETISEDISVDTSMKNKDEMPTTVVSLSTDLKSGVCLSDQFN 960
QY 961 SVNFSEAGTEVTYDEDSQRPFFVKYATLINSKPSGTGEQGLNINSVTKCFSSKNSPL 1020
DB 961 SVNFSEAGTEVTYDEDSQRPFFVKYATLINSKPSGTGEQGLNINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFITLSDQHPNIIISPHLTFSGLDELKLEGNFPENNKKSIYVL 1080
DB 1021 KDSFNSSSWEIEAQAFITLSDQHPNIIISPHLTFSGLDELKLEGNFPENNKKSIYVL 1080
QY 1081 GVTSTKKRESGVLITDKSRVSPFPAPCLFTDIRVLQDSCSHFVNINILGTSSKKTFFAS 1140
DB 1081 GVTSTKKRESGVLITDKSRVSPFPAPCLFTDIRVLQDSCSHFVNINILGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 2
LEPR_RAT STANDARD; PRT; 1162 AA.
AC Q62959; Q63007; P70493; P70494; P70495; Q63385; Q63386; Q54805;
AC P97589; Q35772;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEP-R OR OB-R FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
RX MEDLINE-9629531; PubMed-8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RA Phillips M.S., Liu Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T.,
RA Hess J.F.;
RA "Leptin receptor missense mutation in the fatty Zucker rat.";
RT Nat. Genet. 13:18-19(1996).
RN [2]
RN SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE-Brain;
RX MEDLINE-9629531; PubMed-8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RA "Substitution at codon 269 (glutamine --> proline) of the leptin
RT receptor (OB-R) cDNA is the only mutation found in the Zucker fatty
RT (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RN SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE-96332408; PubMed-8769097;
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```
RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H.,
RA Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary
RT DNAs -- identification of a missense mutation in Zucker fatty (fa/fa)
RT rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RN SEQUENCE FROM N.A. (VARIANT B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
RA Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE-96212906; PubMed-8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from
RT Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RN SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
RT "Analysis of rat leptin receptor gene.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE OF 594-878 FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
RA Ma Z.;
RT "Identification of a leptin receptor in islet.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
RC STRAIN-SPRAGUE-DAWLEY;
RA Chien E.K., Hara M., Rouard M., Yano H., Phillippe M., Polonsky K.S.,
RA Bell G.I.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RN VARIANT FA PRO-269.
RX MEDLINE-96314329; PubMed-8690163;
RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
RA Leibel R.L.;
RT "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
RT (lepr).";
RL Diabetes 45:1141-1143(1996).
CC CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC CC -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
CC CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
CC CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
CC CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
CC CC WHICH COULD BE SECRETED.
CC CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
CC CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC CC -!- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
CC CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
CC CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
CC CC TISSUE.
CC CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC CC -----
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CC CC -----
DR EMBL; U52966; AAC52587.1; -.
DR EMBL; D84550; BAA12697.1; -.
DR EMBL; D84551; BAA12698.1; -.
DR EMBL; D85557; BAA12830.1; -.
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DR EMBL; D85558; BAA12831.1; -.
DR EMBL; D85559; BAA12832.1; -.
DR EMBL; U60151; AAB06616.1; -.
DR EMBL; D84125; BAA12230.1; -.
DR EMBL; D84126; BAA12231.1; -.
DR EMBL; AB011006; BAA24899.1; -.
DR EMBL; U67207; AAB40654.1; -.
DR EMBL; AF007818; AAB63201.1; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00441; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Polymorphism; Alternative splicing.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 1162 LEPTIN RECEPTOR.
FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 840 860 POTENTIAL.
FT DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 318 FIBRONECTIN TYPE-III 1.
FT DOMAIN 535 621 FIBRONECTIN TYPE-III 2.
FT DOMAIN 736 821 FIBRONECTIN TYPE-III 3.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 275 275 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 514 514 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 668 668 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 686 686 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 695 695 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 726 726 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOLIC 894 PETE -> RADTL (IN ISOFORM A).
FT VARSPLIC 895 1162 MISSING (IN ISOFORM A).
FT VARSPLIC 890 892 PET -> VTV (IN ISOFORM C).
FT VARSPLIC 893 1162 MISSING (IN ISOFORM C).
FT VARSPLIC 797 805 DNFTPIERY -> GNCVTLLN (IN ISOFORM E).
FT VARSPLIC 806 1162 MISSING (IN ISOFORM E).
FT VARIANT 269 269 Q -> P (IN FA).
FT CONFLICT 2 2 T -> M (IN REF. 4).
FT CONFLICT 12 12 H -> P (IN REF. 6).
FT CONFLICT 34 34 K -> R (IN REF. 6).
FT CONFLICT 751 752 CV -> SL (IN REF. 7).
FT CONFLICT 846 846 I -> V (IN REF. 8).
SQ SEQUENCE 1162 AA; 130832 MW; BA7AC2CA2D2E62AF CRC64;

Query Match 76.5%; Score 4784.5; DB 1; Length 1162;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;

QY 1 MTCQKFCVVLHWEFYVITAFNLSPYTPWRFKLSCHMPNSTDYVFLLPAGLSKNTSNS 60
DB 1 MTCQKFCVVLHWEFYVITAFNLSPYTPWRFKLSCHMPNSTDYVFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKFNSSGTHFSNKTTHCCFSEQRDCNSCADNIEGKTFVSTYNSLVF 120
DB 61 KGAEALVEAKFNSTGIYVSELSKTFHCCFGEQGNCSALTNGTEGKTLASVVKPLVF 120
QY 121 QOIDANWITQWLKGDGLKFLICYVESLFPKLNFRNRYNKVHLLYLVPEVLEDSPLVPQKGS 180
DB 121 ROLGNWIDIECKMMKGDGLFTICHMEPLKPNKFNKDYDSKVHLLYDLPEVIDDLPPLPKDS 180
QY 181 FQWVHCNCSVHCCCLVPVPTAKLNDTLMLCKLTSGTGVIFQSPFLMSVQPINMYVKPDPP 240
DB 181 FQWVHCNCSVHCCCLVPVPTAKLNDTLMLCKLTSGTGVIFQSPFLMSVQPINMYVKPDPP 240

Db 181 FQWVHCNCSVHCCCLVPVPTAKLNDTLMLCKLTSGTGVIFQSPFLMSVQPINMYVKPDPP 239
QY 241 LGLHMEITDDGNLKLISWSSPPLVPPPLQYQVKSSENSTTVIREADKIYSAISLLVDSILP 300
DB 240 LGLRMEVTDGNLKLISWDSQTKAPEPQYQVYLENS-TIVREAAEIVSDISLLVDSVLP 298
QY 301 GSSYEVQVGRKRLDGGIWSQWSTPRVTTQDVIVFPFKILTSVGSNSVSHCIYKKNKI 360
DB 299 GSSYEVQVGRKRLDGSVMSDWSLPQLFTQDMVFPFKILTSVGSNASFCCTIYKNEQT 358
QY 361 VPSKEIVVMNLAEKIPQSOYDVVSDHVSQVYTFNFNLNLTGKRGKFTYDAVYCCNEHCHH 420
DB 359 TSSKQIVVMNLAEKIPETQYNTVSDHISKYTFSLNKAATPRPKRFTYDAVYCCNEQACHH 418
QY 421 RYAEIYVIVDNNINISCEITDGYLTGMTKRWSTSTIOSLAESTIQLRYHRSSLYCSIPSIH 480
DB 419 RYAEIYVIVDNNINISCEITDGYLTGMTKRWSPSTIOSLVGSTVQLRYHRSLYCPNPISIR 478
QY 481 PISEPKDCYLOSDFEYECIFQIFLLSGYTMIRINHSLGSLDSOSPPTCVLPDSVVKPLPP 540
DB 479 PISEPKDCYLOSDFEYECIFQIFLLSGYTMIRINHSLGSLDSOSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEIITINGLLKLSHEKPVFPENNLOFQIRYGLSGKEVQMKMYEYDAKSKSVSLPV 600
DB 539 SSVKAEIITINGLLKLSHEKPVFPENNLOFQIRYGLSGKEVQMKMYEYDAKSKSVSLPV 598
QY 601 PDLCAVAVQVRCRLDGLGYWSNMSPAYTVVMDIKVPMRGPEPWRIRINGDTMKKNV 660
DB 599 PDLCAVAVQVRCRLDGLGYWSNMSPAYTVVMDIKVPMRGPEPWRIRINGDTMKKNV 658
QY 661 TLLKPLMKNSLCSQVRYVINHHTSCNGTWSVDGNTHTKFTFLMTEQAHVTVLAINSI 720
DB 659 TLLKPLMKNSLCSQVRYVINHHTSCNGTWSVDGNTHTKFTFLMTEQAHVTVLAINSI 718
QY 721 GASVANFNLTSPWPKVNIQSLSAYPLNSCVTSVNLSPDSYKLVYIIEWKNLND 780
DB 719 GASVANFNLTSPWPKVNAVOSLSAYPLNSCVTSVNLSPDSYKLVYIIEWKNLND 778
QY 781 GEIKWLRISSYKYYIHDHFIPIEKYOFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
DB 779 DGMKWLRISSYKYYIHDHFIPIEKYOFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 838
QY 841 GLYIVTVPIISSILLGLTLISHQMKLFWEDVPNPKNSWAQGLNFORPTEHFLFI 900
DB 839 GLYIVTVPIISSILLGLTLISHQMKLFWEDVPNPKNSWAQGLNFORPTEHFLFI 898
QY 901 KHTASVTCGILLPETISEDIVTSNKNKDNMTPTVVSLLSTT-DLEKGSVCISDQF 959
DB 899 KHTASVTCGILLPETISEDIVTSNKNKDNMTPTVVSLLSTT-DLEKGSVCISDQF 958
QY 960 NSVNFSEAEGETVYDEDSQRPVFKYATLISNPKSPSETGEBEQGLINSVTKCFSSKNSP 1019
DB 959 NSVNFSEAEGETVYDEDSQRPVFKYATLISNPKSPSETGEBEQGLINSVTKCFSSKNSP 1018
QY 1020 LKQSFNSWEIEAQAFITLSDQHNIIISPHLTFSEGDELKLGEPNPEENNKKSIY 1079
DB 1019 LKQSFNSWEIEAQAFITLSDQHNIIISPHLTFSEGDELKLGEPNPEENNKKSIY 1077
QY 1080 LGVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFA 1139
DB 1078 LGVTSIKKRESGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLTSSKKTFA 1136
QY 1140 SYMPOFOTCSQTQTHIMENKMCIDLTV 1165
DB 1137 PYMPOFOTCSQTQTHIMENKMCIDLTV 1162
RESULT 3
LEPR_MOUSE
ID LEPR_MOUSE STANDARD; PRT; 1162 AA.
AC P48356; O35686; Q61215; Q64309; O54986;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219
 GN LEP-R OR OBR OR DB)
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 [1]
 RN SEQUENCE FROM N.A. (VARIANT A).
 RC TISSUE=Choroid plexus;
 RX MEDLINE=96128129; PubMed=8548812;
 RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
 RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
 RA Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;
 RT "Identification and expression cloning of a leptin receptor, OB-R.";
 RL Cell 83:1263-1271(1995).
 [2]
 RN SEQUENCE FROM N.A. (VARIANT B).
 RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;
 RX MEDLINE=96190816; PubMed=8608603;
 RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
 RA Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
 RA Dyk G.M., Tepper R.I., Morgenstern J.P.;
 RT "Evidence that the diabetes gene encodes the leptin receptor:
 RT identification of a mutation in the leptin receptor gene in db/db
 RT mice.";
 RL Cell 84:491-495(1996).
 [3]
 RN SEQUENCE FROM N.A. (VARIANTS A TO E).
 RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;
 RX MEDLINE=96231997; PubMed=8628397;
 RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
 RA Lee J.-I., Friedman J.M.;
 RT "Abnormal splicing of the leptin receptor in diabetic mice.";
 RL Nature 379:632-635(1996).
 [4]
 RN SEQUENCE FROM N.A. (VARIANT C).
 RC STRAIN=BA1B/C; TISSUE=Liver;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J.,
 RA Mikhail A., Platika D., Snodgrass H.R.;
 RT "Novel B219/OB receptor isoforms: possible role of leptin in
 RT hematopoiesis and reproduction.";
 RL Nat. Med. 2:585-589(1996).
 [5]
 RN SEQUENCE FROM N.A. (VARIANT B).
 RC STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=Hypothalamus;
 RX MEDLINE=97462708; PubMed=9322335;
 RA Igel M., Becker W., Herberg L., Joost H.G.;
 RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
 RT in the New Zealand obese mouse.";
 RL Endocrinology 138:4234-4239(1997).
 [6]
 RN SEQUENCE FROM N.A. (VARIANTS A AND B).
 RC STRAIN=FVB/N; TISSUE=Spleen;
 RX MEDLINE=96270520; PubMed=8692797;
 RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
 RA Skoda R.C.;
 RT "Defective STAT signaling by the leptin receptor in diabetic mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
 [7]
 RN SEQUENCE FROM N.A. (VARIANT E).
 RC STRAIN=129/J;
 RX MEDLINE=98008913; PubMed=9344648;
 RA Chua S.C., Koutaris I.K., Han L., Liu S.M., Kay J., Young S.J.,
 RA Chung W.K., Leibel R.L.;
 RT "Fine structure of the murine leptin receptor gene: splice site
 RT suppression is required to form two alternatively spliced
 RT transcripts.";
 RL Genomics 45:264-270(1997).
 CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC CC -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS: A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN
 CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.
 CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND
 CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:
 CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
 CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 CC EMBL; U42467; AAA93014.1; -
 CC EMBL; U46135; AAC52408.1; -
 CC EMBL; U49106; AAC52420.1; -
 CC EMBL; U49107; AAC52421.1; -
 CC EMBL; U49108; AAC52422.1; -
 CC EMBL; U49109; AAC52423.1; -
 CC EMBL; U49110; AAC52424.1; -
 CC EMBL; U52915; AAC52599.1; -
 CC EMBL; Y10298; CAA71343.1; -
 CC EMBL; U58861; AAC52705.1; -
 CC EMBL; U58862; AAC52706.1; -
 CC EMBL; U58863; AAC52707.1; -
 CC EMBL; AF039456; AAB95334.1; -
 CC EMBL; AF039443; AAB95334.1; JOINED.
 CC EMBL; AF039444; AAB95334.1; JOINED.
 CC EMBL; AF039445; AAB95334.1; JOINED.
 CC EMBL; AF039446; AAB95334.1; JOINED.
 CC EMBL; AF039447; AAB95334.1; JOINED.
 CC EMBL; AF039448; AAB95334.1; JOINED.
 CC EMBL; AF039449; AAB95334.1; JOINED.
 CC EMBL; AF039450; AAB95334.1; JOINED.
 CC EMBL; AF039451; AAB95334.1; JOINED.
 CC EMBL; AF039452; AAB95334.1; JOINED.
 CC EMBL; AF039453; AAB95334.1; JOINED.
 CC EMBL; AF039454; AAB95334.1; JOINED.
 CC EMBL; AF039455; AAB95334.1; JOINED.
 CC HSP; P40189; IBOU.
 CC MGD; MGI:104993; Lepr.
 CC InterPro; IPR002996; CRIA.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003529; Hematopo_receptor_L_F2.
 CC Pfam; PF00041; fn3; 3.
 CC SMART; SM00060; FN3; 3.
 CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Polymorphism; Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1162 LEPTIN RECEPTOR.
 FT DOMAIN 22 839 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 840 860 POTENTIAL.
 FT DOMAIN 861 1162 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 236 318 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 535 621 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 736 821 FIBRONECTIN TYPE-III 3.
 FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	345	345	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	431	431	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	514	514	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	622	622	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	657	657	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	668	668	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	686	686	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	695	695	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	698	698	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	726	726	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	VARSPLIC	890	894	PETE -> RIDTL (IN ISOFORM A).	
FT	VARSPLIC	895	1162	MISSING (IN ISOFORM A).	
FT	VARSPLIC	890	892	PET -> VTV (IN ISOFORM C).	
FT	VARSPLIC	893	1162	MISSING (IN ISOFORM C).	
FT	VARSPLIC	890	900	PETEHLFTKH -> DISFHEVFIFR (IN ISOFORM D).	
FT	VARSPLIC	901	1162	MISSING (IN THE ISOFORM D).	
FT	VARSPLIC	797	805	DNPIEKY -> GNCVTFMD (IN ISOFORM E).	
FT	VARSPLIC	806	1162	MISSING (IN ISOFORM E).	
FT	VARIANT	541	541	V -> I (IN STRAIN NOZ).	
FT	VARIANT	651	651	V -> I (IN STRAIN NOZ).	
FT	VARIANT	1044	1044	T -> I (IN STRAIN NOZ).	
FT	CONFLICT	140	140	F -> I (IN REF. 6).	
FT	CONFLICT	720	720	A -> T (IN REF. 5).	
SQ	SEQUENCE	1162 AA;	130788 MM;	OEIE75B076BA60A2 CRC64;	
Query Match 76.2%; Score 4766.5; DB 1; Length 1162;					
Best Local Similarity 75.4%; Pred. No. 0;					
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;					
Qy	1	MICQKFCVLLHWEIYVITAFNLSYPTIPWRFKLSCHMPNPNSTYDFLLPAGLSKNTNS	60		
Db	1	MMQCFYVLLHWEIYVITAFNLSYPTIPWRFKLSCHMPNPNSTYDFLLPAGLSKNTNS	60		
Qy	61	NGHYETAVEPKFNSGTHFNSLSKTFHCCPSEORNCSLCADNIEGKTFVSTVNSLVF	120		
Db	61	KGAEAIVEAKFNSGTHFNSLSKTFHCCPSEORNCSLCADNIEGKTFVSTVNSLVF	120		
Qy	121	QOIDANWITQCKGLDKLFTICVYVESLFKNLFRNRYKVLHLYLPEVLEDSPLVPQKGS	180		
Db	121	ROLGVNWDIECKMKGDLFLFICHEMPLKPNPKNYDSKVHLLYDLPEVIDDSPLPLKDS	180		
Qy	181	FOMVHCNCSVHCCBCLVPVPTAKUNDLLMCLKITSQGVIFQSPMLSVQPINWYKPDPP	240		
Db	181	FOTVQCNCSLRG-CCHVPVPRAKUNLALMYLEITSAGVSQSPMLSLQPLMLVYKPDPP	239		
Qy	241	LGLHMEITDDGNLKYSWSSPPLVPFPLOYOVKYSNSTVIREADKIVSATSLLVDSILP	300		
Db	240	LGLHMEITDDGNLKYSWSSPPLVPFPLOYOVKYSNSTVIREADKIVSATSLLVDSILP	298		
Qy	301	GSSYEVOVRKRLDGPWSDMSTPRVFTTQDVYFPFKILTSVGSNSVSHFCIYKKNKI	360		
Db	299	GSSYEVOVRKRLDGPWSDMSSPQVFTTQDVYFPFKILTSVGSNSVSHFCIYKKNKI	358		
Qy	361	VPSKEIVWMNLAEPKQSDVSDHVSQVTFNMLNETKPGKTTYDAVYCCNEHECHH	420		
Db	359	ISSKQIVWMNLAEPKQSDVSDHVSQVTFNMLNETKPGKTTYDAVYCCNEHECHH	418		
Qy	421	RYAEIYVIVDNNISCTDGYLTCTKRWSTSTIOSLAESTIQLRYHRSLSYCSIDIPSTH	480		
Db	419	RYAEIYVIVDNNISCTDGYLTCTKRWSPSTIOSLGVSTVQLRYHRSLSYCSIDIPSTH	478		
Qy	481	PISEPKOCYLOSDGYECFQIFLLSGYTMIRNHSLSGSDSPPTCVLPDSVVKPLPP	540		
Db	479	PISEPKOCYLOSDGYECFQIFLLSGYTMIRNHSLSGSDSPPTCVLPDSVVKPLPP	538		
Qy	541	SSVKAETITNIGLLKISKEKVPFPENNLOFQTRYGLSKEVQWKMVEYVDAKSVSPLV	600		
Db	539	SNVKAETITNIGLLKISKEKVPFPENNLOFQTRYGLSKEVQWKMVEYVDAKSVSPLV	598		
Qy	601	PDLCAVYAVQVCKRLDGLGYWNSNPNAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV	660		

Db	599	SDLCAVYVYVQVRRRLDGLGYWNSNPNAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV	658		
Qy	661	TLLMKPLKNDKSLQSVQRYVINHTSCNGTWSEYDGNHKTETFLWTEQAHVTVVLAINSI	720		
Db	659	TLLMKPLKNDKSLQSVRYVVKHRTAHNGTWSEYDGNHKTETFLWTEQAHVTVVLAINSL	718		
Qy	721	GASVANFNLTSWPMKSNVIVQSIQSAVPLNSCVTVSVILSPDKLMYFIEKWNKLNED	780		
Db	719	GASLVNENLTSWPMKSNVIVQSIQSAVPLNSCVTVSVILSPDKLMYFIEKWNKLNED	778		
Qy	781	GEIKWLRISSSVKYVYIHDHFIPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA	840		
Db	779	DMKWLRIPIPSNVKFIYIHDHFIPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA	838		
Qy	841	GLYIVTVPIIISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNFQKPEFHLFI	900		
Db	839	GLYIVTVPIIISSSILLGLTLISHQRMKLLFWEDVNPKNCSWAQGLNFQKPEFHLFI	898		
Qy	901	KHTASVTCGPLLLEPETISEISVDTSWKNKDEMPPTVVSLLSTT-DLEKGSVCISQF	959		
Db	899	KHAESVIFGPIIPEPEISEISVDTWKNKDEMPPTVVSLLSTT-DLEKGSVCISQF	958		
Qy	960	NSVNESEAEGETVYEDESQRPVYKATLISNSKPSSETGEOGLINSVTKCFSSKNSP	1019		
Db	959	NSANFSGSQVTVCEDECQKQPSVKYATLVNSDKLVETDEEQGFIRSPVSNCSNNSP	1018		
Qy	1020	LKDFSSNSWETAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNPFPEENNDKKSYY	1079		
Db	1019	LKDFSSNSWETAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNPFPEENNDKKSYY	1077		
Qy	1080	LGVTISIKRESQVLLTDKSRVSCPPAPCLFTDIRVLQSDCSHFVENNINIGTSSKKTFA	1139		
Db	1078	LGVTISIKRESQVLLTDKSRVSCPPAPCLFTDIRVLQSDCSHFVENNINIGTSSKKTFA	1136		
Qy	1140	SYMFOFQCTSTHIMENKMCIDLTV	1165		
Db	1137	PYMPQFQCTSHIMENKMCIDLTV	1162		
RESULT 4					
IL6B_MOUSE STANDARD; PRT: 917 AA.					
ID	IL6B_MOUSE	STANDARD;	PRT:	917 AA.	
AC	Q00560;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin				
DE	6 signal transducer) (Membrane glycoprotein 130) (GP130).				
GN	IL6ST.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ICR; TISSUE=Macrophage;				
RX	MEDLINE=92291532; PubMed=1602143;				
RA	Saito M., Yoshida K., Hibi M., Taga T., Kishimoto T.;				
RT	"Molecular cloning of a murine IL-6 receptor-associated signal				
RT	transducer, gp130, and its regulated expression in vivo.";				
RL	J. Immunol. 148:4066-4071(1992).				
CC	- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR				
CC	IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING				
CC	SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,				
CC	RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,				
CC	AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN				
CC	EMBRYONIC DEVELOPMENT.				
CC	- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,				
CC	SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED				
CC	EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE				
CC	CELLS.				

RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RL Cell 63:1149-1157(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE-Synovium;
 RX MEDLINE-20341529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osakada F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis."
 RL J. Clin. Invest. 106:137-144(2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE-21269388; PubMed=11098061;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "Determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130."
 RL J. Biol. Chem. 276:8244-8253(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE-98169383; PubMed=9501088;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130."
 RL EMBO J. 17:1665-1674(1998).
 CC -!- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL-6, LIF, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for
 CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
 CC complex, resulting in the formation of high-affinity IL-6 binding
 CC sites, and transduces the signal. Does not bind IL-6. May have a
 CC role in embryonic development (By similarity).
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1) and
 CC secreted (isoform 2).
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2/gp130-
 CC RAPS; are produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -!- DISEASE: gp130-RAPS is an autoantigen found in rheumatoid
 CC arthritis (RA) but it is not specific to patients with RA.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- DATABASE: NAME-PRO; NOTE-CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
 CC -----
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 CC -----
 DR EMBL; M57230; AAA59155.1; -;
 DR EMBL; AB015706; BAA78112.1; -;
 DR PIR; A36337; A36337.
 DR PDB; 1BQU; 26-AUG-98.
 DR MIM; 600694; -;
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003962; FNIII_repeat.
 DR InterPro; IPR003529; Hematopo_receptor_L_F2.
 DR Pfam; PF00041; fn3; 3.
 DR PRINTS; PR00014; FNTYPEIII.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 KW Repeat; 3D-structure; Alternative splicing.
 FT SIGNAL 1 22
 FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 620
 FT DOMAIN 642
 FT DOMAIN 918
 FT DOMAIN 120
 FT DOMAIN 124
 FT DOMAIN 222
 FT DOMAIN 324
 FT DOMAIN 325
 FT DOMAIN 424
 FT DOMAIN 518
 FT DOMAIN 613
 FT DOMAIN 725
 FT DOMAIN 755
 FT DISULFID 28
 FT DISULFID 48
 FT DISULFID 103
 FT DISULFID 134
 FT DISULFID 144
 FT DISULFID 172
 FT DISULFID 182
 FT DISULFID 458
 FT CARBOHYD 43
 FT CARBOHYD 43
 FT CARBOHYD 83
 FT CARBOHYD 131
 FT CARBOHYD 131
 FT CARBOHYD 157
 FT CARBOHYD 227
 FT CARBOHYD 379
 FT CARBOHYD 383
 FT CARBOHYD 553
 FT CARBOHYD 564
 FT CARBOHYD 564
 FT VARSPLIC 325
 FT VARSPLIC 330
 SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;
 Query Match 5.5%; Score 345.5; DB 1; Length 918;
 Best Local Similarity 19.8%; Pred No. 1.4e-15;
 Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;
 QY 337 PPKILTSGVSNFRCIYKK---ENKIVPSKEIVWMNLAEPQSDVDVSDHVKVTF 393
 DB 33 PESPVVQLHSNFTAVCLVCKEKCMDYFHVNAVIVKTN-HFTIPKEQYTIIRNTASSVTF 91
 QY 394 FNLNTRKRGKTYDAVCCNEHECHHRYAEIYVDV-----NINISC-ETDGYLTK 444
 DB 92 TDI-----ASLNQLTCNLTFTGQLEQNVYGIITISGLPPKPKNLSICVINEG--KK 141
 QY 445 MTRCWSTSTIQSLAESTLQLRVHRSLSYCSIDPSIHPISSEPKDCYVLSQSGFYECI--FQP 502
 DB 142 MCEWDGG-----RETHLETNFTLASEWAT-----HKFA---DCKAKRDTPTSCIVDYST 188
 QY 503 IFLSGYTMIRINHSGLSDSPPTCVIPDSVVKLPSPSSVKAETIN-----IGLLKISW 558
 DB 189 VYFVN-IEWVEAEALGKVTSDHINFDPVYKVKPNPHNLS---VINSEELSSILKLTW 244
 QY 559 EXP-----VFPENNLFQIRYCLSGKEVQWKMYEVDKSKSVSLPVDL--CAVYAVQV 611
 DB 245 TNPSIKSVIILKYNIOYRTKDAST-----WSQIPPEDTASTRSFTVQDLKPFTEYVFR 299
 QY 612 RCKRLDGLCYWNSNPAYTVMYDIKVPMPGPEFWRINGDTMKKEKNVTLWKPLMKND 671
 DB 300 RCKMEDGKGYSDNSEEASGIYYEDR-PSKAPSFYWKIDPSHTQGYRTVOLWKTLPPPE 358
 QY 672 SLCSVQRYVINHHTSCNGTWSDEVDGNH---TKFTFLWTEQAHVTVVLAINSIGASVANF 727
 DB 359 ANGKILDYEVT-----LTPWKSHLQNYTVNATKLVNLTNDRYLATLTVRNLVGKSDAAV 413
 QY 728 NLTFSPWPKSVNIVOSLSAYPLNNSCVIVSWILSDYKLYMFIIEKNKLNEDGE--IKW 785
 DB 414 LTPACDFQATHPVMDLKAFP-KDNMLWYEWTPRESVK--KYILLEWCYLSDKAPCIDTM 470
 QY 786 LRISSSVKKYIYDHFPIETKYOFSLYPIFMEGVGKPKII----- 825
 DB 471 QOEDGTVHRTYLRGNLAESKCVLITVTPVIADGPGSPESIKAYLKQAPPKSGPTVTKVY 530
 QY 826 -----NSFTQDOIEKHQSADGLY- 843
 DB 531 GKNEAVLEWDLQPDVQNGFIRNYTFYRTIIGNETAVNVDSSTHTYLSLTSOT-LYM 589
 QY 844 -----VIVPVISSSI-LLLGTLILLSHQR--MKK 869

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Db 590 VRMAAYTDEGGKDGDEFTTTPKFAQGEIAIVVPVCLAFLLTLLGLVFCNKRLDIKK 649
QY 870 LEWEDVPNPKNSWAQGLNFQKPFTEFHLFIKHTASVTCGPIILLLEPETISEDIVSTWSK 929
Db 650 HIWPNVDPSPKSHIAQWSPHTTP-----RH-----NFN 677
QY 930 NKDEMPPTVVSLSTDLKSGVCSIQSFNSVNSEABGTVEYDESDORPPF---VKY 986
Db 678 SKDQM-----YSDGNFTDVSVEIEAND---KKPFPEDLKS 710
QY 987 AFLINSKPSTGEQGLINSVTKCFSSKNSPLKXDSFNS 1028
Db 711 LDLFKKEINTEGSHSGIGSS---CMSSSRPSISSDENES 749

RESULT 6
ID IL6B_RAT STANDARD; PRT; 918 AA.
AC P40190;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (gp130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92340; ; NOT_ANNOTATED_CDS.
DR PIR; A44257; A44257.
DR HSP; P40189; 1BOU.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat.
FT SIGNAL.
FT CHAIN 1 22 POTENTIAL.
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.

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FT DOMAIN 23 618 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 619 640 POTENTIAL.
FT DOMAIN 641 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 124 221 FIBRONECTIN TYPE-III 1.
FT DOMAIN 222 323 FIBRONECTIN TYPE-III 2.
FT DOMAIN 324 422 FIBRONECTIN TYPE-III 3.
FT DOMAIN 423 516 FIBRONECTIN TYPE-III 4.
FT DOMAIN 517 612 FIBRONECTIN TYPE-III 5.
FT DOMAIN 724 754 SER-RICH.
FT DISULFID 28 54 BY SIMILARITY.
FT DISULFID 48 103 BY SIMILARITY.
FT DISULFID 134 144 BY SIMILARITY.
FT DISULFID 172 181 BY SIMILARITY.
FT DISULFID 457 465 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECFF087F7 CRC64;

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Query Match 5.4%; Score 339.5; DB 1; Length 918;
Best Local Similarity 20.8%; Pred. No. 3.7e-15;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

QY 327 VFTQDVI-----YFPFKILTVSGNSVPHCIYKXENKIYPSKE---IWMNMLAE 374
Db 14 IFLTTSIGQLVEPCGIYFPVVGQSGNFTATCVLKKRCLQVSVNATYIVWKNHV- 72
QY 375 KIPQSDYDVVSHVSKVTFENLNETPRGKFTYDAYV-----CCNEHECHHRAELVVI- 428
Db 73 AVPKQGVTVINRTASSVTF-----TDVVFNQVQLTCNLSFGQIQSNVYGIT 119
QY 429 -----DVYINIS-ETDGYLTMTKCRWSTSTQSLAESTLQLRYHRSSLYCSDPSIH 480
Db 120 ILSGYPDPDPTNLSCLVNEG--KNMLCQ-----LDPGRETYLETNYTLKSEATE----- 167
QY 481 PISEPKDCVQLQSDGFECI--FOPIFLSGYTMIRINISLGLSDSPPTCVLPDVSVKPL 538
Db 168 ---KFPDCRTK-HGTSSCMMGYTPYFVN-IEYVVEAENALGNVSSEPIINFDPVKVKPS 222
QY 539 PPSSVKAETITNI-GLLKISW-----EKVPENNNLQFOIRYGLSGKEVQWKMYEYDAK 592
Db 223 PHNLVSVTNSBELSLKLAWNSGLDSILRLKASDIQYRKDAST-----WIOVPLEDIV 277
QY 593 KSVSLVPDPL--CAYVAVQVRCRLDGLGYSNWSNPAYTVVMDIKVPMRGPFWRIN 650
Db 278 SPRTSFTVQDLKPFTEYVFRIRSIKENGKGYWSDWEASGTYVEDR-PSKAPSEWTKVN 336
QY 651 GDTMKKEKNVTLWKPLMKNDLSCVQRY--VINHTSCNGTWSVEDVGNUTKFTFLWTEQ 708
Db 337 ANHPQYRGLRIWKLPLSEANGKITLDYEVLTQSKSVSQTYTV---NGTEILVNLTN 393
QY 709 AHTVTVLAINSIGASVANFNLTFSWPMKV-NIVQSLASVPLNSSGVIVSWILSPSDYKL 767
Db 394 RVASLAARNVVGKSPATV-LTIPGSHFKASHVVDLKAFF-KDNLWVW-TPPSKPV 449
QY 768 MYFIEWKNLNEDGEI--KWLRISSSKYKYIHDHPIPIEKYQFSLYPIPMGVGKXP--- 822
Db 450 NKVILEMVLSENPCIPDQDQEDGVNTHLRGSLLESKCYLITVTPVPPGGPGSPESM 509
QY 823 -----KI 824
Db 510 KAYLQAAPSKGPTVRTKKVKGNEAVLEMDHLPDVQNGFIRNYSIRTSYSGKEMVVR 569

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QY 825 INSFTODDIEKHQSDAGLY-----VIVPVVLS 852
Db 570 DSSHTYTLSSLSST-LYMHVMAAYTEEGKDGPEFTTTLFAQGEIAIVVPVCLAF 628
QY 853 SI-LLLTGLLISHOR--MKLFWEDVPNPKNCWSAQLNFQKPEHFLF-----YKHTA 904
Db 629 LLTTLGLVLCFKNRDLIKKHHPNVPDPKSHIAQWSPHTPP--RHFNPSKQDMYSDA 685
QY 905 SVTCGPLLLEPETISEDIVSTSWKNKDEMPPTVVVSLSTTDLEK----- 950
Db 686 NPT-----DVSVEITEANKKPCDDKLKSL-----DLFKKEKISTEGHSGIG 728
QY 951 GSVICISQNSVNFSAEGTEVYDEBSORO--PFVKYATLNSKPSPTGEQGLNLS 1008
Db 729 GSSCMSSRSPTSSSSE-----ENESAQSTASTVQYSTVHSHYRHOVPSVQVFSRSE 780
QY 1009 VTK-CFSSKNSP----LKDSFSSNSEEIAQAFILSDQHPNIIISPLHT 1052
Db 781 STOPLDSRERPDQLVDSVDSGDILPRQYFKSCSQPG-ASPDVS 828
RESULT 7
GCSR_MOUSE STANDARD; PRT; 837 AA.
AC P40223;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R).
GN CSF3R OR CSFGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90235283; PubMed-2158861;
RA Fukunaga R., Ishizaka-Ikeda E., Seto Y., Nagata S.;
RT "Expression cloning of a receptor for murine granulocyte colony-
stimulating factor.";
RL Cell 61:341-350(1990).
RN [2]
RP STRUCTURE BY NMR OF 225-333.
RX MEDLINE-97331327; PubMed-9187659;
RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the Wsxs
motif of the granulocyte colony-stimulating factor receptor and its
interaction with ligand.";
RL Nat. Struct. Biol. 4:498-504(1997).
CC -!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS AT
THE CELL SURFACE.
CC -!- SUBUNIT: DIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN BONE MARROW.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M58288; AAA37673.1; -.
DR PIR; A34898; A34898.
DR PDB; 1GCF; 22-OCT-97.
DR MGD; MGI:1339755; Csf3r.
DR InterPro; IPR002996; CRIA.

DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo__receptor_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 1.
KW PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Repeat; 3D-structure.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 837 GRANULOCYTE COLONY STIMULATING FACTOR
RECEPTOR.
FT DOMAIN 26 626 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 627 650 POTENTIAL.
FT DOMAIN 651 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 118 118 IC-LIKE C2-TYPE DOMAIN.
FT DOMAIN 122 228 FIBRONECTIN TYPE-III 1.
FT DOMAIN 229 333 FIBRONECTIN TYPE-III 2.
FT DOMAIN 334 431 FIBRONECTIN TYPE-III 3.
FT DOMAIN 432 528 FIBRONECTIN TYPE-III 4.
FT DOMAIN 529 624 FIBRONECTIN TYPE-III 5.
FT DISULFID 132 143 BY SIMILARITY.
FT DISULFID 249 296 BY SIMILARITY.
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 837 AA; 93406 MW; 42295989E2C8531 CRC64;

Query Match 5.0%; Score 313; DB 1; Length 837;

Best Local Similarity 20.0%; Pred. No. 2e-13;

Matches 183; Conservative 125; Mismatches 311; Indels 298; Gaps 40;

QY 337 PPKILTSVGSNVSFHC-IYKKNKIVPSKEIVMMMLAEKIPQSDYDVYSD--HVSKVTF 393
Db 33 PP--VVRIGDPVLASCTISPNCSKLDQQAQILWRLODEIOPGDRQHLPDGTQESLITL 90
QY 394 FNLNETKPKGFTY-----DAVYCNEHECHHRYAELXVIDVNIINISCTDGYLFKMTK 447
Db 91 PHLNYTQ--AFLFCLVPWEDSVQLLDAQELHAGYPPA---SPSNLSCLMLHLTTNSLVC 143
QY 448 RWSTSTQSLAESTLQLRVHRSLSYCDIPSHPISEPKCYLQSDGFYECIFQP----- 502
Db 144 QMEPGPETHLPTSFI-LKSFRR-----ADCCYQGGDTIPDCVAKKRONNC 187
QY 503 -----IFLLSGYTMIRINHSLGSLDSPPTCVLPDSVVKPLPPSSVKAETITNI----- 551
Db 188 SIPRKNLLLYQYMAIWQAEENMLGSSESPKCLDPMQVVKLEPPMLQALDIDGVVSHQP 247
QY 552 GLLKISWEKVPFENNL--QFQIRYGLSKEVQWKMYEYDAKSKSVSLPVPDLCA---- 605
Db 248 GCLWLSW-KPWKPSEYMEQECRLYQPLKGANWTL--VFHLPPSSKQDF---ELCLGHOA 301
QY 606 --YAVQVRCKRLDGLGYWNSWNSPAYTVMDIKVPRGPEFWRIINGDMTKKEK----- 658
Db 302 PVTYLMRCIRSSLPGFWSWPS-PG-----LQURPTWKAP-----TIRLDWCQKKQLDPGT 352
QY 659 -NVTLLWKLPMKNDLSQVRYVINHTS-----CNGTWSDEDVGNHKTFTFLWTEQ 708
Db 353 VSVQLFWKFTPLQEDSGOIQGYLLSNWSPDHQODIHLNNT-----QLSCIFLLPSE 405
QY 709 AHTVTVALNSIGASVANENLTFSWPMKVNIVQSLSAYPLNSCVISVW---ILSPSDY 765
Db 406 AQNVTLVAYNKAGTSSPT---TVVLENEGPAVTGLHAMAQDLNTIWDWEAPSLPQGY 462
QY 766 KLMYFIENK----NLNEDGEIKWLRISSVKKYIYTHDHFPIEIKYQFSLYPIFMGVGK 821


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Db 463 -----LIEWEMSPYNNYSKSWMIEPNNGNTGILLKNDINFPQIXRITVAPLYPGIVGP 517
QY 822 PKIINSFT-----
Db 518 PNVYTFAGERAPPAPALHLKHVGTWQAELWVPEAPRLGMIPLTHYTFWADAGDSHF 577
QY 830 -----QDDTEKHQSAGLY-----
Db 578 SVTLNISLHDFVLKLEFASLVHYVLMATSRAGSNSTGLTURTLDPSDLNIFLGILCLV 637
QY 849 IISSELLIGTLISHQRMKLFWDVNPKNCSNAQGLNFQKPTFEHLFIKHTASVTC 908
Db 638 LLSTCVV--TWLCKRRGKTSFWSVDVDPAPHSLSLW-----
QY 909 GLLLEPETISEDISVDTSWKNKDEMPVTVVSLLSTLDLEKGSVCIS--DQPNVSNFS-- 965
Db 675 -PTIMEET---FQLPSFW-----DSSVPSITKITELEEDKKRPTHWDSSESGSLP 722
QY 966 -----EAGTEVTEYEDSORQPFVKYATLISNKPSETGEE-----Q 1002
Db 723 ALUQAVYVQGDPREIS-----NOSQP-----PSRTGDQVLYGQVLESPTSPGVM 766
QY 1003 GLINSVTKCFSSKNPLKDSFNSWEIEAQAFILSDQHPN-----IISPHLTFS--- 1054
Db 767 QYIRSDSTOPLGGTSPSKSYENIWFHSRQETEV--PQPNQEDDCVFGPPDFPLEF 824
QY 1055 -----EGLELLKLEGNF 1067
Db 825 GLQVHGVEE---QGGF 837

RESULT 8
LIFR_HUMAN STANDARD; PRT; 1097 AA.
AC P42702;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leukemia inhibitory factor receptor precursor (LIF-R).
GN LIFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92007727; PubMed=1915266;
RA Gearing D.P., Thut C.J., Vandenbos T., Gimpe S.D., Delaney P.B.,
RA King J., Price V., Cosman D., Beckmann M.P.;
RT "Leukemia inhibitory factor receptor is structurally related to the
RL IL-6 signal transducer, gp130."
RL EMBO J. 10:2839-2848(1991).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY
CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF
CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
CC -!- SUBUNIT: HETEROIMER COMPOSED OF LIFR AND GP130.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A
CC MEMBRANE-BOUND AND A SECRETED FORM.
CC -!- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS
CC MAY ARISE BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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CC EMBL; X61615; CAA43805.1; -.
DR MIM; 151443; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
KW Alternative splicing; Repeat.
FT SIGNAL 1 44 POTENTIAL.
FT CHAIN 45 1097 LEUKEMIA INHIBITORY FACTOR RECEPTOR.
FT DOMAIN 45 833 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 834 858 POTENTIAL.
FT DOMAIN 859 1097 CYTOPLASMIC (POTENTIAL).
FT DISULFID 55 65 BY SIMILARITY.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 426 426 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 652 652 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 680 680 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 729 729 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 787 787 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1097 AA; 123742 MW; C8602897E359FCE5 CRC64;

Query Match 4.7%; Score 294.5; DB 1; Length 1097;
Best Local Similarity 19.2%; Pred. No. 5.3e-12;
Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;

QY 161 LLYLPEVLEDSPLVPQKGSFQMVHC-----NCS-----VHECC----- 194
Db 35 LLYLMNVNSQ-----KKGAPHDLKCVTNLQVWNCWSKAPSGTGRGTDEYECIENRSRS 89

QY 195 -----ECLVPVPTAKLNDTLMLCKITSGGVIFQSPINMVQPINMKVPPGLHMEIT- 248
Db 90 CYOLEKTSIKIPALSHGDEITINSLHDFGSSSTKFTLNEQVSLI-PDTPEILNLSADF 148

QY 249 DGNLKIWSPPPLVPFPLOYQVQKYSNSTTVIR-----EADKIVSATSLI----- 294
Db 149 STSTLYLKWNRGVS-FPHRSNVIV---ETKVLKESMELVKLVTHNTTLNGKDTLHWS 204

QY 295 --VDSLTPGSSYEVR-----CKRLDGPICWSQSWSPRVFT---TODVIYFPKILTSVG 345
Db 205 WASDMPLECAIHFEIVELIDNLHPSGLSEWSDSWPKVNSWIPDSQTKVFPQDKVILVG 264

QY 346 SNVSFHCIVKKNKIVPSKEIVMMNLAKEIPQSQDQVW---SDHVSQVTFNLTNLTQPR 402
Db 265 SDITCCV-----SQEKV-----LSALIGHTNCPILHLDGENVA-TKIRNISVASS 310

QY 403 GKFTYDAVCCNEHCHRYAEIYVIDVNVINISCEPDGYLTMTKWCWSSTQSLA---E 459
Db 311 GT---NWFTTEDNIFGTIFAGYPPDTPQNLNCETHD-LKEIICSWNPGRVATLVGPA 366

QY 460 STLQLRYHRSSLYCSDIPSIHRISEPKCYLOSDFGYECIFQIFLLSGYTWIRNHS 519
Db 367 TSYTLVESFSGYVRLKRAEPTNES-----YQLLQFQMLPQOEIYNETLNAHNP 416

QY 520 GSILDSPTCVLPDPSVVKPLPPSSVKAETINIGLLKISWEKP-----VFPEN 566
```

Db 417 GRSQSTILVNITEKVY-PHTPTSFVKV-DINSTAVKLSWHLPGFAKINFLCEIEIKSN 474
QY 567 NLQFOIRVGLSGKEVQWMEYVDYDAKSKSVLPVPDLCVAVAVQVRCRLDGLGYSWNS 626
Db 475 SVQORNTYIKVE-----NSSYLVALDKLNPYTYTFRICS-TETFWKWSKS 523
QY 627 NPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNVTLLMKPLMKNSLCSQVQVINHHITS 686
Db 524 NKKQHLTEAS-PSKGPDTRWESSD---GKNLIYWKPLPNEA---NGKILSYNVS 574
QY 687 CNG-----TWSDVGNHVKFTPLWTEQAHVTVLAINSIGASVANFNLPSPMKSKNIV 741
Db 575 CSDEETOSLSIPDQHQAEIRLDKNDYIISVAKNSVSGSPPKIASMEIPDLKTE 634
QY 742 QSLSAVPLNSCVIYSWILSPS---DYKLMYFIIEKN--LNEDGEIKWLRI-SSSVKY 795
Db 635 QVQGM-----GKILITWHYDPNMTCDY-----VIKWCNSRSEPCMDMRKVPNSSTEV 685
QY 796 YIHDHIFIEKYOFSLYPIFMEG-----VG-----KPKIINSFTQDD----- 832
Db 686 IESDEFRCIRYNFFLYGCRNGYQLLRSMICYIEELAPIVAPNFTVEDTSADSLVKWE 745
QY 833 -----TEKHSD----- 839
Db 746 DIPVEPLRGLRGYLFYFGKERDTSKMRVLESGRSDIKVKKNITDISQTLRIADLQGT 805
QY 840 -----AGLYVI-----VPIIISILLTLLISHOR--M 867
Db 806 SYHLVLRAYTDGCVGPEKSMYVTKENSVGLLIALLIPVAVITVGVVTSILCYRKREWI 865
QY 868 KKLFWEDVPNPKNCWAQGLNFQK-----PETFEHLFKHTASVTCGPLL 912
Db 866 KETFPDTPNPENC---RALQPKSGVCGSSALKTKLENNPCPNNVLETRSFAF--PKI 920
QY 913 LPEPTISEDISVDTSKNKDENMPTTVVYLLSTTDLEKGSVC---ISDFNSVNFSEARG 969
Db 921 ETEIIS---PVAERPDORSDEPNHVWV-----SYCPPIIEEIPNPADEAGG 968
QY 970 T-EVYTED-ESORQPFVYATLINSKPSKETGEQGL-----INSSVTKCFS- 1014
Db 969 TAQVIYIDVQSMYQF-----QAKPEEQENDPVGAGYKQPHLPINSTVEDIAAE 1019
QY 1015 ---SKNSPLKDSFNSWEIEAQAFILSDQHPNIISP 1049
Db 1020 EDLDKTAGYRPOANVTW-----NLVSP 1042

RESULT 9
GCSR_HUMAN STANDARD; PRT; 836 AA.
AC G99062;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)
DE (CD114 antigen).
GN CSF3R OR GCSFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91079757; PubMed=2147944;
RA Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman D.,
RA Park L., Sorensen E., March C.J., Smith C.A.;
RT "Expression cloning of a human granulocyte colony-stimulating factor
RT receptor: a structural mosaic of hematopoietin receptor,
RT immunoglobulin, and fibronectin domains.";
RL J. Exp. Med. 172:1559-1570(1990).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;
RX MEDLINE=91062348; PubMed=1701053;
RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
RT "Three different mRNAs encoding human granulocyte colony-stimulating
RT factor receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8702-8706(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92091782; PubMed=1530796;
RA Seto Y., Fukunaga R., Nagata S.;
RT "Chromosomal gene organization of the human granulocyte colony-
RT stimulating factor receptor.";
RL J. Immunol. 148:259-266(1992).
RN [4]
RP DOMAINS STRUCTURE
RX MEDLINE=92007729; PubMed=1717255;
RA "Functional domains of the granulocyte colony-stimulating factor
RT receptor.";
RL EMBO J. 10:2855-2865(1991).
RN [5]
RP STRUCTURE BY NMR OF 227-334
RX MEDLINE=97331327; PubMed=9187659;
RA Yamasaki K., Naito S., Anaguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the WSXWS
RT motif of the granulocyte colony-stimulating factor receptor and its
RT interaction with ligand.";
RL Nat. Struct. Biol. 4:498-503(1997).
RN [6]
RP 3D-STRUCTURE MODELING OF 125-331.
RX MEDLINE=98037802; PubMed=9368043;
RA Layton J.B., Iaria J., Smith D.K., Treutlein H.R.;
RT "Identification of a ligand-binding site on the granulocyte colony-
RT stimulating factor receptor by molecular modeling and mutagenesis.";
RL J. Biol. Chem. 272:29735-29741(1997).
CC -!- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
CC EVENTS AT THE CELL SURFACE.
CC -!- SUBUNIT: DIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
CC OF THE RECEPTOR.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: GCSFR-1 (SHOWN HERE),
CC GCSFR-2, GCSFR-3 AND GCSFR-4/D7; SEEM TO BE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES
CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
CC -!- DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME;
CC ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
CC -!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD114 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd114.htm".
CC -----
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CC -----
CC EMBL; X55721; CAA39253.1; -
CC EMBL; X55720; CAA39252.1; -
CC EMBL; S71484; AAB20660.1; -
CC EMBL; M59818; AAA63176.1; -
CC EMBL; M59819; AAA63177.1; -
CC EMBL; M59820; AAA63178.1; -
CC PIR; JH0329; JH0329.

"Three different cDNAs encoding mouse D-factor/Lif receptor.";

J. Biochem. 115:557-562(1994).

- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY WITH GPI30. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.

- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GPI30.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A MEMBRANE-BOUND AND A SECRETED FORM.

- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS MAY ARISE BY ALTERNATIVE SPLICING.

- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN, AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF THE SECRETED FORM.

- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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EMBL; S73496; AAC60698.1; -

DR EMBL; S73495; AAC60697.1; -

DR EMBL; D26177; BAA05165.1; -

DR EMBL; D17444; BAA04258.1; -

DR MGD; MGI:96788; Lifr; CRIA.

DR InterPro; IPR002996; Lifr.

DR InterPro; IPR003961; FN.III.

DR InterPro; IPR003529; Hematopo_receptor_L_F2.

DR Pfam; PF00041; fn3; 4.

DR SMART; SM00060; FN3; 3.

DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.

KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

KW Alternative splicing; Repeat.

FT SIGNAL 1 43 POTENTIAL.

FT CHAIN 44 1092 LEUKEMIA INHIBITORY FACTOR RECEPTOR.

FT DOMAIN 44 828 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 829 853 POTENTIAL.

FT DOMAIN 854 1092 CYTOPLASMIC (POTENTIAL).

FT DISULFID 53 63 BY SIMILARITY.

FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 421 421 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 453 453 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 476 476 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 647 647 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 658 658 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 675 675 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 724 724 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 782 782 N-LINKED (GLCNAC. .) (POTENTIAL).

FT VARSPLIC 718 719 AP->EA (IN SECRETED ISOFORM).

FT VARSPLIC 720 1092 MISSING (IN SECRETED ISOFORM).

SQ SEQUENCE 1092 AA; 122573 MW; 6F02BBC8E154DE70 CRG64;

Query Match 4.5%; Score 281.5; DB 1; Length 1092;

Best Local Similarity 18.8%; Pred. No. 4e-11;

Matches 217; Conservative 177; Mismatches 392; Indels 371; Gaps 57;

QY 178 KGSFQVHCNCVSHVCECECLVPP-----TAK-----LNDTLMC--LKITSGGVFQSP- 225

DB 45 KRGVODLKCTTNNMRVNDCTNPAPLGVSGVTGKDIKDRFHSHCPLETTNNKIPALSPG 104

QY 226 -----LMSVQPINMKVDPDPPLGLHMEITDD---GNLKISNWS--PPLVPP 265

DB 105 DHEVTINLVNGFQSKFTLNKEDVSLIPETPEI---LDLSADFFTSLLKWNDRGSLPH 161

QY 266 P--LOYQVKYSENSTTVIREADKIVSATSL------VDSILPGSSYVQVVRGK 311

DB 162 PSNATWEIKVLONPT---EPVALVLTNMLSGKDTVOHNNWTSDDLPLQCATHSVIRW- 217

QY 312 RLDGPGI-----WSDWSTPRVFT---QDVIYFPFKILTSVGSNVSFHCYKKNKIVPS 363

DB 218 HIDSHPHSGYKESDWSPLKNISWIRNTETNVFPQDVVLGASNMKTC-----MSPT 270

QY 364 KEIYVMM-NIAEKIPOSQYDVVSHVSKVTFEFLNETKPRCK-----FTYDAVYCCNEHC 418

DB 271 KVLSEQIGNTLRPLIHLYGQTVAIHI-----LNIPVSENSGTNFIITDDDV----- 317

QY 419 HRYRAEL---YVDVNIINISCETDGYLTMTKCRWSTSTIQSL-----AESTL----- 462

DB 318 ---YGTVVFAFPDVPQKLSCEHD-LKEICSWNPQRIGLVGRNTEYTLFESISGK 373

QY 463 QLRVHR-----SSLYCSDIPSIPISEPKCYLQSDGFEYCIQPIFLLSGYTWIRINH 517

DB 374 SAVFHRIEGLTNETYRLGV-QMHPGQEIHN-----FTLTG-----RN 409

QY 518 SLGSLDSPPTCVLSDSVVVKPLPPSSVRAEITINIGLLKISKEKP-VPENNLQFQIRVGL 576

DB 410 PLGQAQSAVVINTVERVA-PHDPYSLKVK-DINSTVTFVSWYLPNGFTKIMLLQIEICK 467

QY 577 SGKEVQMKMYEYDAKSKSVSLPVDL--CAVYAVQVRCRLDGLGYWMSNMSPAYTVVM 634

DB 468 ANSKKEVNATIRGAEDSTYHVAVDKLNPYATYFRVRCSS-KTFWKWSRWSDEKRLHT 526

QY 635 DIKVPMRGPEFWRIINGDTMKKEKNVLLKPLMKNSLCSQVRYVIVNHHTSCNGTWSED 694

DB 527 E-ATPSKGPDTWREWSSD---GKNLIYVWKPLPINEA---NGKILSYNVS----- 571

QY 695 VGNHTKFTFLTEQAH-----TVTVLANISGASVANFNLTSPWMSKVINQVS 743

DB 572 LNEETQSVLEIFDPOHRAEIOLSKNDYIISVVARNSAGSPSPKIASMEIPNDITVQQA 631

QY 744 LSAYPLNSSCVIVSWILSPS---DYKLMYFTIEWKN--LNEDGEIKWLRI--SSSYKYYI 797

DB 632 VGL---GNRIFLWRHDPNNTCDY-----VIKWCNSSRSEPCLLDWRKVSNSTETVIE 682

QY 798 HDHFTPIBKYSFYLPIMEG-----VG-----KPKIINSFTQDD----- 832

DB 683 SDQFQGVRYNFYLYGCTNOGYQLRSIIGYVEELAPIVAPNFTVEDTSADSLVKWDDI 742

QY 833 -----TEKHOSDAGL----- 842

DB 743 PVEELRGFLRGYLFYQKGERDTPKTRSLRPHSHDIKKNITDISOKTLRIADLOGKTSY 802

QY 843 -----YVIVPVISSILLGLTLLSHOR--MKK 869

DB 803 HVLRYATHGGLGPEKSMFVVTKENSGLIIAILIPVAVAVIVGVVTSILCYRKREMIKE 862

QY 870 LFWEVDPNPKNCNAQGLNFOKPEFHLFIKHTASVTCGPPLLLEPEPTEISEDISVDTSWK 929

DB 863 TFYPDIPNENC---KALQFKSVCEGSKNALKTLEMNFCPT-----NNVEYLESRS 910

QY 930 NKDEMPITVVVSLSTTDLKGSV-----CISDQFNSVNSEAG-TEVTYE 975

DB 911 IVPKIEDTEIISPAVERGSEVDPENHVVVSYCPPIIIEEITNPADEVGGSQVVI 970

QY 976 D-ESORQPFVKYATLISNKPSETGEEQGLINSSVTKCFSSKNSPKDKDSFNSSMEIEAQ 1034

DB 971 DVQSMYQPAK-----AEEQDV-----DPV----- 991

QY 1035 AFFILSDQHPNI---ISPHLTFSEGLDELLKLEGFPENNDKKSIIYLGVTISIKRSG 1091

DB 992 ---VVAGYKPKQMLPISPVEDTAAEDDEEGTAGYRPOANVTWNL-----VSPDSPRS-- 1042

QY 1092 VLLTDKSRVSCFPFPAPC 1108

CC LOW AFFINITY.

CC -1- SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH

CC AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND

CC IL12RB2.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: U64199; AAB36676.1; -.

CC HSSP: P40189; LBOU.

CC MGP: MG1-1270861; IL12rb2.

CC InterPro: IPR002996; CRIA.

CC InterPro: IPR003961; FN.III.

CC InterPro: IPR003962; FN.III.repeat.

CC InterPro: IPR003529; Hematopo_receptor_L_F2.

CC Pfam: PF00041; fn3; 4.

CC PRINTS: PR00014; FNTYPEIII.

CC SMART: SM00060; FN3; 3.

CC PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.

CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

CC SIGNAL 1 20

CC OR 23 (POTENTIAL).

CC CHAIN 1 874 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.

CC DOMAIN 21 639 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 640 656 POTENTIAL.

CC DOMAIN 657 874 CYTOPLASMIC (POTENTIAL).

CC DOMAIN 137 230 FIBRONECTIN TYPE-III 1.

CC DOMAIN 240 322 FIBRONECTIN TYPE-III 2.

CC DOMAIN 436 523 FIBRONECTIN TYPE-III 3.

CC DOMAIN 534 622 FIBRONECTIN TYPE-III 4.

CC CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 874 AA; 98196 MW; 582E4D21BF1FBD67 CRC64;

Query Match 3.5%; Score 220; DB 1; Length 874;

Best Local Similarity 20.3%; Pred. No. 4.2e-07;

Matches 166; Conservative 95; Mismatches 286; Indels 270; Gaps 42;

QY 433 NISCTEDGYLTWKTCRWSTSTTOSLAES-TLQRYHRSSLYCSDPSIHPISEPKDCYIQ 491

Db 142 NITSCVQEGENGTVACSWNSGKTYLKTNYTLQLS-GPNLNTCQ-----KOCF-- 187

QY 492 SDGFYEC-----IFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPSSVK 544

Db 188 SNRONCRNLDGINLSPDLAESIRTVRTAINDGNSSSLPHTTFFLDIVPLPLPMDIR 247

QY 545 ABITINIGLLKIS-----WB-KPVFPNNLQFOIRYGLSGKEVQWKMYEYVDKSKSV 596

Db 248 -----INFLNAGSGRGLOWEDEGVVNLQRYQLNSTS-----WNMVAATNAGK-- 294

QY 597 SLVPDPL--CAVYAVQVRCK-RLDGLGYSWNSNPAYTVMDIKVPMRGP-----EFWRII 649

Db 295 -YDLRLRPFTTEYEFQISSKHLHSG-GWSNWSSESIRT-----RTPPEEPVGLDIW-YM 346

QY 650 NGDTMKKKNVTLMLKPLMKNDSLCSVORYVINHHSTSCNGTWSVEDVGNHTKTFELMTE-- 707

Db 347 KODIDYDROQISLFWKSLNPSEARGKILHYQVTLQEVTKKTKTLQNTTRHTS-----WTRVI 402

QY 708 ---QAHTVTVLAINSGASVANFNLTFSWPMKSNIV-----OSLSAYPLNSSCV 754

Db 403 PRTGAWTASVSAANSKGASAP-----THINIVDLCGTGLLAPHOVSAKSENMDI 452

QY 755 IVSWILSP---SDYKLMYFIEMKLNEDGEI-----KWLK-----ISSVKKYVI 797

Db 453 LVTW--QPPKKADSAREVIVEMRAL-QPGSITKPPHWRIPPDNMKSALISENIKPYIC 509

QY 798 LDH-----HFTPI-----EKYQ-----808

Db 510 YEIRVHAISESGGSSIRGDSKHKAPVSGPHITAITEKKERLFIKSWTHIPFPQRCIL 569

QY 809 -FSLYPIFMGVGPKII-----NSFTQDDIEKH-----836

Db 570 HYRIYWKERDSTAQELCEIQYRRSQNSHIPISLQPRVTVVLMWTAVTAAGESPQGNERE 629

QY 837 ---QSDAGLVIVPVIISSIIILLGLLISHQRMK-----KLEW--EDVENPKNCW 883

Db 630 FCPQGGKANKKAFVISSICIAITVGTFSIRYFQKAFITLLSTLKPQWYSRTIPDPANSTW 689

QY 884 AGLNLFQKPFTEHFIKHTASVTCGPLLEPETISEDISVDTSWKNKDEMPTTVVSL 943

Db 690 VR-----KY-----PILEEKIQLPD-NLLMAWPTPEPEPLIHEVL 726

QY 944 -----STTDLEKGSVCISDQFNSVNFSEAEGETVYVEDESQROP 982

Db 727 YHMIPVVRQPYFVKRCOGQGYSTSKODAMYANTPATGTLTAEQLVNLKYVLESRDP 786

QY 983 FVKYATLIS-----NSKPSGETGEQGLINSVTKFCFSKNSPLKDSFNSNWEIAQ- 1034

Db 787 DSKLANLTSPLTVPVNYLPS-----HEGYLPSNIEDLSPEADP-----TDSFDLEHQH 836

QY 1035 ---AFILSDQHPNII-SPHLTFSE---GLDELKLE 1064

Db 837 ISLSIFASSSLRPLPGGERLTLDRKMGYDSLMSNE 873

RESULT 14

PRLR_CHICK

ID PRLR_CHICK STANDARD; PRT: 831 AA.

AC Q04594;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Prolactin receptor precursor (PRL-R) (CPRLP).

GN PRLR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEGHORN; TISSUE=Kidney;

RX MEDLINE=93075121; PubMed=1445292;

RA Tanaka M., Maeda K., Okubo T., Nakashima K.;

RT "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence.";

RL Biochem. Biophys. Res. Commun. 188:490-496(1992).

CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DR EMBL; U22924; AAA75039.1; -.
DR HSP; P16471; LBP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemato_p_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANS 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
FT CARBOHYD 831 AA; 94394 MW; 220916320f77FAC1 CRC64;
SQ SEQUENCE 831 AA; 94394 MW; 220916320f77FAC1 CRC64;

Query Match 3.0%; Score 190; DB 1; Length 831;
Best Local Similarity 17.4%; Pred.No. 4.2e-05;
Matches 159; Conservative 126; Mismatches 276; Indels 354; Gaps 42;

QY 229 VQPINNVKPPDPLGLHMETDDGNLKISWS--SPPLVP-----FPLOYQVKSYS 277
DB 119 VDVTSIVQSPVNLTEFORANIMYLWAKWSPLLADASSNHLHYHLRLKPEKEW 178
QY 278 TVVIREAKIVSATLLVDLSILPGSSYEVQVGRKRLDGGIWSMDSTPRVFTQDVIVFP 337
DB 179 EVV-----PVGVTQCKINRLNAGMRYVQVR-CMLD-PGENSEWSSER----- 220
QY 338 PKILTSVGSNVSFHCYIKKENIV-----PSKE--IVVMNLAELKIPQSOYDVSDHYSK 390
DB 221 -RILISGG-----LSPEKPTTKCRSPERETFCWV----- 251
QY 391 VTFFNLNETKPRGKFTYDAVYCCNEHECHRYAELYVDVININISCEITDGYLTMTCRWS 450
DB 252 -----KPG-----LD-----GGHPTNYLLYS 268
QY 451 TSTIQSLAESTLQRLYHRSSLYCSIPSHPISEPKDYL--QSDGFYECIFQPIFLLSG 508
DB 269 KEGEQVVE-----CPD-----YRTAGPNSCVFDKKHTSFV-----TV 301
QY 509 YTWIIRINHSIGSLDPPPCVLPDPSVVRKLPSSVKAET-----T 548
DB 302 YNITVKATNMGNSSDPHYVDVTVIVQDPDPAVNTLELKPINKPKYLMLTWSPPLAD 361
QY 549 INIGLLKISWEKVPENNLOFOIRYGLSGKGVQWKMYEVDYDAKSKVSLPVPDLCAVYA 608
DB 362 VRSGLWTLDELRLKPEEGEWEVTF--VGQOTQYKMFSLNPKK-----YI 406
QY 609 VQVRKRLDGLGYGWSNWSNPAYTVVYMDIKVPMRGPEEFWRINIGDTMKKEKNVTLLMKPL- 667
DB 407 VQTHCKP-DHHSWSWSSSEN-----IEIP-----NDFRVKD---MIVWIVLG 446
QY 668 MKNDLSGVQRYVINHHSCNTWSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANF 727
DB 447 VLSSLICLLM-----SWTMVLKGYRMITFILPPVP-----GPKIKGI 483
QY 728 NLTFSPNPMKSVNIQVSL--AYPLNSSCVSVISWLLSPDYKLMYFTIEWKNLNDEGEIKW 785
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Db 484 DTHLLETCKSEELLSALGCHGFPPTSDC-----EELLIEY 518
QY 786 LRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKRP-----KIINSFTODDIEKHQSDAG 841
Db 519 LEVEDS-----EDH-----QLMP--SHDSGRPSKNAKITLTKETDRDGRGSCDS- 560
QY 842 LYVIVPVIIS-----SSILLTGTLTLLSHQMKKLFWEDV-----PNP 878
Db 561 -----PSLLSEKRETCALPSALQIQDVRDQVQAKKGRKSWESYCVASERKALLFNESA 615
QY 879 KNCMW-AQGLNFKQKPETFEHLFI-----KHTASVTCGPLLLEPE-----TISEDIS 923
Db 616 KSTWPAVOLPNQPPPTPAYHSIVFAANKITSTTTNNVAAVLVENEERHQSLYSISSETIS 675
QY 924 -----VDTSMKNKDEMMPPTTVVSLSTTDLEKGSVCISDQFNVS- 962
Db 676 GGMKEOEEMENLHSKTQTQTVQVRQNRSEKLPFLNALMDYVEVHK---VRQDEBPTVL 732
QY 963 -NFSAEGTEVTYEDESQRPVFKYATLISN-----SKPSETGE 1000
Db 733 LKHKEKSGKIEKTYTISGASKETKYSTVMNHNLVLMPSRVLHTPTSOEPAKETSQNP 792
QY 1001 EOGLINSSVTKCFSS 1015
Db 793 QGQVETNMSYCMTA 807
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Search completed: August 15, 2002, 16:36:09
Job time: 719 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:20:00 ; Search time 54.95 Seconds
(without alignments)
2037.199 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICOKFCVLLHWEFIIVIT.....QTCSTQTHIMENKMDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR J1-1
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4784.5	76.5	1162	PC4184	leptin receptor, O
2	4766.5	76.2	1162	S68438	leptin receptor, s
3	3793	60.6	900	S68440	leptin receptor, s
4	3785	60.5	892	S68439	leptin receptor, s
5	3785	60.5	894	S68437	leptin receptor, s
6	3729	59.6	895	S74225	leptin receptor, i
7	3340	53.4	805	S68441	leptin receptor, s
8	366	5.9	917	I49699	glycoprotein I30 -
9	345.5	5.5	918	A36337	membrane glycoprot
10	339.5	5.4	918	A44257	interleukin-6 sign
11	313	5.0	837	A34898	granulocyte colony
12	294.5	4.7	1097	S17308	leukemia inhibitor
13	288.5	4.6	863	C38252	granulocyte colony
14	284	4.5	783	JH0329	granulocyte colony
15	281.5	4.5	1092	JX0312	differentiation-st
16	277	4.4	771	B38252	granulocyte colony
17	251.5	4.0	2302	T14328	prolactin receptor
18	220	3.5	830	I50455	prolactin receptor
19	209.5	3.3	831	J01655	titin - rabbit (fr
20	191.5	3.1	6805	S20901	titin - rabbit (fr
21	188	3.0	26926	I18344	hypothetical prote
22	182.5	2.9	1471	T19506	fibronectin - Afri
23	177	2.8	2481	A43908	hypothetical prote
24	174	2.8	1375	T13822	frizzled gene prot
25	172	2.8	1896	T08851	Down syndrome cell
26	170	2.7	1232	T43027	neural cell adhesi
27	169.5	2.7	1443	I50600	neogenin - chicken
28	166.5	2.7	2029	1 TDFPLK	protein-tyrosine-p
29	166	2.7	3488	2 T34418	hypothetical prote

30	165	2.6	630	2	I51086	prolactin receptor
31	165	2.6	1326	2	T13823	frizzled gene prot
32	160	2.6	1197	2	T30581	neural cell adhesi
33	159	2.5	2340	2	I48310	kinase-related pro
34	158	2.5	1825	2	C88400	protein H19W22.1 l
35	158	2.5	1825	2	T32828	hypothetical prote
36	158	2.5	2338	2	I73957	kinase-related pro
37	156	2.5	1000	2	I46521	titin - rabbit (fr
38	154.5	2.5	2386	1	FNHU	fibronectin precu
39	153.5	2.5	440	2	JL0144	interleukin-6 rece
40	153.5	2.5	460	2	JL0145	interleukin-6 rece
41	153.5	2.5	610	2	A36116	prolactin receptor
42	150.5	2.4	310	2	A29884	prolactin receptor
43	150.5	2.4	412	2	A41070	prolactin receptor
44	150.5	2.4	5005	2	F82884	hypothetical prote
45	148.5	2.4	610	2	A34631	lactogen receptor

ALIGNMENTS

RESULT 1
PC4184
leptin receptor, Ob-Rb - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 13-Mar-1997, #text_change 01-Dec-2000
C:Accession: JC4895; JC4896; JC4897; PC4184; JC4797
R: Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; Ta
Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
A:Reference number: JC4895; MUID:96332408
A:Accession: JC4895
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1162 <TA3>
A:Cross-references: DDBJ:D85558; NID:gl526441; PIDN:BAA12831.1; PID:d1013515; PID:gl5
A:Accession: JC4896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TA2>
A:Cross-references: DDBJ:D85557
A:Accession: JC4897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796, 'G', 1157-1158, 'TVLLLN' <TA3>
A:Cross-references: DDBJ:D85559
R: Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 224, 597-604, 1996
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A:Reference number: PC4184; MUID:96255531
A:Accession: PC4184
A:Molecule type: mRNA
A:Residues: 840-1162 <IID>
A:Cross-references: DDBJ:D84550
R: Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from zucker f
A:Reference number: JC4797; MUID:96212906
A:Accession: JC4797
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <IID>
A:Cross-references: DDBJ:D84125; NID:gl374707; PIDN:BAA12230.1; PID:gl374708
A:Experimental source: adipose cell
C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa)
C:Genetics:
A:Gene: fa
C:Keywords: appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>
F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 76.5%; Score 4784.5; DB 2; Length 1162;
Best Local Similarity 75.6%; Pred. No. 6.5e-303;

Matches 882; Conservative 118; Mismatches 161; Indels 5; Gaps 5;			
QY	1	MICQKFCVLLHWEFIVITAFNLSPYITPWREKLSOMPNSYDYVFLLPAGLSKNTSNS	60
Db	1	MTQKQFVYVLLHWEFLVITAFNLALAYPTSPWREKLCFAPSTTDDSLSPAGVNPNTSSL	60
QY	61	NGHYETAVERPKFNSSGTHFNKSLTKTHCFCRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	KGASEALVEAKNSTGIYVSELSKTIHFCCFGNEQGCNSALTCNTEGKTLASVVKPLVF	120
QY	121	QQIDANNIOCWLGDKLKLFCYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPQKS	180
Db	121	RQLGVNWDIECMWKGDLTLFICHMEPLTKNPKNYDSKVLHLLDPLVEIDDLPLPLKDS	180
QY	181	FQWVHCNCSVHECECECLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMSVQPINNAKPDPP	240
Db	181	FQVOCNCSVRE-CECHVPVPRAKVNALLMYLEITSAGVSFQSPMSLQPLMLVVKPDPP	239
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQVQKYSNSTTVIREADKTVSATSLLVDSILP	300
Db	240	LGLRMEVTDGNNLKISWDSQTKAPFPLOYQVQKYLENS-TIVREAAEIVSDTSLLVDSVLP	298
QY	301	GSSVEVQVRKRLDGPGLGWSDMSTPRVFTTQDVLYFPKILTSVGSNVSPHCYKKNKI	360
Db	299	GSSVEVQVRKRLDGPGLGWSLQPLFTQDVWVFPKILTSVGSNASFCCYKKNQNT	358
QY	361	VPKSEIIVWNNLAEKIPQSOQYDVVSHVSKVTFNLTNETPRGKFTYDAYVCCNEHCCH	420
Db	359	ISSKQIIVWNNLAEKIPETOYNTVSDHISKVTFNLTNETPRGKFTYDAYVCCNEQACHH	418
QY	421	RYAELVYIDVNNISCTDGYLTKWTCRWSSTTQSLAESTLOLRHRSLYCSDIPSIIH	480
Db	419	RYAELVYIDVNNISCTDGYLTKWTCRWSPTQSLVGSTVQLRYHRSLYCPDNPISIR	478
QY	481	PISPEKCYLQSDGFYECIEQPIFLLSGYTWINHINSLGSDSPPTCVLPDSVVKPLPP	540
Db	479	PTSLKNCVILQTDGFCVQPIFLLSGYTWINHINSLGSDSPPTCVLPDSVVKPLPP	538
QY	541	SSVKAETITNIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMEVYDAKSKSVSLPV	600
Db	539	SNVKAETITNIGLLKISWEKVPFPENNLOFQIRYGLNGKEIQMKTHEVFOAKSKASLPV	598
QY	601	PDLCAYTAVQVRKRLDGLGYWSNWSNPATVTVNDIKVPMRGPEFWRRIINDTMKKEKNY	660
Db	599	SDLCAYVYVQVRKRLDGLGYWSNWSNPATVTVNDIKVPMRGPEFWRRIINDTMKKEKNY	658
QY	661	TLWKKPLMKNDLSLCVQRYVYINHTSCNCTWSESDVGNHTKFTPLWTDQAHTVIVLAINSI	720
Db	659	TLWKKPLMKNDLSLCVQRYVYVYKHTAHNGTWSQDVGNQTLTLWAEASHTVIVLAINSI	718
QY	721	GASVANPLTFSWPMKSNVIVQSILSAYPLANSSCVIVSWILSPSDYKLMYFIIEMKNNLED	780
Db	719	GASLVNPLTFSWPMKSNVAVQSILSAYPLSSSCVILSWILSPNDYSLYLVIEWKNNLND	778
QY	781	GETKWLRISSVKKYYIHDHPIEPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA	840
Db	779	DGKKWLRISSVKKYYIHDHPIEPIEKYQFSLYPIVMEGVGKPKIINGFTKDDIAKQONDA	838
QY	841	GLYVIVPVIISSLLTLLGTLISHORMKKLFWDVDPNPKNCSNAQGNLFQKPTFEHLFI	900
Db	839	GLYVIVPVIISSLLTLLGTLISHORMKKLFWDVDPNPKNCSNAQGNLFQKPTFEHLFT	898
QY	901	KHTASVTCGPLLLEPETISEDIVSDTSWKNKDEMPTTVVYLSLSTT-DLEKGSVCISDQF	959
Db	899	KHAESVIFGPLLLEPEVPSVEISVDTAWNKKNDEMVPAAWVSLTLTPDSTRGSGICISDQC	958
QY	960	NSVNFSAEGETVYDESQRPQPVKYATLISNKSPTSETGEOGLINSSVTKCFSSKNSP	1019
Db	959	NSANFSAQSTQGTCEDECQSQSPVKYATLVSNVKTVETDEEQAIIHSSVSQCIAKHSP	1018
QY	1020	LKDSFSSNSWEIEAQAFILSDQHPNIIISPLTFSEGLDLELLKLEGNFPENNDDKSIYY	1079
Db	1019	LROSFSNSWEIEAQAFILSDQHPNIIISPLTFSEGLDLELLKLEGNFPENNDDKSIYY	1077

QY	1080	LGVTSSIKKRESGVLLTDKSRVSCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKRTFA	1139
Db	1078	LGVSNGKRENDMLLTDEAGVLCFPFAHCLFSDIRILQESCSHFVENNINLGTSG-KNFV	1136
QY	1140	SYMPQQTCTQTHKIMENKMDLTV	1165
Db	1137	PYMPQFQSCSTHSHKIENKMDLTV	1162
RESULT 2			
S68438			
leptin receptor, splice form Ob-Rb - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000			
A:Accession: S68438; S68441			
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;			
Nature 379, 632-635, 1996			
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.			
A:Reference number: S68437; MUID:96231997			
A:Accession: S68438			
A:Status: nucleic acid sequence not shown			
A:Molecule type: mRNA			
A:Residues: 564-1162 <LEE>			
A:Cross-references: EMBL:U49107; NID:g1195486; PIDN:AAC52421.1; PID:g1195487			
A:Experimental source: splice form Rb; tissue hypothalamus			
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996			
A:Note: only a part of the translation is shown			
A:Accession: S68441			
A:Status: nucleic acid sequence not shown; translation not shown			
A:Molecule type: mRNA			
A:Residues: 1-796, 'GMCVLFMD' <LEE2>			
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493			
A:Experimental source: splice form Re; tissue hypothalamus			
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996			
A:Note: this sequence from splice form Re is included to produce a complete sequence			
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:			
C:Genetics:			
A:Gene: Ob-Rb			
C:Keywords: alternative splicing; appetite			
Query Match 76.2%; Score 4766.5; DB 2; Length 1162;			
Best Local Similarity 75.4%; Pred. No. 9.6e-302;			
Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;			
QY	1	MICQKFCVLLHWEFIVITAFNLSPYITPWREKLSOMPNSYDYVFLLPAGLSKNTSNS	60
Db	1	MMCQKQFVYVLLHWEFLVITAFNLALAYDISPWKFKLFCGPPNTTDDSLSPAGAPNNASAL	60
QY	61	NGHYETAVERPKFNSSGTHFNKSLTKTHCFCRSEQDRNCSLCADNIEGKTFVSTVNSLVF	120
Db	61	KGASEALVEAKFNSSGTHFNKSLTKTHCFCRSEQDRNCSLCADNIEGKTLASVVKASVF	120
QY	121	QQIDANNIOCWLGDKLKLFCYVESLFKNLFNRYNKKVHLLYVLPVLEDSPLVPQKS	180
Db	121	RQLGVNWDIECMWKGDLTLFICHMEPLTKNPKNYDSKVLHLLDPLVEIDDLPLPLKDS	180
QY	181	FQWVHCNCSVHECECECLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMSVQPINNAKPDPP	240
Db	181	FQVOCNCSLURG-CECHVPVPRAKLNALLMYLEITSAGVSFQSPMSLQPLMLVVKPDPP	239
QY	241	LGLHMEITDDGNLKISWSSPPLVPFPLOYQVQKYSNSTTVIREADKTVSATSLLVDSILP	300
Db	240	LGLHMEVTDGNNLKISWDSQTKAPFPLOYQVQKYLENS-TIVREAAEIVSATSLLVDSVLP	298
QY	301	GSSVEVQVRKRLDGPGLGWSDMSTPRVFTTQDVLYFPKILTSVGSNVSPHCYKKNKI	360
Db	299	GSSVEVQVRKRLDGPGLGWSWSQVFTTQDVVYFPKILTSVGSNASFHCYKKNQI	358
QY	361	VPKSEIIVWNNLAEKIPQSOQYDVVSHVSKVTFNLTNETPRGKFTYDAYVCCNEHCCH	420
Db	359	ISSKQIIVWNNLAEKIPQIYISIVDRVSKVTFNLTNETPRGKFTYDAYVCCNEQACHH	418

QY 421 RYAELYVIDVNNISCTDGYLTWKTCRWSTSIQSLAESTLQLRVYHRSSLYCSDPISIH 480
 Db 419 RYAELYVIDVNNISCTDGYLTWKTCRWSPSTIQSLVSTVQLRYHRSSLYCPDSPSIH 478
 QY 481 PISEPKDCYLQSDGFYECIQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDPSVWKPPLP 540
 Db 479 PTSEPKNCVLQRDGFYECVQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDPSVWKPPLP 538
 QY 541 SSVKAEITINIGLLKISWEKPPENNLQFOIRYGLSGKEVQMKVEYVDAKSKSVSLPV 600
 Db 539 SNVKAETIVTGLLKVSEKPPENNLQFOIRYGLSGKEIQWKTHEVDAKSKSALLV 598
 QY 601 PDLCAVAVQVRKRLDGLGYSNWSNPAITYVMDIKVPMRGPEEFWRIINGDMTKKEKNV 660
 Db 599 S DLCVAVTVQVRCRLDGLGYSNWSSPATLVMDVPMRGPEEFWKKMGDDVTKKERNV 658
 QY 661 TLLWKPLMKNDLSLCSVORYVINHHTSCNGTWSDEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
 Db 659 TLLWKPLTKNDLSLCSVRYVYVVKHTAHNGTWSDEDVGNRTNLTLFWTEPAHTVTVLAVNSL 718
 QY 721 GASVANENLTFSPMSKVNTVOSISAYPLANSCTVIVSWILSPDYLKMYFLIEKKNLNE 780
 Db 719 GASLVNENLTFSPMSKVSAVESAYPLSSCVILSWTLPDDYSLLYLVIEWKILNE 778
 QY 781 GEIKWLRISSVKKYYITHDFIPIEKYQFSLYIFEMEGVGKPKIINSFTODDIEKHQSDA 840
 Db 779 DGMKWLRIPSNVKKFYIHDNFIPIEKYQFSLYIFEMEGVGKPKIINGFTDAIDKQQND 838
 QY 841 GLYIVIVPVISSLLTGLTLLISHQMKKLFWEVDVPMKNCWQAQGLNFQKPFTEHFLFI 900
 Db 839 GLYIVIVPIISSCVLLTGLTLLISHQMKKLFWDVPMKNCWQAQGLNFQKPFTEHFLT 898
 QY 901 KHTASVTCGPIILLEPETISEDISVDTSWKNKDEKMPITVYVSLSTT-DLEKSGVVCISDQF 959
 Db 899 KHAESVIFGPIILLEPEPISEISVDATAKNKDEMPVPAKVSLLLLTTPDESSSICISDQC 958
 QY 960 NSVNFSAEGTEVYIYEDSORPPVKYATILSNKSPSETGEBQGLINSSVTKCFSSKNSP 1019
 Db 959 NSANFSQSGTQVTCDECORQSPVKYATIVSNKLVETDEBQGFTHSPVSNCSISSNHSP 1018
 QY 1020 LKDSFSNSWEIAQAFIILSDQHPNIIISPHLTFSEGLDKLLKLEGNFPENNDKKSIY 1079
 Db 1019 LRQSFSSSSWETAQTFELSDQQTWISQLSFS-GIDELLELEGFSFPEHNREKSVCY 1077
 QY 1080 LGVTSIKRRSGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGSSTKTF 1139
 Db 1078 LGVTSVNRRESGVLLTGEAGILCTFPAQCLFSDIRILQERCSEHFVENNLSLGTSG-ENFV 1136
 QY 1140 SYMPOFOTCSTOYHKIMENKMCDLTV 1165
 Db 1137 PYMPQFQTCSTHSHKIMENKMCDLTV 1162

RESULT 3
 S68440
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
 C:Accession: S68440
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fnd Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68440
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-900 <LEE>
 A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491
 A:Experimental source: tissue hypothalamus
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68440
 C:Genetics:

Query Match		60.6%	Score 3793;	DB 2;	Length 900;
Best Local Similarity		76.8%	Pred. No. 1.4e-238;		
Matches	691;	Conservative	83;	Mismatches 124;	Indels 2;
		Gaps			
Qy	1	MICQKFCVLLHWEFIYIVTAFLNLSYPITPWRFKLSMPNPNSTYDYLPLDAGLSKNTNS	60		
Db	1	MMCKQFYVLLHWEFLYIAALNLAYISPWKFKLCGPPNTTDDSFSLSPAGPNNASAL	60		
Qy	61	NGHYETAPEKFNSSGTHFSNLKSTTPHCCFRSPQDRNCSLCADNTEGKTFTVSTVNSLVF	120		
Db	61	KGASEAIVEAKFNSSGIYVELSKTVPHCCFGNEQGNCSALTDNTEGKTLASVVKASVF	120		
Qy	121	QQIDANNICQWLKGDULKFCYVESLFKNLFRNYNTKVHLLYVLPEVLEDSPLVPKGS	180		
Db	121	ROLGVNWDIECWKMGDLTLFCHMEPLPKPNFKNYDKVHLLYDLPEVIDDSPLPLPKDS	180		
Qy	181	FOMYHCNCSVHECECLVPVPTAKLNDTLMLCKLITISGGVIFOSPMSVQPINVKVPDPP	240		
Db	181	FQVQCNCISURG-CCECHVPVPRAKLNTALLMYLEITSAGVSFQSPMSLQPMVLVADPP	239		
Qy	241	LGLHMEITDDGNLKSISWSSPLVPFPPLQYQVKYSENSTTVIREADKIVSATSLVDSILP	300		
Db	240	LGLHMEVTDGNNLKISNDSQTMAPPFLQYQVKYLENS-TIVREAAEIVSATSLVDSVLP	298		
Qy	301	GSSYEVOVQRKRLDGPGLWSDWSTPRVFTQDVIYPPPKILT SVGSNVSPHCIIYKKNKI	360		
Db	299	GSSYEVOVRSKRLDGSVGSWSSPQVFETTDVYVFPFKILT SVGSNAPHCIIYKKNQI	358		
Qy	361	VPSEIYVMMNLAEKIPQSOYDVVSDVSHVSKVTFFNLNETKPRGFTYDAYCYCNEHECHH	420		
Db	359	ISSKQIVWMNLAEKIPIQYISVSDRVSKVTSNLKATPRGKFTYDAYCYCNEQACHH	418		
Qy	421	RYAEIYIDVNVINTSCETDGYLTKMTCRWSTSTISQSLAESTLQIRYHRSSLYCSDIPSIIH	480		
Db	419	RYAEIYIDVNVINTSCETDGYLTKMTCRWSPSTISQSLVGSTVOLRYHRRSLYCDPSPIH	478		
Qy	481	PISPKDCYLQSDGFCYICFOPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540		
Db	479	PTSPKNCVLQDGFYECVQPIFLLSGYTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	538		
Qy	541	SSVKAETITIGLLKISWEKPVFPENNLQFOIRYGLSGKEVQMKWEYVYDAKSYSVSLPV	600		
Db	539	SNVKAETIVTGLLKISWEKPVFPENNLQFOIRYGLSGKEIQMKTHEVFOAKSKSASLLV	598		
Qy	601	PDLCAVAVQYRCRRLDGLGWSNWSNPATVYNDIKVPMRGPEFWRIINCQDTMKKEKNV	660		
Db	599	SDLCAVYVQYRCRRLDGLGWSNWSNPATVLMVDMVKVPMRGPEFWRKMDGDTYKKERNV	658		
Qy	661	TLLMKPLMKNDSLCSQVRYVINHHSTCNGTWSGDVGHNTKFTFLWTBQAHVTVLAINSI	720		
Db	659	TLLMKPLTKNDSLCSRRYVYVKHRTAHNGTWSGDVGNRTNLTFLWTBPAHTVTVLAVNSL	718		
Qy	721	GASVANFNLTSPWMSKVNIVQSLSATPLNNSCVIVSWILLSPSDYKLMYFIIEKKNLNE	780		
Db	719	GASLVNFNLTSPWMSKVSAYESLSAYPLSSCCVILSWTILSPDYSLLYLVIEMKILNE	778		
Qy	781	GEIKWLRTSSSVKYYIYTHDRPIETKEQYFSLPIYFMGVGCKPKIINFTODDTTEKHQSDA	840		
Db	779	DCMKWLRTSPVKKFYIHDNFIPIETKEQYFSLPIYFMGVGCKPKLIINGFTKDAIDKQONDA	838		
Qy	841	GLYIVTVIISSSILLGTLTLLISHORMKKLFWEVDVPPKNCNSWAQGLNFQKPTFEHLFI	900		
Db	839	GLYIVTVIISSCVLLGLTLAISORMKKLFWDVDPVPPKNCNSWAQGLNFQKDISLHEVFI	898		

A:Gene: Ob-Rd

C:Keywords: alternative splicing; appetite; transmembrane protein

F:840-860/Domain: transmembrane #status predicted <TMM>

RESULT 4

S68439

leptin receptor, splice form Ob-Rc - mouse

RESULT	4
S68439	
leptin receptor, splice form Ob-Rc - mouse	

C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68439; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; F
 Nature 379, 632-635, 1996
 A>Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68439
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 684-892 <LEP1>
 A:Cross-references: EMBL:U49110; NID:g1195488; PIDN:AAC52422.1; PID:g1195489
 A:Experimental source: splice form Rc; tissue hypothalamus
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Accession: S68441
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, 'GNCTVLFMD' <LEP2>
 A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Note: this sequence from splice form Re is included to produce a complete sequence
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68
 C:Genetics:
 A:Gene: Ob-Rc
 C:Keywords: alternative splicing; appetite

Query Match 60.5%; Score 3785; DB 2; Length 892;
 Best Local Similarity 77.3%; Pred. No. 4.5e-238;
 Matches 689; Conservative 81; Mismatches 119; Indels 2; Gaps 2;

QY 1 MICOKFCVLLHWFYIVITAFNLSYPTPWRFKLSQMPNSTYDYELLPLAGLSKNTSNS 60
 DB 1 MMCOKFYVLLHWFELVIAALNAYLSPWKFALFCGPNPTDDSLPAGAPNNASAL 60
 QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCRSPQDRNCSLCADNIEGKTFVSTVNSL 120
 DB 61 KGASEAIVEAKFNSSGTHFNSLKTTHFCRSPQDRNCSLCADNIEGKTFVSTVNSL 120
 QY 121 QQDANNNIOCLWGLDKLFICYVESLFKNLFRNYNKKVHLLYVLPVLEDSPLVPKGS 180
 DB 121 RQLGVNWDIECKWKGDLTLFICHMEPLKPNFKNYDSKVHLLYDLPVDDSPPLPKDS 180
 QY 181 FQVHCNCSVHECECLVPVPTAKLNTLLMCLKITSGGVIFQSPMSVOPINNVKPDPP 240
 DB 181 FQVHCNCSVHECECLVPVPTAKLNTLLMCLKITSGGVIFQSPMSVOPINNVKPDPP 240
 QY 241 LGLHMEITDGNLKSISWSSPPLVFPLOQYQVYSENSTTVIREADKTVSATSLVDSILP 300
 DB 240 LGLHMEITDGNLKSISWSSPPLVFPLOQYQVYSENSTTVIREADKTVSATSLVDSILP 300
 QY 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVYFPFKILTSVGSNVSPHCYKKNKI 360
 DB 299 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVYFPFKILTSVGSNVSPHCYKKNKI 358
 QY 361 VPSKEIIVWNNLAKIPQSQDYVSVHVKVTFNFKLNETPRGKFTYDAYVCCNEHCCH 420
 DB 359 ISSKQIIVWNNLAKIPQSQDYVSVHVKVTFNFKLNETPRGKFTYDAYVCCNEHCCH 418
 QY 421 RYAEYVIDVNNISCTDGYLTKMTCTWSTSTIQSLAESTLQRYHRSLYCDIPSIH 480
 DB 419 RYAEYVIDVNNISCTDGYLTKMTCTWSTSTIQSLAESTLQRYHRSLYCDIPSIH 478
 QY 481 PISPKDCYQLQSGFYECIFQPIFLLSGYTWMIRINSLGSLDSPPTCYLPSVVKPLPP 540
 DB 479 PTSEPKNCVQLQSGFYECIFQPIFLLSGYTWMIRINSLGSLDSPPTCYLPSVVKPLPP 538
 QY 541 SSVKAEITINIGLKISWEKVPFPENNLQFIQRYGLSGEKVQWKEVYDAKSKSVSLPV 600
 DB 539 SNVKAETIVNTGLLKVSWEKVPFPENNLQFIQRYGLSGEKVQWKEVYDAKSKSVSLPV 598
 QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPATVTVMDIKVPMRGPEFWRINGDTMKKEKNV 660

DB 599 SDLCVAVVQVRCRDLGLGYSWNSNPATVTVMDIKVPMRGPEFWRINGDTMKKEKNV 658
 QY 661 TLLWKPMLKNDSCSVORYVNHHTSCNGWSEVDVGNHTFTFTFLWTQAHVTVTLAINSI 720
 DB 659 TLLWKPMLKNDSCSVORYVNHHTSCNGWSEVDVGNHTFTFTFLWTQAHVTVTLAINSI 718
 QY 721 GASVANENLTFSPWMSKVNTVQSLSAVPLSSSCVIVSWILSPSDYKLMYFIENKLNED 780
 DB 719 GASVANENLTFSPWMSKVNTVQSLSAVPLSSSCVIVSWILSPSDYKLMYFIENKLNED 778
 QY 781 GEIKWLRISSVKRYIHDHFIPIEKYQFSLPIFMGVGPKPIINSFTQDDIEKHSDA 840
 DB 779 DGMKWLRISSVKRYIHDHFIPIEKYQFSLPIFMGVGPKPIINSFTQDDIEKHSDA 838
 QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQK 891
 DB 839 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQK 889

RESULT 5

S68437
 leptin receptor, splice form Ob-Ra - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
 C:Accession: S68437
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
 Nature 379, 632-635, 1996
 A>Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68437
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-894 <LE>
 A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
 A:Experimental source: splice form Ra; tissue hypothalamus
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
 C:Genetics:
 A:Gene: Ob-Ra
 C:Keywords: alternative splicing; appetite

Query Match 60.5%; Score 3785; DB 2; Length 894;
 Best Local Similarity 77.3%; Pred. No. 4.6e-238;
 Matches 689; Conservative 81; Mismatches 119; Indels 2; Gaps 2;

QY 1 MICOKFCVLLHWFYIVITAFNLSYPTPWRFKLSQMPNSTYDYELLPLAGLSKNTSNS 60
 DB 1 MMCOKFYVLLHWFELVIAALNAYLSPWKFALFCGPNPTDDSLPAGAPNNASAL 60
 QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCRSPQDRNCSLCADNIEGKTFVSTVNSL 120
 DB 61 KGASEAIVEAKFNSSGTHFNSLKTTHFCRSPQDRNCSLCADNIEGKTFVSTVNSL 120
 QY 121 QQDANNNIOCLWGLDKLFICYVESLFKNLFRNYNKKVHLLYVLPVLEDSPLVPKGS 180
 DB 121 RQLGVNWDIECKWKGDLTLFICHMEPLKPNFKNYDSKVHLLYDLPVDDSPPLPKDS 180
 QY 181 FQVHCNCSVHECECLVPVPTAKLNTLLMCLKITSGGVIFQSPMSVOPINNVKPDPP 240
 DB 181 FQVHCNCSVHECECLVPVPTAKLNTLLMCLKITSGGVIFQSPMSVOPINNVKPDPP 240
 QY 241 LGLHMEITDGNLKSISWSSPPLVFPLOQYQVYSENSTTVIREADKTVSATSLVDSILP 300
 DB 240 LGLHMEITDGNLKSISWSSPPLVFPLOQYQVYSENSTTVIREADKTVSATSLVDSILP 298
 QY 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVYFPFKILTSVGSNVSPHCYKKNKI 360
 DB 299 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVYFPFKILTSVGSNVSPHCYKKNKI 358
 QY 361 VPSKEIIVWNNLAKIPQSQDYVSVHVKVTFNFKLNETPRGKFTYDAYVCCNEHCCH 420
 DB 359 SNVKAETIVNTGLLKVSWEKVPFPENNLQFIQRYGLSGEKVQWKEVYDAKSKSVSLPV 598
 QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPATVTVMDIKVPMRGPEFWRINGDTMKKEKNV 660

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Db 359 ISSKQIWWNRNLAETPEIQSYIVSDRVSKVTFPSNLKATPRGKFTYDAYVCCNEQACHH 418
QY 421 RYAELVIVDVNINISCTDGYLTMTKCRNSTSTIQSLAESTLQLRVHRSLKCSIDIPSIH 480
Db 419 RYAELVIVDVNINISCTDGYLTMTKCRNSPSTIQSLVSTVOLRYHRRSLKCPDPSPIH 478
QY 481 PISEPKDCYLOSGDFEYCFQPIFELLSGYTMTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKNCVLQRDGFECYFQPIFELLSGYTMTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKTSWEKPFPPENNLOQIRYGLSGKEVQMKTEYVDYDAKSKSVSLPV 600
Db 539 SNVKAETINTGLLKYSWEKPFPPENNLOQIRYGLSGKEIQWKTEHVFDAKSKASLLV 598
QY 601 PDLCAVYAVOVCRKRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 SDCAVYVYVQVRCRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRKMDGDVTKKERNV 658
QY 661 TLLWKPLMKNDLSLCVQRYVINHHTSCNGTWSDEVCNHTKFTFLMTEQAHVTVLAINSI 720
Db 659 TLLWKPLTKNDLSLCVRYVVKHRTAHNGTWSDEVCNHTKFTFLMTEPAHTVTVLAVNSL 718
QY 721 GASVANFNLTFSWPMKSKVINQSLSAYPNLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 719 GASLVNFNLTFSWPMKSKVAVESLSAYPLSSSCVILSWTSLSPDYSLLYLVIEWKILNED 778
QY 781 GEIKWLRISSVKKYIYHDFPIEKYQPSLYPIFMEGVGKPKLIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRIIPSNVKKFYIHDNFPIEKYQPSLYPVFMEGVGKPKLIINGFTKDAIDKQONDA 838
QY 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWDVDPNPKNCSWAAGLNFOK 891
Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKKLFWDVDPNPKNCSWAAGLNFOK 889

RESULT 6
leptin receptor, isoform Ob-Rf - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
C:Accession: S74225
R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
FEBS Lett. 392, 87-90, 1996
A:Title: A novel leptin receptor isoform in rat.
A:Reference number: S74225; MUID:96368027
A:Accession: S74225
A:Molecule type: mRNA
A:Residues: 1-895 <WAV>
A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213
A:Experimental source: strain Sprague-Dawley; tissue type brain
C:Genetics:
A:Gene: rob-R
C:Keywords: appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 59.6%; Score 3729; DB 2; Length 895;
Best Local Similarity 76.5%; Pred. No. 2e-234;
Matches 682; Conservative 84; Mismatches 123; Indels 2; Gaps 2;

QY 1 MICOQKFCVLLHWEFYIVITAFNLNLSYIPTPRPKLSKMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MTCQKRYVLLHWEFYIVITAFNLNLSYIPTPRPKLSKMPNPNSTYDSDFLSPAGVFNNTSSL 60
QY 61 NCHYETAPEPKFNSSGTHFSNLKSTTFHCCFSEQRNCSLCAADNIEGKTFVSTVNSLVF 120
Db 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFGEQNGNCSALTGNTGKTLASVVPPLVF 120
QY 121 QQIDANNQCWLKGLKFLICYVESLFRNLFNRYNKHVLLYVLPVLEVDLSPLVPQKGS 180
Db 121 RQLGVNWDIECNMKGDLTLFICHMEPLLNPKFNKNDYKVVHLLYDLPEVIDDLDLPLPLKDS 180
QY 181 FQMVHCNCSVHECCCECLVPVPVPAKLNLDLTLMLCLKITSGGVIFQSPMLSVQPINNWKPDPP 240
```

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Db 181 FQVQCNCVRE-CECHVPVPRAKVNTALLMYLEITSAGVSFOSPLMSLOPMLVVPDPP 239
QY 241 LGLHMEITDDGNLKISWSPPPLPFPPLQYQVYSENSTTVIREADKIVSATLSLVDLSLP 300
Db 240 LGLRMEVTDGDNLKISWDQSOTKAPFPLOQYKYLENS-TIVREAAETVSDTSLVDVSLP 298
QY 301 GSYEVQVQVGRKRLDGPICGWSNSTPRVFTTQDYVPPPKILTSGVSNVSHCIYKKNKI 360
Db 299 GSYEVQVRSKRLLDGGVMSDLSLPQLFTTQDMYFPFKILTSGVSNASFCYKKNQOT 358
QY 361 VPSKEVWMMNLAETKIQSOYDVVSDHVSKVTFENLNETKPRGKFTYDAYVCCNEHECHH 420
Db 359 ISSKQIWWNRNLAETPEIQSYIVSDRVSKVTFPSNLKATPRGKFTYDAYVCCNEQOCH 418
QY 421 RYAELVIVDVNINISCTDGYLTMTKCRNSTSTIQSLAESTLQLRVHRSLKCSIDIPSIH 480
Db 419 RYAELVIVDVNINISCTDGYLTMTKCRNSPSTIQSLVSTVOLRYHRRSLKCPDPSPIR 478
QY 481 PISEPKDCYLOSGDFEYCFQPIFELLSGYTMTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKNCVLQRDGFECYFQPIFELLSGYTMTWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKTSWEKPFPPENNLOQIRYGLSGKEVQMKTEYVDYDAKSKSVSLPV 600
Db 539 SNVKAETINTGLLKYSWEKPFPPENNLOQIRYGLSGKEIQWKTEHVFDAKSKASLPV 598
QY 601 PDLCAVYAVOVCRKRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 SDCAVYVYVQVRCRLDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRKMDGDVTKKERNV 658
QY 661 TLLWKPLMKNDLSLCVQRYVINHHTSCNGTWSDEVCNHTKFTFLMTEQAHVTVLAINSI 720
Db 659 TLLWKPLMKNDLSLCVRYVVKHRTAHNGTWSDEVCNHTKFTFLMTEPAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSKVINQSLSAYPNLNSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
Db 719 GASLVNFNLTFSWPMKSKVQWQSLSAYPPLSSSCVILSWTSLSPDYSLLYLVIEWKNLND 778
QY 781 GEIKWLRISSVKKYIYHDFPIEKYQPSLYPIFMEGVGKPKLIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRIIPSNVKKFYIHDNFPIEKYQPSLYPVFMEGVGKPKLIINGFTKDDIAKQONDA 838
QY 841 GLYVIVPVIISILLGLTLLISHQRMKKLFWDVDPNPKNCSWAAGLNFOK 891
Db 839 GLYVIVPIIISCVLLGLTLLISHQRMKKLFWDVDPNPKNCSWAAGLNFOK 889

RESULT 7
leptin receptor, splice form Ob-Re - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68441
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-805 <LE>
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Re; tissue hypothalamus
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: for alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Re
C:Keywords: alternative splicing; appetite

Query Match 53.4%; Score 3340; DB 2; Length 805;
Best Local Similarity 76.2%; Pred. No. 3.5e-209;
```

Matches 608; Conservative 73; Mismatches 115; Indels 2; Gaps 2;

QY 1 MICOKFCVLLHWEFIYITAFNLSPYIPTRFKLSCHMPNPNSTYDYFLPAGLSKNTS 60
 Db 1 MMCKOFVYVLLHWEFLYIAALNLAYIPSPWPKLFPGPNTTDDSGFLSPAGAPNNASAL 60

QY 61 NGHYETAVERPKFNSGTHFNSLKTFFHCCFRSEQDRNCSLCAJNTEGKTFVSTVNSLVF 120
 Db 61 KGASEATVEAKFNSGGIYVPELSKTVFHCFCGNEQONCSALTDNTEGKTLASVKNASVF 120

QY 121 QQTDAANNIOCLWGLDKLFICVSVESLFKNLFRNYKYVHLLVYLVLEVDSPVPOKGS 180
 Db 121 RQLGVNWDIECMWKGDLTLFICHEPELPKNPFKNYDSKVLHLLDPEVIDDPLPLKDS 180

QY 181 FQMVHCNCSVHECCCLVPPVPTAKLNDTLMLCKITSGGVFOSPLMSVQPINMKVPDPP 240
 Db 181 FQVQNCNSLURG-CECHVPPVRAKLNALMLYLEITSAGVSFOSPLMSQPLMLVVPDPP 239

QY 241 LGLHMETDDGNLKIWSSSPPLFPFLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
 Db 240 LGLHMETDDGNLKIWSQSQTMAPFLOQVQKYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 301 GSSYEVOVKRDLGDCGINSWSTPRVFTQDVYIPPPKILTSVGVNSVPHCIYKKENKI 360
 Db 299 GSSYEVOVKRDLGDCGINSWSTPRVFTQDVYIPPPKILTSVGVNSVPHCIYKKENKI 358

QY 361 VPSKEIVMMNLAEKIPQSDYDVSDHVSQVTFPFLNETKPRCKFTYDAYVCCNEHECHH 420
 Db 359 ISSKQIWWRNLAELPEIQSYISVRSVKVTFESNLKATPRGKFTYDAYVCCNEQACHH 418

QY 421 RYAEVLVIDVINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRVHRSLSYCDIPSIIH 480
 Db 419 RYAEVLVIDVINISCTDGYLTKMTCRWSPSTIQSLVSGTVQLRVHRSLSYCDIPSPSIH 478

QY 481 PISEPKDCYLOSDFEYECIFQPIFLISGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 540
 Db 479 PTSEPKNCVLORDGFYECVFQPIFLISGYTMWIRINHSLSGLDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLTKISWEKVPENNLOFQIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
 Db 539 SNYKAEITVNTGLKYSWEKVPENNLOFQIRYGLSGKEIQWKTHEVEDAKSKSASLLV 598

QY 601 PDLCAVAVOVKRLDGLGYSWNSNPAYVYVMDIKVPMRGPEFWRINGEDTMKKEKNV 660
 Db 599 SDCAVAVYVQVRCRLDGLGYSWNSNPAYVYVMDIKVPMRGPEFWRKMDGDVTKERNV 658

QY 661 TLLWKLPMKNDSCSVQRYVINHTSCNGTWSDEVDGNGHTKFTFLWTEQAHTVTVLAINSI 720
 Db 659 TLLWKLPMKNDSCSVQRYVINHTSCNGTWSDEVDGNGHTKFTFLWTEQAHTVTVLAINSL 718

QY 721 GASVANFNTFSWPMKVNIVQSLAYSAPLNSCVIYVSWTILSPSDYKLMYFIEWKNLNED 780
 Db 719 GASLVNFLTFSWPMKSVASVESLSAYPLSSSCVILSWTILSPDDYSLILYLVIEWKILNED 778

QY 781 GEIKWLIRISSVKKYIYH 798
 Db 779 DGMKWLIRIPSNVKKFYIH 796

RESULT 8
 I49699
 Glycoprotein 130 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
 C:Accession: I49699; I48370
 R:Saico, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
 J. Immunol. 148, 4066-4071, 1992
 A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
 A:Reference number: I48370; MUID:92291532
 A:Accession: I49699
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>

A:Cross-references: GB:M83336; NID:g193591; PIDN:AAA37723.1; PID:g193592
 A:Accession: I48370
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-917 <RES>
 A:Cross-references: EMBL:X62646; NID:g840816; PIDN:CAA44515.1; PID:g840817
 C:Genetics:
 A:Gene: gp130
 C:Superfamily: cytokine receptor homology
 C:Keywords: glycoprotein
 F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 5.9%; Score 366; DB 2; Length 917;
 Best Local Similarity 20.9%; Pred No. 1.2e-15;
 Matches 191; Conservative 140; Mismatches 338; Indels 244; Gaps 42;

QY 323 STPRVFTQDVYF-----PPKILTSVGVNSVPHCIYKK-----ENKIYP 362
 Db 2 SAPRIWLAQALLFFLTSTESIGQLLEPCGYIYPEFVVQVQSGNFTALCVLKEACLOHYVYN 61

QY 363 SKRIWMMNLAEKIPQSDYDVSDHVSQVTFPFLNETKPRCKFTYDAYVCCNEHECHHRY 422
 Db 62 ASYIWKTNHA-AVPREQVTVINRTTSSVFTDV--VLPVSQLT-----CNTLSFGQIE 112

QY 423 AELYVI-----DYNINISC-ETDGYLTKMTCRWSTSTIQSLAESTLQLRVHRSLSY 473
 Db 113 QNYGVYMLSGPPDPDPTNLTCLIVNEG--KNMLCQWDPG-----RETYLETNYTLASEWA 165

QY 474 SDIPSTHPISEPKDCYLOSDFEYECI--FOPIPLLSGYTMWIRINHSLSGLDSPPTCVLP 531
 Db 166 TE-----KFPDC--QSKHGTSCMVSYMPTVYN-IEVWVEANALKVSSESINFDP 214

QY 532 DSVVKKPLPSSVKAETINI-GLLKISWEKVPENNLOFQIRYGLSG-----KEYQ--- 582
 Db 215 VDKVETPPYINLSVTNSEELSSILKLSW-----VSSGLGGLLDLSDIQYRT 261

QY 583 -----WKMEYVDVDAKSKSVSLPVPDL--CAVAVOVKRLDGLGYSWNSNPAYTVVMD 635
 Db 262 KDASTWIQVPLEDTMSPRTSFTQDLKPTTEYVFRIRSIKDSKGYWSDSEASQTTVE 321

QY 636 IKVPMRGPEFWRINGEDTMKKEKNVTLKPLMKNDSCSVQRY--VINHTSCNCTWSE 693
 Db 322 DR-PSRPPSFYKTNPSHGQYRSVRLINKALPLSEANGKILDYEVILTQSKSVSQTYT 380

QY 694 DVGNNHKTFTLWTEQAHTVTVLAINSIGASVANFNLTFSWP-MSKVNIVQSLAYSAPLNS 752
 Db 381 ---TGTELVNLTNDRYVASLAARNKVGSAAY-LTIPSPHYTAAYSVVNLKAFP-KDN 435

QY 753 CVIVSWILSPSDYKLMYFIEWKNLNEDGEI--KWLIRISSVKKYIYHDHFTPIEKYQFS 810
 Db 436 LLWVWV--TPPPKPVSKYLEWCVLSENAPCEDWQEDATVNRTHLGRLLLESKYQIT 493

QY 811 LYPFMEG----- 818
 Db 494 VTPVFATPGGSESLKAYLKQAPARGPTVRTKVGKNEAVLAWDOIPIVDDQNGQIRNYS 553

QY 819 -----VGPKPII---NSFTQDDIEKHQSDAGLY----- 843
 Db 554 ISYRTSVGKEMVHVVDSSHTETLSSLSDT-LYVYRMAAYTDEGKDGPEFTFTPKFA 612

QY 844 -----VIYVPIISSI-LLLTGLTLLISHQR--MKLIFWEDVPNPKNCNWAQGLNFQKPT 894
 Db 613 QGEIEAIVVPVCLAPLTLTLLGVLCFNKRLIKKHIPNVPDPSPKSHIAQNSPHPPP-- 670

QY 895 FEHLFKHTASVTCGPLPILLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEK---- 950
 Db 671 -RHNFNSKQDMQSDGNF-----TDVSVVEIEANKKPCPDD----LKSVDLFFKKEV 717

QY 951 -----GVCISDQFNSVNFSEAGTEVYIEESQORQ--PFVKYATLISNKPSET 998
 Db 718 STEGHSGLGGSCSMSSSRPSISSNE-----ENESAQSTASTVEYTVVHSGYRHQV 769

QY 999 GEEQGLINSSVTK-CFSSKNSP-----LKDSFSNSSWEIEAQAFILSDQHNPILSPHLTF 1053
Db 770 PSVQVFSRSESTQPLDSEERPEDQLVDSDVGDGDEILPROPYPKONCSOPE-ACPEISH 828
QY 1054 SEGDELLEKLEGN 1066
Db 829 PERSNOV--LSGN 839

RESULT 9
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:HiBi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:9108484
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <H1B>
A:Cross-references: GB:M57230; MID:g186353; PIDN:AAA59155.1; PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST; GP130
A:Cross-references: GDB:126725; OMTM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 5.5%; Score 345.5; DB 2; Length 918;
Best Local Similarity 19.8%; Pred. No. 2.6e-14;
Matches 163; Conservative 119; Mismatches 305; Indels 235; Gaps 33;

QY 337 PPKILTSVGSNVSFHCYIKK---ENKIVPSKEIVWMNLAEKIPQSDVVDVSHVKYTF 393
Db 33 PESPVVQLHSNFTAVCVLKEKCMDFHVNANVIVWKTN-HFTIPKEQYTIINRTASSVTF 91
QY 394 FNLNETKPRGKFTYDAVYCCNEHCHEHRYAEIYDIV-----NINISC-ETDGYLT 444
Db 92 TDI-----ASLNQLTCNLITFGLEQNVYGIITISGLPEKPKNLSCLVNEG--KK 141
QY 445 MFCRSTSTQSLASTQLRYHRSLSYCSIDPSTHPISEPKDCYLQSDGFYECI--FQP 502
Db 142 MRCEDDGG-----RETHLETNFTLSEWAT-----HKEA---DCKAKRDTPTSCVDYST 188
QY 503 IFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKAETIN-----IGLLKISW 558
Db 189 VYFVN-IEVWVEAENALGKVTSDHINFDVPVYKVPKPNPHNLS---VINSEELSSILKLTW 244
QY 559 EXP-----VFPENNLFQITRYGLSGKEVQWKMYEYVDADSKSVSLPVPDL--CAVYAVOV 611
Db 245 TNPSIKSVILKYNQYRKDAST-----WSQIPPEDTASTRSSFTVQDLKPFTEVFPRI 299
QY 612 RCKRLDGLGYNSNWPAYTVVMDIKVPMRGPEFWRLINGDTMKKKNVTLWKPLMKND 671
Db 300 RCKMDGKGYNSDWEASEAGITYEDR-PSKAPSFYKIDPSHTQGYRTVQLVWKTLPPE 358
QY 672 SLCSVQRVYVNHHTSCNGTWSVDGNH---TKFTFLWTEQAHTVTVLAINSIGASVANF 727
Db 359 ANGKILDVEVT-----LFRWKSHLQNYTVNATKLVNLTNDRLATPLVRNLVGKSDRAV 413
QY 728 NLTFSPWPSKVNIVQSLGAYPLNSNCVIVSWILSPDSVKLMYFIIEWKNLNDGE--IKW 785
Db 414 LTIPACDQOATHPVMDLRAF-P-KDNMLWETWTPRESVK--KYILEWCVLSDKAPCITDW 470
QY 786 LRISSVKKYIYTHDHPLEPKYQFSLYPIFMGEGVKPKII----- 825
Db 471 QOEDGTVHRTYLRGNLAESKCVLITVTPVYADPGSPESIKAYLKQAPSPKGTPTVTKKV 530

QY 826 -----NSFTQDDIEKHQSAGLY- 843
Db 531 GKNEAVLEWDQLPVDVQNGFIRNYTIFYRTIIGNETAVNDSSTHTYTLSSUTSDT-LXM 589
QY 844 -----VIVPVISSSI-LLIGTLLISHQR--MKK 869
Db 590 VRMAAYTDGGKDGPEFTTTPKFAOGEIEAIVVPVCLAFLLTLLGLVLCFNKRDLIKK 649
QY 870 LFWEVDVNPKNCSWAGLNFQKPFTEHFLFIKHTASVTCGPIILLPEPITISEDISVDTSWK 929
Db 650 HIWPNVDPFSKSHIAQWSPHTPP-----RH-----NFN 677
QY 930 NKDEAMPTTVVLLSTTDLEKGSVCISQFNSVNFSEAGTEVTVEDESOROPF---VKY 986
Db 678 SKDQM-----YSDGNFTDVSVEIAND---KKFPFEDLAS 710
QY 987 ATLISNKPSETGEGGLINSVTRKFSKNSPLKDSFNS 1028
Db 711 LDLFKKEKINTEGHSSGIGSS---CMSSSRPSISSDENES 749

RESULT 10
A44257
Interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transduc
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein
F:134-315/Domain: cytokine receptor homology <CRS>

Query Match 5.4%; Score 339.5; DB 2; Length 918;
Best Local Similarity 20.8%; Pred. No. 6.3e-14;
Matches 185; Conservative 141; Mismatches 326; Indels 237; Gaps 40;

QY 327 VFTTQDVI-----YFPKILTSVGSNVSFHCYIKKENKIVPSKE---IYWMNLAE 374
Db 14 IFLTTEISIGLVEPCGYIYPPVQVQSGNFTATCVLKEKCLQVYSVNAVYIWKTNHV- 72
QY 375 KIPQSQYDVVDVSHVKYTFNINETKPRGKFTYDAVY-----CCNEHCHEHRYAEIYV- 428
Db 73 AVPKEQVTVINRTASSVTF-----TDVVVFQNVLTNLTSLFGQIQNYGIT 119
QY 429 -----DVNINISC-ETDGYLTMTKRWSTSTIQSLAESTLQLRVHRSLSYCSIDPSIH 480
Db 120 ILSGYPDPDPTMNLSCIVNEG--KNMLCQ-----LDPRGYLETNLTLSKSEWATE----- 167
QY 481 PISEPKDCYLQSDGFYECI--FQPIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPL 538
Db 168 ---KFPDCKTK-HGTSSCMGTYPIYFVN-IEVWVEAENALGNSVSEPINFDPDVVKPS 222
QY 539 PPSSVKAETINI-GLLKISW-----EKPVPFENNLFQIRYGLSGKEVQWKMYEYVDK 592
Db 223 PPHNLVSTNSEELSSILKLVNLSGLDSILRLKSDIQYRTKDAST-----WIQVPLEDTV 277
QY 593 SAKSVSLPVPDL--CAVYAVOVCKRLDGLGYNSNWPAYTVVMDIKVPMRGPEFWRIIN 650
Db 278 SPTSFTVODLPKPFTEYVPIRSIKENGKGYSDWSEASGTYEDR-PSKAPSFYKVN 336
QY 651 GUTMKKEKNVTLWKPLMKNDSLCSVQRV--VINHHTSCNGTWSVDGNHTFTFLWTEQ 708
Db 337 ANHPQEYRSARLIWKTLPLESEANGKILDVVLVTQSKSVQIYTV---NGTELIVNLTN 393

QY 709 AHTVTVLAINSGASVANFNLPFSWPMKSV-NIVQSLASAPLNSCVIVSWILSPSDYKL 767
Db 394 RYVASLAARNVGVKSPATV-LITPGSHFKASHPVVDLKAFF-KDNLWVEM--TPSPKPV 449
QY 768 MYFIEWKMLNDEGEI--KWLRISSVKYIYIHDHPIEIKYQFSLYPIFMGVGKPV---822
Db 450 NKYLEWCVLSNSPCIPQWQEDGVNTRHLRGSLLSKCYLITVTPVPPGGPGSPESM 509
QY 823 -----KI 824
Db 510 KAYLKOAPSKGFTVTKVKVGKNEAVLEWDHLPVDVQNGFIRNYSISYRTSVGKEMVVR 569
QY 825 INSFOTDIEKHQSDAGLY-LYVHVMAAYTEBGGKDPETFTTLKFAQGEIYAVVPCIAF 628
Db 570 DSHTETYLSSLSST-LYVHVMAAYTEBGGKDPETFTTLKFAQGEIYAVVPCIAF 628
QY 853 SI-LLGTLLISHQ--MKKLFWEDVPNPKNSWAQGLNFQKPEFELF-----TKHTA 904
Db 629 LLTTLGLVLCFNKRLIKKHIPNPVDPSPKSHIAQWSPHTP--RHNFNKQDMYSDA 685
QY 905 SVTCGPLLPEPITISEDIVSDTSWKKNDKEMPTTVVSLSTTDLEK-----950
Db 686 NTF-----DVSVEIEANKRCPDLDKSL-----DLFKKEKISTEGHSGGIG 728
QY 951 GSVICISQFNSVNFSAEGTEVYDEDSQR--PFVKYATLISNSKPSSETGEEQGLINS 1008
Db 729 GSSCMSSSRPSISSE-----ENESAQSTASTVOYSTVHSGYRHOVPSVQVFSRSE 780
QY 1009 VTK-CFSSKNP-----LKDSFNSWEIEAQAFILSDQHPNIIISPLT 1052
Db 781 STQPLDLSBERPDLQVDSVSGDEILPRQOYFKQSCQPG-ASPDVS 828
RESULT 11
A34898
granulocyte colony-stimulating factor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 05-Nov-1999
C:Accession: A34898
R:Fukunaga, R.; Ishizaka-Ikeda, E.; Seto, Y.; Nagata, S.
Cell 61, 341-350, 1990
A:Title: Expression cloning of a receptor for murine granulocyte colony-stimulating factor
A:Reference number: A34898; MUID:90235283
A:Accession: A34898
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-837 <FUK>
A:Cross-references: GB:M50288; NID:g193454; PIDN:AAA37673.1; PID:g193455; GB:M32699
C:Keywords: transmembrane protein

Query Match 5.0%; Score 313; DB 2; Length 837;
Best Local Similarity 20.0%; Pred. No. 2.9e-12;
Matches 183; Conservative 125; Mismatches 311; Indels 298; Gaps 40;
QY 337 PKILTSVGSNVSFHC-IYKKNKIVPSKEIYVMMMLAEIKPOSQVDVSD--HVSKVTF 393
Db 33 PP--VVRGLDGPVLASCTISPNSCKLQQAQKILRLQDEPTQCDRQHLPDGTQESLITL 90
QY 394 FNLNETKPKGKFTY-----DAVCCNEHECHRYAELVIDVININISCTDGLYFKMTC 447
Db 91 PHLNYTQ---AFLFCLVPWEDSVQLDDQAEHLHAGYPPA---SPSNLSCLMLHLLTNSLVC 143
QY 448 RWSTSIQSLAESTLQRLYHRSLYCSIDPSIHPISPKDCVYLQSDGFYECIFQP-----502
Db 144 QWEPGPETHLPFSFI-LKSFRRS-----ADCOVQGTIPDCVAKKQNNC 187
QY 503 -----IFLLSGYTMIRINHSLGSLDSPPTCVLPDSVVKPLPPSPSVKAEITINI-----551
Db 188 SIPRKNLLLYQYMAIWWQAEENMLGSSSEPKCLDPMVDVVKLEPMLQALDIPDVVSHQ 247
QY 552 GLLKISWEKVPFPENL--QFQIRYGLSGKEVQWKMVEYDASKSVSLPVPDLCA-----605

Db 248 GCILWSW-RPMKSEPMEOCELRYPOLKGANWTL--VFHLPPSKDQF---ELCGLHOA 301
QY 606 -YVAVQVCRKRLDGLGYWNSNPNPAYTVVMDIKVPMRGPPEFNRIINGDTMKKEK-----658
Db 302 PYVTQMRCIRSSLSLPGFWS-PSG-----LQRPMTKAP-----TIRLDTWCQKKQLDPGT 352
QY 659 -NVTLLWKPLMKNDLSLCSVQRYVINHTIS-----CNGTWSIEDVGNHTKFTFLWTEQ 708
Db 353 VSVQLFWKPTPLQEDSGOIQGYLLSWNSPDHQODIHLNNT-----QLSCIFLLPSE 405
QY 709 AHTVTVLAINSGASVANFNLPFSWPMKSVNIVQSLASAPLNSCVIVSW---ILSPSDY 765
Db 406 AQNVTLVAYNKAGTSPT--TVVLENEGPAVTGLHAMAQDLNTTWDWEAPSLPQGY 462
QY 766 KLMYFIEWK---NLNEDGEIKWLISSSVKYIYIHDHPIEIKYQFSLYPIFMGVGK 821
Db 463 -----LIEWEMSSPSYNNYSKSWIEPNIGITGILLKDNINPFQLYRITVAPLYQIVGP 517
QY 822 PKIINSFT-----CNGTWSIEDVGNHTKFTFLWTEQ 708
Db 518 PNVYITFAGERAPPAPALHLKHVGTWQAQLEWVPEAPRLGMIPLTHYTFIWADAGHSF 577
QY 830 -----QDDTEKHQSDAGLY-----VIVPV 848
Db 578 SVTLNLSLHDFVLKHLPEASLYHVLMAYSRAGSTNSTGLTLRTLDPSDLNIFLGLCLV 637
QY 849 ITSSILLGLTLLISHQMKLFWEDVPNPKNSWAQGLNFQKPEFELFHKHTASVTC 908
Db 638 LLSTTCVV--TWLCCRRKGTFSWSDVDPDAHSSLSWL-----674
QY 909 GPULLEPETISEDIVSDTSWKKNDKEMPTTVVSLSTTDLEKSGVCIS-DQFNSVNF--965
Db 675 -PTIMTEET---FQLPSEW-----DSSVPSITKITELEDKPKTHWDSSESSNGSLP 722
QY 966 -----EAGTEVYDEDSQRPFVKYATLISNSKPSSETGEE-----Q 1002
Db 723 ALVQAVYVLOGDPREIS-----NOSQP-----PSRTGDQVLYGVLESPTSPGVW 766
QY 1003 GLINSVTKFCFSKNSKLDKDSFNSNWSWEIEAQAFILSDQHPN-----IISPLTFSS---1054
Db 767 QYIRSDSTQPLGGPTSPKSYENIWFHSRPOETFV--PQPPNQEDDCVGGPFPDFPLFQ 824
QY 1055 -----EGLDELLKLEGNF 1067
Db 825 GLQVHGVEE---QGGF 837
RESULT 12
S17308
leukemia inhibitory factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S17308
R:Gearing, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Pr
EMBO J. 10, 2839-2848, 1991
A:Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 sign
A:Reference number: S17308; MUID:92007727
A:Accession: S17308
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1097 <GEA>
A:Cross-references: GB:X61615; NID:g34365; PIDN:CAA43805.1; PID:g34366

Query Match 4.7%; Score 294.5; DB 2; Length 1097;
Best Local Similarity 19.2%; Pred. No. 7e-11;
Matches 215; Conservative 179; Mismatches 385; Indels 339; Gaps 52;
QY 161 LLVVLPEVLDSPLVPQKGSFQWVHC-----NCS-----VHECC-----194
Db 35 LLYLMNQVNSQ-----KKGAPHLKCVTNLQVWNCWKAAPSCTGRGTDEYVCIEIENRSR 89

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QY 195 -----ECLVPVPTAKLNDTLMLCKLITSGVIFQSPMLSVQPINVMKPPDPLGLHMEIT- 248
Db 90 CVOLEKTSIKIPALSHGDYEITINSUHDGFSSTKFTLNEQNVSLI-PDTPETILNSADF 148
QY 249 DGNLKAISWSSPLVPFPFQYQVKYSNSTVIR-----EADKIVSATSLI----- 294
Db 149 STSTLYLKNDRGSV-FPHRSNVIV---EIKVLKRESMELVKLVTINT'NLNGKDTLHHWS 204
QY 295 --VDSILPGSSVEQVVR-----GKRLDGPGLWSDWSPRPVFT---TQDVYIFPPKILTSVG 345
Db 205 WASDMPLECAIHFEIRCVYIDNLFHSGLEWSDWSPVKNISWIPDSQTKVFPQDKVILVG 264
QY 346 SNVSFHCYKKNKIYPSKEIYVWMLAEKIPQSQVDV---SDHVSKYVTFPFLNLTETPR 402
Db 265 SDITFCV-----SQEKV-----LSALIGHTNCPLIHLDGENVA-IKIRNISVSASS 310
QY 403 GKFTYDAVYCCNEHCHRYAEIYVDVINISCEFTDGYLTCKTCRWSTSTQSLA---E 459
Db 311 GT---NVVFTEDNIFGTVFAGYPPDTPQOLNCETHD-LKEIICSWNPGRTALVGPRA 366
QY 460 STIQLRYHRSLLYCDIPSTHPISEPKDCYLOSQDGYECIFQPIFLLSGYTMWIRINHSL 519
Db 367 TSYTLVESFSGKYVRLKRAEAPNES-----YQLLFQMLPNOEIYNTFLNAHNPL 416
QY 520 GSLDSPCTCLVPSVVKPLPPSPSVKAEITINIGLLKISWEK-----VPEP 566
Db 417 GRSQSTILVNITDKV-PHTPTSFVKY-DINSTAVKLSWHLPGNFAKINFLCBIETIKKSN 474
QY 567 NLOFIQIRYGLSGKEVQWKYEVYDAKSKSVLFPVDPDLCAVYAVQVRCRLDGLGYWSNWS 636
Db 475 SVQEQRNVTIKGVE-----NSSYLVALDKLAPYLTLYTRIRCS-TETPWKWSKWS 523
QY 627 NPAYTVMDIKVPMRGPPEFWIRINGDTMKKEKNVTLLWPLMKNDSLCSVQRVVIHHST 686
Db 524 NKKOHLTTEAS-PSKPGDTWREWSSD---GKNLIYWKPLPINEA---NGRIKLSYNVS 574
QY 687 CNG-----TWSEDDVGNHTFTFLWLTQAHVTVTALNISGASVANFLNFSWPMKSNVIV 741
Db 575 CSDEETQSLEIPDPQHKAEIRLKDNDYIISVANKSVSSPPSKIASMEIPNDLKE 634
QY 742 QSLSAYPLNSCIVVSWILSPS---DYKLMYFIEWKN-LNEDGEIKWLRI-SSSVKKY 795
Db 635 QVYGM---GKGILLWHYDPNMTCDY-----VIKWCNSRSEPCMLDMRKVPNSNTEV 685
QY 796 YIHDHPIPIEKYQSLYPIFMEG-----VG-----KPKIINSFTQDD----- 832
Db 686 IESDEPRGIRYNFFLYGCRNQYLLRSMIGVIEBELAPIVAFNFTVEDTSADSIIVKWE 745
QY 833 -----IEKHQSD----- 839
Db 746 DIPVEELRGFLGYLFYFGKGERDTSKMRVLESGRSDIKVKNTIDISOKLTRIADLOGKT 805
QY 840 -----AGLYVI-----VPVLISSILLGLPGLLSHOR--M 867
Db 806 SYHLVLRAYTDGGVGPESKSMYVTKENSVCGLITAILIPVAVAVIVGVVTSILCYRKREWI 865
QY 868 KKLFWEDVNPKNCSWAQGLNFQK-----PETEHLFIKHTASVTCGPLL 912
Db 866 KEFFYPDIPNPENC---KALQFOKSCVCEGSSALKTLLEMPNCTPNNVLEVLETSFSAF--PKI 920
QY 913 LEPETISEDIVDTSWKNKDEMPTTWSLLSTTDLEKGSVC---ISDQFNVSYNFSEAG 969
Db 921 EDTEIIS---PVAEREDRSDAEPENHVUV-----SYCPPIIEEETPNPAADGAG 968
QY 970 T-EVTVED-ESQRQPVVKYATLISNKPSETGEEQSL-----INSSVTKFS- 1014
Db 969 TAQVIVIDQSMYQP-----QAKPEEQENDPVGAGYKPMHLPINSTVDIAAE 1019
QY 1015 ---SKNSPLKDSFNSNSWEIEAQAFILSDQHPNIIISP 1049
Db 1020 EDLDKTAGYRQPOANVTW-----NLVSP 1042
```

```
RESULT 13
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C:Date: 14-Jun-1991 #sequence-revision 30-Jan-1993 #text-change 05-Nov-1999
C:Accession: C38252; A38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A>Note: Clones pHG11 and pHG5
A:Accession: A38252
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X5721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A>Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A>Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: lp35-lp34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F:25-860,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TM>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred
```

Query Match 4.6%; Score 288.5; DB 2; Length 863;

Best Local Similarity 20.0%; Pred. No. 1.2e-10;

Matches 156; Conservative 125; Mismatches 280; Indels 219; Gaps 38;

QY 341 LTVSGSVNPFHCYKKE-NKIVFSKEIYVWMLAEKIPQSQVDVSD--HVSKVTFNLN 397

Db 35 IVHLGDPITASCITKQNCNSHLDPEPQILWRLG-AELQPGGRQRLSDGTQESTITPLN 93

QY 398 ETRKPRGFTYDAVYCCNEHCHRYAEIYVD-----VNINISCTDGYLTKMT 446

Db 94 HTQ-----AFVSC-----CLWNGNSLQILDQVELRAGYPPAIPHNLSCMLNLTSSLI 141
QY 447 CRWSTSTIOSLABS-TLOLRHYHSSLYCSDIPSIHPISPEKDCYLOSDGYECI-----499
Db 142 COMEPGETHLPSTFTLKSKSRG-----NCOTQGDSTLDCVPPKDGQS 184
QY 500 -----FQPIFLSGYTMWIRINHSLGSDSPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLYQNMGIWQAEALGTSMSPOLCLDPMVVKLEPPMLRTMDSPEA-AP 243
QY 549 INTGLLKISWEKVPFP--ENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPVP-----601
Db 244 PQAGCLQLCWE-PWQPGELHINOKCELHKKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCV-----YAVQVRCKLDGLGYSWNSNPAYTVVMDIKVPMRGP-----EFWRIIN 650
Db 292 YELCGLLPATAYTQIRCIKWPPLGHSWDS-PS-----LELRTTERTAPTVRDLTWNR---343
QY 651 GDTMKKEKNVTLWKPLKNDLSQVRYVINHTS-----CNGTWSEDVGNHTKF 701
Db 344 -QRLDPTVOLFWKVPLEEDSGRIQGYVSWRPSQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTOAHTVTVLAINSGASVANFNLTFSWPMKVNIVQSLSAYPLNSSCVIVSWILS 761
Db 396 TFLPSEAQVAVLVAAYNSAGTSRPT-PVWFS--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSYKLMYFIIEW-----KNLEDGEIKW-LRISSSVKKYYIHDFPIEKYQSLYP 813
Db 451 PPNWPGQYVIEGLGPPSPASNSNK-----TWMEQNGRATGFLLENIRFPQYELIYVTP 506
QY 814 IFMEGVGKPKIINFTQDDIEKHOSDAGL-----YVIVPVTISSLILLGLTLLI 862
Db 507 LYQDTMGPSQHVYAYSQEAMAPSHAPELHLKHICKTWAQLEWVPEPELGKSPLTHTY---563
QY 863 SHORMKKLFWEVDPNPKNCWAQGLNFPQ-----KPTFEHLFIK-----HTASVT 907
Db 564 -----IFW---TNAQNQSFSAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 613
QY 908 CGPLLEPETISEDIV-----DTSW-----KNKDEMPPTVVVLLSTDLLE 949
Db 614 LTLMTLTPEGSELHIILGLFLLLLTCLCGTAWLCCSPNKNPLWPSVDPDPAHSLGSW 673
QY 938 --TWVSL-----STTDLEKGSV---CISDQFNVSFSEAEGETVEYDEESQRP 982
Db 674 VPTIMEELCPROGWLQGTSENRAITPHPCVQDAFQLPGLTPTTKITLVLEDEKPP 733

RESULT 14

JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
C:Accession: JH0329; S21608
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <IAR>
A:Cross-references: GB:X5720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
A:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <M
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match

4.5%; Score 284; DB 2; Length 783;

Best Local Similarity 20.3%; Pred. No. 2e-10;
Matches 153; Conservative 121; Mismatches 287; Indels 192; Gaps 35;
QY 341 LTSVGSNVSFHCYKKE-NKIVPSKETVWMMNLAERIKPOSOYDVSD--HVSXVTFENLN 397
Db 35 IVHLGDPITASCIIKONCSHLDPQLLRIG-AELQPGGRQORLSDGTQESIIITPHLN 93
QY 398 ETRPRGKFTYDAYVCNEHECHRYAELVVID-----VNIISCTDGYLTKMT 446
Db 94 HTQ-----AFVSC-----CLWNGNSLQILDQVELRAGYPPAIPHNLSCMLNLTSSLI 141
QY 447 CRWSTSTIOSLABS-TLOLRHYHSSLYCSDIPSIHPISPEKDCYLOSDGYECI-----499
Db 142 COMEPGETHLPSTFTLKSKSRG-----NCOTQGDSTLDCVPPKDGQS 184
QY 500 -----FQPIFLSGYTMWIRINHSLGSDSPPTCVLPDSVVKPLPP-----SSVKAET 548
Db 185 HCCIPRKHLLYQNMGIWQAEALGTSMSPOLCLDPMVVKLEPPMLRTMDSPEA-AP 243
QY 549 INTGLLKISWEKVPFP--ENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPVP-----601
Db 244 PQAGCLQLCWE-PWQPGELHINOKCELHKKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCV-----YAVQVRCKLDGLGYSWNSNPAYTVVMDIKVPMRGP-----EFWRIIN 650
Db 292 YELCGLLPATAYTQIRCIKWPPLGHSWDS-PS-----LELRTTERTAPTVRDLTWNR---343
QY 651 GDTMKKEKNVTLWKPLKNDLSQVRYVINHTS-----CNGTWSEDVGNHTKF 701
Db 344 -QRLDPTVOLFWKVPLEEDSGRIQGYVSWRPSQAGAILPLCNTT-----ELSC 395
QY 702 TFLWTOAHTVTVLAINSGASVANFNLTFSWPMKVNIVQSLSAYPLNSSCVIVSWILS 761
Db 396 TFLPSEAQVAVLVAAYNSAGTSRPT-PVWFS--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSYKLMYFIIEW-----KNLEDGEIKW-LRISSSVKKYYIHDFPIEKYQSLYP 813
Db 451 PPNWPGQYVIEGLGPPSPASNSNK-----TWMEQNGRATGFLLENIRFPQYELIYVTP 506
QY 814 IFMEGVGKPKIINFTQDDIEKHOSDAGL-----YVIVPVTISSLILLGLTLLI 862
Db 507 LYQDTMGPSQHVYAYSQEAMAPSHAPELHLKHICKTWAQLEWVPEPELGKSPLTHTY---563
QY 863 SHORMKKLFWEVDPNPKNCWAQGLNFPQ-----KPTFEHLFIK-----HTASVT 907
Db 564 -----IFW---TNAQNQSFSAILNASSRGFVLHGLEPASLYHIHLMAASQAGATNSTV 613
QY 908 CGPLLEPETISEDIV-----DTSW-----KNKDEMPPTVVVLLSTDLLE 949
Db 614 LTLMTLTPEGSELHIILGLFLLLLTCLCGTAWLCCSPNKNPLWPSVDPDPAHSLGSW 673
QY 950 KGSVCISDQFNVSFSEAEGETVEYDEESQRP 982
Db 674 VPTIMEEDAFQLPGLTPTTKITLVLEDEKPP 706
RESULT 15
JH0312
differentiation-stimulating factor/leukemia inhibitory factor receptor 1 precursor -
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C:Accession: JX0312; JC2181; S38942
R:Tomida, M.; Yamamoto-Yamaguchi, Y.; Hozumi, M.
J. Biochem. 115, 557-562, 1994
A:Title: Three different cDNAs encoding mouse D-factor/LIF receptor.
A:Reference number: JX0312; MUID:94334302
A:Accession: JX0312
A:Molecule type: mRNA
A:Residues: 1-1092 <TOM>
A:Cross-references: DDBJ:D26177; NID:q473718; PIDN:BAA05165.1; PID:d1005707; PID:g825
A:Accession: JC2181
A:Molecule type: mRNA
A:Residues: 1-717, 'EA' <TOM1>

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: August 15, 2002, 16:18:50 ; Search time 101.13 Seconds
(without alignments)
1279.551 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEPIVIT.....QTCSTQTHKIMENKMCIDLIV 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6254	100.0	1165	18 AAW24051	Human WSX receptor
2	6254	100.0	1165	22 AAE12609	Human Ob receptor
3	6254	100.0	1220	18 AAW34500	Obesity receptor D
4	6250	99.9	1165	22 AAE12551	Human Ob receptor
5	6246	99.9	1165	20 AAY13474	Peptide Seq ID No:
6	6240	99.8	1165	18 AAW19116	Human Ob receptor.
7	5809	92.9	1221	19 AAW62544	Human ob-receptor
8	4831.5	77.3	970	18 AAW34499	Obesity receptor C
9	4826	77.2	896	18 AAW24052	Human WSX receptor
10	4826	77.2	923	18 AAW24053	Human WSX receptor
11	4826	77.2	972	18 AAW34497	Obesity receptor A

12	4826	77.2	999	18 AAW34498	Obesity receptor B
13	4819.5	77.1	958	18 AAW36214	Human OB-R variant
14	4819.5	77.1	958	18 AAW31911	Human OB-R variant
15	4819.5	77.1	958	18 AAW19535	Human OB-R variant
16	4819.5	77.1	958	18 AAW22773	Human haematopoietin
17	4816.5	77.0	960	17 AAR88910	Haematopoietin rec
18	4814	77.0	896	18 AAW50003	Human OB-R variant
19	4814	77.0	904	18 AAW50002	Human OB-R variant
20	4813	77.0	908	17 AAR88911	Haematopoietin rec
21	4811	76.9	898	17 AAR88912	Haematopoietin rec
22	4799	76.7	908	18 AAW19536	Variant form of hu
23	4785	76.5	896	18 AAW14841	Human haematopoietin
24	4784.5	76.5	1162	18 AAW34257	Rat wild-type ob r
25	4784.5	76.5	1162	18 AAW32398	Rat ob receptor (w
26	4778.5	76.4	1162	18 AAW23399	Rat ob receptor (f
27	4770.5	76.3	1162	18 AAW19115	Murine long form O
28	4770.5	76.3	1162	22 AAE12615	Murine long form O
29	4766.5	76.2	1162	20 AAY13473	Peptide Seq ID No:
30	4574	73.1	883	19 AAW62543	Human ob-receptor
31	4554	72.8	839	18 AAW34502	Obesity receptor p
32	4421	70.7	815	20 AAY05701	Human OB receptor
33	4337	69.3	804	18 AAW34501	Obesity receptor p
34	4214.5	67.4	1015	18 AAW34259	Rat ob receptor is
35	3793	60.6	900	18 AAW22105	Murine leptin rece
36	3787	60.6	892	18 AAW34260	Rat ob receptor is
37	3787	60.6	894	18 AAW37337	Ob protein recepto
38	3787	60.6	895	18 AAW34258	Rat ob receptor is
39	3785	60.5	894	18 AAW24064	Murine WSX recepto
40	3785	60.5	894	18 AAW19114	Murine short form
41	3781	60.5	894	22 AAE12608	Murine short form
42	3781	60.5	894	18 AAW37338	Ob protein recepto
43	3479	55.6	842	18 AAW22102	Murine leptin rece
44	3340	53.4	805	18 AAW22106	Murine leptin rece
45	3143	50.3	783	18 AAW24054	Murine WSX recepto

ALIGNMENTS

RESULT 1
AAW24051
ID AAW24051 standard; Protein; 1165 AA.
XX
AC AAW24051;
XX
DT 17-MAR-1998 (first entry)
XX
Human WSX receptor variant 13.2.
XX
Human; WSX receptor; variant 13.2; identification; purification;
ligand; activator; antibody; agonist; proliferation; obesity;
differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
Type II diabetes; polycystic ovarian disease;
cardiovascular disease; osteoarthritis; dermatological disorder;
hypertension; insulin resistance; hypercholesterolaemia;
hypertriglyceridaemia; cancer; cholelithiasis.
XX
OS Homo sapiens.
XX
PN WO9725425-A1.
XX
PD 17-JUL-1997.
XX
07-JAN-1997; 97WO-US00325.
XX
20-JUN-1996; 96US-0667197.
XX
08-JAN-1996; 96US-0585005.
XX
(GETH) GENENTECH INC.
XX
Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
Rodrigues ML.

DR WPI; 1997-372864/34.
DR N-PSDB; AAT85575.
XX
PT WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours
XX
PS
PS ClaIm 2; Pages 81-85; 219pp; English.
XX
XX The present sequence is the human WSX receptor variant 13.2,
CC which can be used to identify and purify ligands and activators.
CC An anti-WSX receptor antibody can be used as an agonist to activate
CC the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.
XX
SQ Sequence 1165 AA;

Query Match 100.0%; Score 6254; DB 18; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVITARNLSYPITPWRFKLSCHMPNSTYDYFLLPAGLSKNTS 60
DB 1 micqkfcvllhweifyvitarnlsypitpwrfrklschmpnstydyfllpaglsknts 60
QY 61 NGHYETAPEPKNSGTHFSNLSKTFHCFRSEQDRNCSLADNTEGKTFVSTVNSLVP 120
DB 61 nghyetapepkfnsqthfshnlskttfhcfrseqdrncsladnlegkthfvtvnslvf 120
QY 121 QQIDANWNTQCVLKGDLKIFCYVESLFKNLFRNYKYVHLLYVLPVEVLEDSPLVPQKGS 180
DB 121 qqidanwnlqcvlkgdlkifcyveslfknlfrnykyvhllyvlpvevledsplvpqkgs 180
QY 181 FQWVHCNCSVHECCCLVPPVPAKLNDTLMLCLKITSGGVIFQSPVMSVQPINWVKPDPP 240
DB 181 fqwvhcnscsvheccclvppvpaklndtlmlclkitsggvifqspvmsvqipnwvkpdpp 240
QY 241 LGLHMEITDDGNLKISWSSPPVLPFLOQVQVYSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitddgnlkiswssppvlpflopqvqvysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEVQVVRGKLDGPGIWSNDSTPRVFTQDVIYFPKILTSVGSNVSFHCIIYKKENKI 360
DB 301 gssyevqvrgrldpgiwsdswstprvftqdvifppkiltsvgsnvsfhcllykknk1 360
QY 361 VPSKEIVWMMNLAEKIPQSOYDVSDHVSQVTFNINLNETKPRGKFTYDVCYCNHECHH 420
DB 361 vpskeivwmnlakkipqsoydvsdhvsqvtfnlnetkprgkftydavycnehechh 420
QY 421 RYAEIYVIDVNTINISCTGYLTWKTCRWSTSTIQSLAESTLQLRVHRSLSYCSDDIPSTH 480
DB 421 ryaeilyvidvntiniscetdgyltkmtcrwststiqslaestlqlrvhrrslycsddipsh 480
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRNIHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylqsdgfyecifqpiifllsgytmwirnihslgsldspptcvlpdsvvkplpp 540
QY 541 SSVKAEITTNIGLLKLSWEKPVFPENNLOFQIRYGLSGREOVQWKEVYVDKSKSVSLPV 600
DB 541 ssvkaeittnigllklswekvpfpennlofqiroyglsgrevowkewyvyvdksksvslpv 600

DB 541 ssvkaeittnigllklswekvpfpennlofqiroyglsgrevowkewyvyvdksksvslpv 600
QY 601 PDLCAVYAYOVCRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 pdlcavyayovcrckrlldglgywsnnsnpaytvvmdikvpmrgpewfriingdtmkkeknv 660
QY 661 TLLWKPMLKNDLSLCSVQRYVINHHTSCNGTWSDEDVGNHTKFTFLWTEQAHTTVVLAINSI 720
DB 661 tllwkpmlkndslcsvqryvinhhtscngtwsedvgnhtkftflwteqahtvtvlainsi 720
QY 721 GASVANFNITFSPWMSKVNIVOSLSAYPLNSCVIVSNILSPSDYKLMYFIIEWKLNLED 780
DB 721 gasvanfnitfswpmkskvnivoslaysplnscviviwnilspdsdyklmfyiiewklnled 780
QY 781 GEIKWLIRISSVKKYIYHDFPIPIEKYQFSLYPIFMGVGPKIINSFTQDDIEKHOSDA 840
DB 781 geikwlirissvkkyyihdfpiipiekyqfslypifmegvgpkilnsftqddiekhosda 840
QY 841 GLYVIVPVISSISLLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPTPEHLFT 900
DB 841 glyvivpviissisllgltllishqrmkklfvedvnpknscswagglnfqkptpehlft 900
QY 901 KHTASVTCGPLLEPETISEDIVSTSWKNKDEMPPTTVVLLSTDLKSGSVCSIDQFN 960
DB 901 khtasvtcgpllepetisedivstswknkdempppttvvllstdlekgsvcsidqfn 960
QY 961 SYNFSAEGETVTEYDESORQPFVKYATLINSKPSKETGEEQGLINSVTKCFSSKNNSPL 1020
DB 961 synfsaegetvteydesorqpfvkvatlinsksketgeegllnsvtkcfssknsp 1020
QY 1021 KGSFNSNSWEIEBAQAFITLSDQHPNITISPHLTFSEGLDELLKLEGNFPENNKKSIYYL 1080
DB 1021 kdsfnssweieaqaftllsdqghpniisphltfsegldeillklegnfpeennkkssiyl 1080
QY 1081 GYVTSIKKRESGVLTKDSRVSCPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 gyvtsikkrsgvlltkdsrvscpfapclftdirvlqdschfvenninlgtsskktffas 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1141 ympqfqtcsqtqhkimenkmdltv 1165

RESULT 2
AAE12609
ID AAE12609 standard; Protein; 1165 AA.
XX
AC AAE12609;
XX
DT 03-JAN-2002 (first entry)
XX Human Ob receptor (ObR) protein.
XX
XX Human; obese receptor; ObR; anorectic; anabolic; body weight disorder;
XX therapy; obesity; cachexia; anorexia.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..20 /label= Signal_peptide
FT Protein 21..1165 /label= Human_mature_ObR_protein
FT Domain 21..839 /label= Extracellular_domain
FT Modified-site 23..25 /note= "Asn is N-glycosylated"
FT Modified-site 41..43 /note= "Asn is N-glycosylated"
FT Modified-site 56..58 /note= "Asn is N-glycosylated"
FT Modified-site 59..61 /note= "Asn is N-glycosylated"
FT

FT Modified-site 73..75 /note="Asn is N-glycosylated"
 FT Modified-site 98..100 /note="Asn is N-glycosylated"
 FT Modified-site 187..189 /note="Asn is N-glycosylated"
 FT Modified-site 206..208 /note="Asn is N-glycosylated"
 FT Modified-site 276..278 /note="Asn is N-glycosylated"
 FT Modified-site 347..349 /note="Asn is N-glycosylated"
 FT Modified-site 319..323 /note="Asn is N-glycosylated"
 FT Region 397..399 /note="Conserved motif of cytokine I receptor family"
 FT Modified-site 433..435 /note="Asn is N-glycosylated"
 FT Modified-site 516..518 /note="Asn is N-glycosylated"
 FT Modified-site 622..626 /note="Asn is N-glycosylated"
 FT Region 624..626 /note="Conserved motif of cytokine I receptor family"
 FT Modified-site 659..661 /note="Asn is N-glycosylated"
 FT Modified-site 670..672 /note="Asn is N-glycosylated"
 FT Modified-site 688..690 /note="Asn is N-glycosylated"
 FT Modified-site 697..699 /note="Asn is N-glycosylated"
 FT Modified-site 728..730 /note="Asn is N-glycosylated"
 FT Modified-site 750..752 /note="Asn is N-glycosylated"
 FT Domain 840..862 /label="Transmembrane_domain"
 FT Domain 863..1165 /label="Cytoplasmic_domain"
 FT US6287782-B1.
 FT 11-SEP-2001.
 FT 29-APR-1998; 98US-0069781.
 FT 27-NOV-1995; 95US-0562663.
 FT 04-DEC-1995; 95US-0566622.
 FT 08-DEC-1995; 95US-0569485.
 FT 11-DEC-1995; 95US-0570142.
 FT 28-DEC-1995; 95US-0583153.
 FT 22-JAN-1996; 96US-0599455.
 FT 26-APR-1996; 96US-0638524.
 FT 03-SEP-1996; 96US-0708123.
 FT 28-MAY-1997; 97US-0864564.
 FT (MILL-) MILLENNIUM PHARM INC.
 FT Tartaglia LA, Tepper RI, Culpepper JA, White DW;
 FT WPI: 2001-624489/72.
 FT N-PSDB; AAD20509.
 FT Identifying compounds for treating body weight disorder, e.g. obesity,
 FT anorexia or cachexia, comprises contacting cell expressing mammalian Ob
 FT receptor protein, JAK2 protein and mammalian SOCS-1 protein with test
 FT compound -
 FT Claim 1; Fig 3; 109pp; English.
 FT The patent discloses obese receptor (OBR) proteins and nucleic acids
 FT encoding them. OBR protein participates in the regulation of mammalian

CC body weight. The invention also relates to a method of identifying
 CC therapeutic compounds for the treatment of a body weight disorder.
 CC The method involves contacting a cell that expresses a mammalian OBR
 CC protein, a JAK2 protein and a mammalian SOCS-1 protein with a test
 CC compound. The method is useful for identifying compounds which modulate
 CC OBR gene expression and gene product activity, which can be used as
 CC agents to control body weight particularly as therapeutic agents for
 CC treating body weight disorders, including obesity, cachexia and anorexia.
 CC The present sequence is OBR protein from human.
 XX
 SQ Sequence 1165 AA;
 Query Match 100.0%; Score 6254; DB 22; Length 1165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MICOKFCVLLHWEFIYVITAFNLSPYIPWRFKLCMPNPNSTYDYVFLPAGLSKNTSNS 60
 DB 1 micqkfcvllhwefiyvitafnlspypwrfklsmpnpsnydyflpagslksntns 60
 QY 61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
 DB 61 nghyetavepkfnsgthfnslnskttfhccfrseqdrncslcadniegktfvstvnslvf 120
 QY 121 QQIDANWNTQCWLKGDILKLFICYVESLFLNLFNRYNYKVHLLYLVPEVLEDSPLVPQKGS 180
 DB 121 qqidanwniqcwlkgdlklficyveslflnlfnykvhllylvlevedsplvpqkgs 180
 QY 181 FQMVHNCNSVHECCGCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINWKPDP 240
 DB 181 fgmvhncnsvehccgclvpvptaklndtlmlcklitsggvifqspmlsvqipnwkpdp 240
 QY 241 LGLHMEITDDGNLKIWSPPPLVFPFLQYQVYSENSTTVIREADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkiwsppplvpfpflqyqvysesttvireadkivsatsilvdsilp 300
 QY 301 GSSYEVQVRGKRLDGGIWSDMSTPRVFTTQDVYPPPKILTSGVSNVSPHCYIKKENKI 360
 DB 301 gssyevqvrqkrlldggiwsdmstprvfttqdvypfpkiltsgvsnvshciykkenki 360
 QY 361 VPSKEIVWMNLAEKIPQSOYDVVSDHVSKVTFPFLNLTNPKRGTFTVAVYCCNEHCCH 420
 DB 361 vpskeivwmnlakelpsqoydvvsdhvskvtfpflnltntpkrgtftvavycnehechh 420
 QY 421 RYAELYVIDVNIINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRHRSSLYCSDIPSIIH 480
 DB 421 ryaelyvidvniiniscetdgyltkmtcrwststiqslaestlqlrhrsslycsdipsih 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSGLSDSPPTCVLPDSVVRPLPP 540
 DB 481 pisepkdcylqsdgfyecifqpifllsgytwirinhsglsdpsptcvipldsvvvrplpp 540
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVYVYDAKSVSPLV 600
 DB 541 ssvkaeitiniigllkiswekvpfpennlofqiiryglsgkevqwmvvyvdaksvsplv 600
 QY 601 PDLICAVYAVOVRCKRLDGLGYNSWNSPAYTVVMDIKVPMRGPEFWIRINGDMTKKEKNV 660
 DB 601 pdlicavyavovrckrldglgynswnspaytvvmdikvpmrgpewfiringdmtkkknv 660
 QY 661 TLLWKPMLKNDLSLCSQRYVINHHTSCNGTWSVDVGNHTKFTFLWTOAHTVTVLAINSI 720
 DB 661 tllwkpmlkndslslcsqryvinhhtscngtwsdvgnhtkftflwteqahvtvtlainsi 720
 QY 721 GASVANFNLTFFSPMSKVNIVQSLAYPLNSCVIVSWILSPDYKLMYRIEWMKLNED 780
 DB 721 gasvanfnltffspmskvnivqslaysplnscvviwswilspdyklmyrieewklned 780
 QY 781 GEIKWLRISSSVKYYIHDHFIEPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
 DB 781 geikwlrisssvkkyyihdhfiepikyqfslypifmgvgkpkliinsftoddiekhqsd 840

QY 841 GLYVIVPVVIAISSILLGLTLLSHQRMKKLFWEDVNPKNCSWAQGLNFQKPFTEHLEFI 900
Db 841 glyvivpvviiassillllgtllshqrmkklfwevnpknkcswaqglnfqkpetfehlfi 900
QY 901 KHTASVTCGPLEPETISEDIVSDTSWKNKDEMPFTTVVLSLLSTTDLEKSGVCISDQFN 960
Db 901 khtasvtcgpllepetisedivsdtswnknkdemmpfttvvlsllsttdleksgvcsisdqfn 960
QY 961 SVNFSEAGTEVTEYDESOROPPVKYATLINSKPSGTGEEOGLINSVTKCFSSKNSPL 1020
Db 961 svnfseagtevtetydesorppvkyatlinskpsgtgeegolinsvtkcfssknspl 1020
QY 1021 KDSFNSWSEIEAQAFFILSDQHPNIIISPHLTFSEGLLELLKLEGNFPEENDDKKSIIYL 1080
Db 1021 kdsfnsweieaqaaffilisdqhpniisphltfsegllellklegnfpeenddkksiiyl 1080
QY 1081 GVTISIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLDSCSHFVENNINLGTSKKTFFAS 1140
Db 1081 gvtisikkresgvlltdksrvscppfapclftdirvldscshfvennlnlgtskktffas 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1141 ympqfotcstqthkimenkmdltv 1165
RESULT 3
AAW34500
ID AAW34500 standard; protein; 1220 AA.
AC AAW34500;
XX
XX 18-MAR-1998 (first entry)
DE Obesity receptor D protein.
DE
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 1..1165 /note= "encoded by AAT98531"
FT Misc-difference 1166 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 1169 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 1187 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 1207 /label= unknown
FT /note= "encoded by stop codon"
FT Misc-difference 1..1165 /note= "encoded by AAT98531"
XX
PN WO9725424-A1.
XX
XX 17-JUL-1997.
XX
XX 02-JAN-1997; 97WO-US00128.
XX
XX 31-DEC-1996; 96US-0774414.
XX 04-JAN-1996; 96US-0582825.
XX (AMGE-) AMGEN INC.
XX Chang M, Fletcher FA, Welcher AA;
XX WPI: 1997-384981/35.
XX
XX
XX

DR N-PSDB; AAT98531.
XX Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 31; Page 76; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor D protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 1220 AA;
Query Match 100.0%; Score 6254; DB 18; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEPIYVITAFNLSPITPWRPKLSCMPNPSTYDFLLPAGLSKNTSNS 60
Db 1 micqkfcvllhwepiyvitafnlspitpwrfrklscmpnpnstydfllpaglskntsns 60
QY 61 NGHYETAVEPKFNSGTFHFNLSKTFPHCCFRSEQRNCSLCADNIEGKTFVTVNSLVF 120
Db 61 nghyetavepkfnsdgthfnlskttfhccfrseqrncslcadniegkttfvatvnslvf 120
QY 121 QQIDANWNIQCWLKGLDKLFCYVESLFKNLFRNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 qqidanwniqcwlkgdlkficyveslfnlfrnykvhllyvlpvledsplvpqkgs 180
QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFSPMSVQPINWVXPDP 240
Db 181 fqwvhcnscsvheccclvpvptaklndtlmlcklitsggvifgspmsvqipnwvxpdpp 240
QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQVQKYSNSTTVIREADKIVSATSLVDSILP 300
Db 241 lglhmeitddgnlkswsppplvpfploqvqkysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEVQVRGKRLDGPINWSDNSTPRVFTQDVYIPFPKILTSVGSNVSFHCYIKKENKI 360
Db 301 gssyevqvrgrldgpgiwsdstprvftqdvyipfpkiltsvgsnvsfhcyikkenki 360
QY 361 VPSKEIYVWVWNLAEKIPQSQDYVSDVSHVSKVTFNLETKPRGKFTYDAYVCCNEHECHH 420
Db 361 vpskeiyvwmnlakekipqsgdyvsvdhvskvtfnlctkprgkftdyavccnehechh 420
QY 421 RYAEELYVIDVNIINISCTDGYLTGMTCRWSTSTIQSLAESTLQLRHYRHSLSYCSIDPSIH 480
Db 421 ryaelvyidvnninisctdgyitkmtcrwststiqslaestqlryhrhslycsidpsih 480
QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 ptsepkdcylqsdgfyecifqipifllsgytmwirinhsllsglspptcvtlpdsvvkplpp 540
QY 541 SSVKABITINIGLLKISWEKVPFPENNLOFQIRYGLISGKEVQWKMYEVDKSKSVSLPV 600
Db 541 ssvkaeitinigllkiswekvpfpennlqfiryglisgkevqwkmyevdaksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGYNSNWSNPATVVMVDIKVPMRGPFWRINGDPTMKKEKNV 660
Db 601 pdlcavyavqvrckrldglgywnsnwspatvvmvdikvpmrgpfwringdptmkkeknv 660
QY 661 TLLWKLPMKNDLSLCSVQRYVINHHHTSCNGTWSDEVGNHKTFTFLWTEQAHTVTVLAINSI 720
Db 661 tllwklpmkndslcsvqrvyvinhhhtscngtwsedvgnhktftflwteqahtvtvlainsi 720
QY 721 GASVANFNLTFFSWPMKSNVINQSLSAYPLNSSCVIYVILLSPSDYKLMVFIIEMKLNED 780
Db 721 gasvanfnltffswpmksnvinqslsayplnsscviyvillspdyklmvfiemklned 780

RESULT	4	
AAE12551		
ID	AAE12551 standard; Protein; 1165 AA.	
XX		
AAE12551;		
XX		
03-JAN-2002	(first entry)	
XX		
Human Ob receptor (ObR) protein mutant (Y1141P).		
XX		
Human; obese receptor; ObR; anorectic; anabolic; body weight disorder;		
KW	therapy; obesity; cachexia; anorexia; mutant; mutuin.	
XX		
Homo sapiens.		
OS	Synthetic.	
XX		
XX		
Key	Location/Qualifiers	
Peptide	1..20	
	/label= Signal_peptide	
Protein	21..1165	
	/label= Human_mature_ObR_protein	
Domain	21..839	
	/label= Extracellular_domain	
Modified-site	23..25	"Asn is N-glycosylated"
	/note=	
Modified-site	41..43	"Asn is N-glycosylated"
	/note=	
Modified-site	56..58	"Asn is N-glycosylated"
	/note=	
Modified-site	59..61	"Asn is N-glycosylated"
	/note=	
Modified-site	73..75	"Asn is N-glycosylated"
	/note=	
Modified-site	98..100	"Asn is N-glycosylated"
	/note=	
Modified-site	187..189	"Asn is N-glycosylated"
	/note=	
Modified-site	206..208	"Asn is N-glycosylated"
	/note=	
Modified-site	276..278	"Asn is N-glycosylated"
	/note=	
Modified-site	347..349	"Asn is N-glycosylated"
	/note=	

CC from the wild-type human ObR protein shown in figure 3 of the
XX specification (AAE12609).

SQ Sequence 1165 AA;

Query Match 99.9%; Score 6250; DB 22; Length 1165;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIIVITAFNLISYPTWRFKLSCLMPNNTSYDYILLPAGLSKNTNS 60
DB 1 micokfcvllhwefiivitaafnlisypwrfklsclmpnntsydyillpaglskntns 60
QY 61 NGHYETAVERKFNFSNGTHFNSLTKTTHFCCHFRSQDRCNLSICADNIEGKTFVSVNSLVF 120
DB 61 ngyetavekfnfngthfnsltkthfchfrsqdrcnlsicadniegktfvsvnslvf 120
QY 121 QQIDANNNIOCWUKGDKLFCYVESLFKNLFRNYYKVHLLYVLPVELEDSPVPOKGS 180
DB 121 qqidanwniqlwkgdklfcyveslfknlfrnynykvhllylvpveledsplvpokgs 180
QY 181 FQWVHCNCSVHECCCECLVPVPTAKLNTLLMCLKITSGGVTFQSPPLMSVQPINWVKDPP 240
DB 181 fqwvhcnscsvheccceclvpvptaklntllmclkitsggvtfqspplmsvqipnwvkdpdp 240
QY 241 LGLHMEITDDGNLIKISWSSPPLVFPLOQYQVYSENSTTVIREADKIVSATSLVDSILP 300
DB 241 lglhmeitddgnlikiswsspplvpfloyqvysensttvireadkivsatsllvdsilp 300
QY 301 GSSYEVOVRKRLDGPQISWDSWTPRVFTTQDVYFPFKILTSVGSNVSFHCYKKNENKI 360
DB 301 gssyevovrgkrlldgpgiswdsdwtpvfttqdvlyfppkiltsvgsnvsfhciykkenki 360
QY 361 VPSKEIIVWNNLAERKIPQSDYDVSDHVSXVTPPNLNETPRGKFTYDAYCCNEHECHH 420
DB 361 vpskeiivwnnlaekipqsdvdyvshvskvtfnlnetprgkftdayccnehechh 420
QY 421 RYAEPLYVIDNINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRYSRSLYCSIDPSIH 480
DB 421 ryaeplyvidninisctdgyltkmtcrwststiqslaestlqlryhsrslsycsidpsih 480
QY 481 PISEPKDCYLOSDGFYECIFQIPLLSGYTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylqsdgfyecifqipllsgytmwirinhsrglsgdspptcvlpdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKVPENNLQIRGLSGKEVQWKMVEYDASKSVSLPV 600
DB 541 ssvkaeitinigllkiswekvpennlqirglsgekvqwmkmyevydasksvslpv 600
QY 601 PDLCAVAVQVRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRINGDTMKKEKNV 660
DB 601 pdlcavavqvrkrlldglgyswnsnpaytvvmdikvpmrgpfwringdtmkkeknv 660
QY 661 TLWKKPLMKNDSCSVORYINHTSCNGTWSEVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 tllwkpimkndscsvoryinhhtscngtwsevdvgnhtkftflwteqahvtvtvlainsi 720
QY 721 GASVANENLTFSPMSKVNIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIEWKNNLED 780
DB 721 gasvanenltfspmskvnivqslsayplnscviviwsilspdykmyfiewknnled 780
QY 781 GEIKWLRISSVKYIYTHDFIERKQFSLYPIFMEGVGKPKIINSFTODDTEKHQSDA 840
DB 781 geikwlrisssvkiyihdfierkqfslypifmegvgkpkiiinsftoddtekhqgsda 840
QY 841 GLYIVPVITSSILLGLTLLISLQRMKKLFWEDVNPKNCSWAQGLNFOKPTFEHLFI 900
DB 841 glyivpvitssillgltllisllqrmkkllfwedvnpknscwaqglnfokptfehlfi 900
QY 901 KHTASVTCGPLLPEPTISEDISVDTSWKNKDEMPTTVVSLSTTDLEKSGVCISQDN 960
DB 901 khtasvtcgpllleptiseedisvdtswknkdempttvvslsttdleksgvcisdqfn 960

QY 961 SVNFSEAGTEVTEYDESRQPFVKYATLISNKSPTGEEQGLINSVTKCFSSKNSPL 1020
DB 961 svnfseagtevteydesqrpfvkayatlinsksptgeeqglinsvckcfssksnpl 1020
QY 1021 KDSFNSWELEAQAFILSDQHNIISPHLTFSEGIDELLKLEGNPFENNNDKKSIIYL 1080
DB 1021 kdsfnsweleaqafilisdqhniisphltfsegidellklegnfpennndkksiiyl 1080
QY 1081 GVTSIKKRESGLVLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 gvtsikresgvlvltkdsrvscppapclftdirvldqscshfvenninlgtsskktffas 1140
QY 1141 YMOFOFOTCSTQTHKIMENKMDLTV 1165
DB 1141 fmpqfotcstqthkimenkmdltv 1165
RESULT 5
AAV13474
ID AAY13474 standard; Protein; 1165 AA.
XX
AC AAY13474;
XX DT 26-JUL-1999 (first entry)
XX Peptide Seq ID No: 4-of-WO9923493.
XX Leptin; phosphorylated leptin receptor; tyrosine phosphatase ID; PTP-ID;
KW modulator; drug; weight loss; adiposity; hypertension; heart disease;
KW type II diabetes; cancer; AIDS; agriculture.
XX Homo sapiens.
XX
XX WO9923493-A1.
XX PQ 14-MAY-1999.
XX PF 27-OCT-1998; 98WO-US22797.
XX PR 26-OCT-1998; 98US-0178691.
PR 31-OCT-1997; 97US-0961809.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX Friedman JM, Li C;
XX WPI; 1999-327025/27.
DR N-PSDB; AAX55588.
XX
XX Identifying modulators agents that modulate leptin activity
XX Disclosure; Page 77-84; 96pp; English.
XX
CC The invention provides a method for identifying modulators of binding of
CC a phosphorylated leptin receptor with tyrosine phosphatase ID PTP-ID).
CC The method comprises: (a) contacting a tyrosine-985-phosphorylated leptin
CC receptor or its phosphorylated fragment with protein PTP-ID or its
CC fragment in the presence and absence of a candidate agent under
CC conditions in which in the absence of the agent the binding of the
CC phosphorylated leptin receptor or fragment with PTP-ID or its fragment
CC can be detected; and (b) detecting the binding of the phosphorylated
CC leptin receptor and PTP ID; where an increase in binding detected in the
CC presence of the agent, indicates that the agent enhances binding, and a
CC decrease in binding in the presence of the agent indicates that the agent
CC is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin
CC receptor-dependent PTP-ID phosphorylation are useful as drugs in weight
CC loss diet regimens. The drugs identified can regulate adiposity and fat
CC content of animals, particularly in mammals. Disorders that can be
CC treated by PTP-ID modulators include obesity and its associated diseases,
CC e.g. hypertension, heart disease and type II diabetes, and weight loss
CC associated with cancer and AIDS. Additionally the agents identified may
CC be useful in agriculture where body weight of domestic animals can be

Qy	961	SVNFSAEAGTEVTYYEDESQRQFVKYATLINSRKPSSETGEEQGLINSVTKCTSSKN SPL	1020
Db	961	svnfseagtevtYeasqrqfvkyatLlnskpsketgeegqlnsvtkcfsskn spl	1020
Qy	1021	KDSFSSSSWEIEAQAFFILSDQHPIIISPHLTFBSGLDELKLEGNFPEENNDKKSIYYL	1080
Db	1021	kdsfssssweieaqaFFILsdqhpiLisphltfsegldeLlklegnfpeenndkkssiyyL	1080
Qy	1081	GVTSIKKRSQVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINIGTSSKKTFFAS	1140
Db	1081	gvtsikkresgvltdksrvscppapclftdirvlqdschfvenninigtsskktffas	1140
Qy	1141	YMPQFQTCSTQTHKIMENKMCDDLTV	1165
Db	1141	ympqfqtctstqthkimenkmedltv	1165
RESULT 6			
ID	AAW19116	AAW19116 standard; Protein; 1165 AA.	
XX	XX		
AC	AAW19116;		
XX	XX		
DT	26-AUG-1997	(first entry)	
XX	XX		
DE	Human Ob receptor.		
XX	XX		
KW	Ob receptor; OBR; cytokine receptor; signal transduction;		
KW	eating disorder; obesity; cachexia; anorexia; bulimia; diagnosis;		
KW	therapy.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
Key	Location/Qualifiers		
FT	Peptide	1..20	
FT		/label= Sig_peptide	
FT	Domain	21..839	
FT		/label= ECD	
FT		/note= "extracellular domain"	
FT	Domain	840..862	
FT		/label= TMD	
FT		/note= "transmembrane domain"	
FT	Domain	863..1165	
FT		/label= CD	
FT		/note= "cytoplasmic domain"	
FT	Peptide	319..323	
FT		/note= "motif conserved in class I cytokine receptors"	
FT	Peptide	622..626	
FT		/note= "motif conserved in class I cytokine receptors"	
FT	Modified-site	23	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	41	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	59	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	98	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	187	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	206	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	276	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	
FT	Modified-site	347	
FT		/label= Glycosylation	
FT		/note= "potential N-linked glycosylation site"	

FT FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 433
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 516
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 624
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 638
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 670
 FT /label= Glycosylation
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 FT 697
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 728
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT 750
 FT /label= Glycosylation
 FT /note= "potential N-linked glycosylation site"
 FT W09719952-A1.
 XX
 XX 05-JUN-1997.
 XX
 XX 27-NOV-1996; 96W0-US19128.
 XX
 PR 03-SEP-1996; 96US-0708123.
 PR 04-DEC-1995; 95US-0562663.
 PR 08-DEC-1995; 95US-0566622.
 PR 11-DEC-1995; 95US-0569485.
 PR 28-DEC-1995; 95US-0570142.
 PR 22-JAN-1996; 95US-0583153.
 PR 26-APR-1996; 96US-0599455.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Culpepper JA, Tartaglia LA, Tepper RI, White DW;
 XX WPI; 1997-310525/28.
 DR N-PSDB; AAT69592.
 XX
 PT Isolated Ob receptor genes and polypeptide(s) - useful to develop
 PT products for diagnosis or treatment of body weight disorders, e.g.
 PT obesity, cachexia, anorexia and bulimia
 XX
 PS Example; Fig 3; 265pp; English.
 XX
 CC Human Ob receptor (OBR) (AAW19116) is a novel polypeptide that
 CC participates in the control of body weight and which is involved in
 CC signal transduction triggered by the binding of its natural ligand,
 CC Ob (leptin). It is a member of the class I cytokine receptor
 CC family. Its amino acid sequence was deduced from a foetal brain
 CC cDNA clone (AAT69592). The receptor corresponds to the long form
 CC mouse OBR (AAW19115). OBR proteins, peptides, antibodies, agonists
 CC and antagonists can be used in the diagnosis and treatment of body
 CC weight disorders such as obesity, cachexia and anorexia.
 XX
 XX Sequence 1165 AA;

Query Match 99.8%; Score 6240; DB 18; Length 1165;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MICQKFCVLLHWEFIVITAFNLSPITPWRKFLSCMPNPNSTYDYFLLPAGLSKNTSNS 60
 DB 1 micqkfcvllhwefflyvitafnlspitpwrkflscmpnpnstydyflpagslknksns 60
 QY 61 NGHYETAVEPKFNSSGTHFNLKTTFFHCCFRSEQDRNCCLCADNIEGKTFVSTVNSLVF 120
 DB 61 nghyetavepkfnssgthfnlskttfhccfrseqdrncalcadniegktfvstvnslvf 120
 QY 121 QQIDANWNTOCWLKGDILKLFICIVESLFLKMLFRNYNYKVHLLYVLPVLEDSPLVPQKGS 180
 DB 121 qqidanwniqcwlkgdilkficyveslfnklnfrnynykvhllvlpvleedsplvpqkgs 180
 QY 181 FQMVHNCNSVHECECECLVPVPTAKLNDTLMLCLKITSGGVIFOSPLMSVOPINMKRPDPP 240
 DB 181 fqmvhncnsvhecececlvpvptaklndtlmlclkitsggvifgspimsvqpinmkvpdpp 240
 QY 241 LGLHMEITDDGNLKIWSPPPLFPLOYQVYKYSKNTTIVREADKIVSATSLLDVSIIP 300
 DB 241 lglhmeitddgnlkiwsspplvpfploqyqvyksensttivreackivsatsllvdsilp 300
 QY 301 GSSYEVQVGRKRLDGPQIWSDMSTPRVFTTQDVIIYPPPKILTSVGSNVSPHCIIYKKNKI 360
 DB 301 gssyevqvrgrldgpgiwsdstprvfttqdvlyfppkiltsvgsnsvthciykkkenk 360
 QY 361 VPSKEIWMNMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDVAVYCCNEHCCHH 420
 DB 361 vpskeiwmnmnlakipqsgdydvvsdhvskvtfeflnetkprgkftydavycnehechh 420
 QY 421 RYAEIYVIDVNIINISCTDGYLTGMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
 DB 421 ryaelyvidvniiniscetdgyltkmtcrwststiqslaestlqlryhrsslycsdipsih 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSLSDSPPTCVLPDSVVRPLPP 540
 DB 481 pisepkdcylqsdgfyecifqpiflisgytmwirinhsisgslpdtcvlpdvsvvrplsp 540
 QY 541 SSVKAEITINIGLLKISWEKVPENNLOFQIRYGLSGKEVQNMKVEYVDAKSKSVSLPV 600
 DB 541 ssvkaeitinigllkiswekvpennlofqiryglsgkevqnmkveyvdaksksvslpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNNSNPATYVVDMLKVPMRGPEFWIRINGDTMKKEKNV 660
 DB 601 pdlcavayavvrckrldglgywsnwnpattyvvdmlkvpmrgefwirindgtmkkeknv 660
 QY 661 TLLWKPLMKNDLSLCSVQRYVINHHTSCNGTWSEDDVGNHTKFTFLWTEQAHVTVLAINSI 720
 DB 661 tllwkpkmndslcsvqrvyinhhtscngtwseddvgnhhtkftflwteqahvtvvlainsl 720
 QY 721 GASVANFNLTFSPMKSKNIVQSLSAYPLNSSCVIYVSWILSPSDYKLMYPIIEWKNLNED 780
 DB 721 gasvanfntfswpmksknivqslsayplnsscvivswilspdyklymylewknlned 780
 QY 781 GEIKWLRISSSVKYYIHDHFIDIEKYQFSLYPIEFMEGVCKPKIINSFTODDIEKHQSDA 840
 DB 781 geikwlri:sssvkyyihdhfidiekyqfslypiiefmegvckpkilnsftoddiekhsda 840
 QY 841 GLYVIVPVIISSTILLGLTLLISHQRMKLFWDVDPNPKNCNSWAQGLNFQKPTFFHLFI 900
 DB 841 glyvivpviisssilllgtllishqrmklfwdvdpnpkncnswaqglnfqkptfehlfi 900
 QY 901 KHTPASVTCGPLLLEPETISEDIVSD7SWKNKDEMPTTVVSVLLSTDTDLKSGVCISDQFN 960
 DB 901 khtcasvtcgpplllepetsedisvds7swknkdempttvvsvllstddleksgvcisdqfn 960
 QY 961 SVNFSAEGTEVYEDESQRPVKYATLISNSKPKETGEEQGLINSSVTKCFSSKNSPL 1020
 DB 961 svnfseagtevyedesqrpvkyatlinskpketgeeqglinsvsvtkcfssknspl 1020
 QY 1021 KDSFSSNSWIEAQAFILSDOHPNIIISPHLTSEGLDELLKLEGNFPENNDKSIYYL 1080
 DB 1021 kdsfssnsweieaqafilisdqhpniisphltfsegldellklegnfpeennnkksiyyl 1080

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Db 179 TFSWKY-----KNSDISSTGRFPFSLRGKGYAANTSQVLPSKDVMOGTDEH 225
QY 228 --CNSRDSGN 236
Db 226 VVCKVQHPNGN 236

RESULT 11
Q9BRV0
ID Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 33.9%; Score 450.5; DB 4; Length 500;
Best Local Similarity 69.0%; Pred. No. 7.2e-29;
Matches 89; Conservative 9; Mismatches 28; Indels 3; Gaps 2;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGNTY 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVHLVQSGAEVMSPGASVRVSKTSYAFHTYSIIWVRQAPGQGLEWMGWSIPSDNTRF 79
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AQKFGQVRVTMTDTSIGTAYMELSLSSDDTAVYYCARDRY--YGSAYHRSYYMDVWG 118
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ARKFGQVRVLTDTSTSTVYMLSLRLSDDTAVYYCAR-RYCSYSCQNDYIIYMDVWG 138
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 119 RGLTVTVSS 127
Db 139 KGLTVTVSS 147
: || |||||

RESULT 12
Q9GYZ2
ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MONOCLONAL ANTI-IDIOYTPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenaea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
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RP SEQUENCE FROM N.A.
RT Song X.T., Feng Z.Q., Guan X.H.;
RT *Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -.
DR HSSP; P01772; 2FE4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG-like; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 33.9%; Score 450; DB 5; Length 119;
Best Local Similarity 67.7%; Pred. No. 1.4e-29;
Matches 86; Conservative 13; Mismatches 20; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGNTY 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLVQSGAEVRRKPGASVRVSKASGYTFGTGYMNVVRQAPGHLEWIGINFSRGITNY 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 AQKFGQVRVTMTDTSIGTAYMELSLRLSDDTAVYYCARDRYGSSAYHRSYYMDVWGR 120
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQKFKDRVTMTDTKSPSTAYMDLRLSLRSADSAVYYCAR-----YYDDHYCLDYWGQ 112
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 TLTVTVSS 127
Db 113 TLTVTVSS 119
: || |||||

RESULT 13
Q9QXE9
ID Q9QXE9 PRELIMINARY; PRT; 117 AA.
AC Q9QXE9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225174; CAB65237.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 32.6%; Score 433; DB 11; Length 117;
Best Local Similarity 64.6%; Pred. No. 3.4e-28;
Matches 82; Conservative 17; Mismatches 18; Indels 10; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFGTGYMYWVRQAPGQGLEWMGWINPNSGNTY 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWKQSHGKSLIEWIGIDINPNGTSY 60
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Thu Aug 15 16:36:04 2002

us-08-779-457-48.rspt

Page 7

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:36:09 ; Search time 28.14 Seconds
(without alignments)
342.614 Million cell updates/sec

Title: US-08-779-457-48

Perfect score: 1329
Sequence: 1 EYLVQSGAEVKKPGASVKV.....SRDSSGNHVVFGGTKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	521	39.2	108	1 LV3A_HUMAN	P01714 homo sapien
2	483	36.3	117	1 HV1G_HUMAN	P23083 homo sapien
3	479.5	36.1	147	1 HV1C_HUMAN	P01744 homo sapien
4	443	33.3	117	1 HV1B_HUMAN	P01743 homo sapien
5	434	32.7	117	1 HV13_MOUSE	P01757 mus musculus
6	429.5	32.3	139	1 HV07_MOUSE	P01751 mus musculus
7	420	31.6	117	1 HV12_MOUSE	P01756 mus musculus
8	415	31.2	120	1 HV03_MOUSE	P01747 mus musculus
9	411	30.9	140	1 HV02_MOUSE	P01746 mus musculus
10	410.5	30.9	120	1 HV50_MOUSE	P06329 mus musculus
11	409.5	30.4	118	1 HV51_MOUSE	P06330 mus musculus
12	395.5	29.8	137	1 HV11_MOUSE	P01755 mus musculus
13	385	29.0	121	1 HV01_MOUSE	P01745 mus musculus
14	381	28.7	138	1 HV48_MOUSE	P03980 mus musculus
15	380.5	28.6	114	1 HV00_MOUSE	P01741 mus musculus
16	377	28.4	111	1 LV3B_HUMAN	P06748 homo sapien
17	376	28.3	117	1 HV1A_HUMAN	P01742 homo sapien
18	368	27.7	117	1 HV09_MOUSE	P01753 mus musculus
19	366	27.5	107	1 LV4C_HUMAN	P01717 homo sapien
20	366	27.5	117	1 HV04_MOUSE	P01748 mus musculus
21	364	27.4	108	1 LV5A_HUMAN	P01719 homo sapien
22	363	27.3	106	1 LV4A_HUMAN	P01715 homo sapien
23	361.5	27.2	120	1 HV1H_HUMAN	P0421 homo sapien
24	361	27.2	136	1 HV15_MOUSE	P01759 mus musculus
25	360	27.1	117	1 HV06_MOUSE	P01750 mus musculus
26	358	26.9	106	1 LV4B_HUMAN	P01716 homo sapien
27	356	26.8	106	1 LV4E_HUMAN	P06889 homo sapien
28	355	26.7	117	1 HV49_MOUSE	P06328 mus musculus
29	353	26.6	125	1 HV1F_HUMAN	P06326 homo sapien
30	352	26.5	117	1 HV10_MOUSE	P01754 mus musculus
31	352	26.5	117	1 HV14_MOUSE	P01758 mus musculus
32	349.5	26.3	119	1 HV38_MOUSE	P01808 mus musculus
33	348.5	26.2	119	1 HV37_MOUSE	P01807 mus musculus

34	348	26.2	117	1 HV52_MOUSE	P06327 mus musculus
35	345.5	26.0	119	1 HV40_MOUSE	P01810 mus musculus
36	340	25.6	106	1 LV4D_HUMAN	P01718 homo sapien
37	336	25.3	111	1 LV2F_HUMAN	P01709 homo sapien
38	336	25.3	117	1 HV05_MOUSE	P01749 mus musculus
39	334.5	25.2	124	1 HV1D_HUMAN	P01760 homo sapien
40	334	25.1	130	1 LV1G_HUMAN	P06316 homo sapien
41	331	24.9	111	1 LV2H_HUMAN	P01711 homo sapien
42	328.5	24.7	122	1 HV3G_HUMAN	P01768 homo sapien
43	327.5	24.6	124	1 HV1E_HUMAN	P01761 homo sapien
44	325.5	24.5	112	1 LV2K_HUMAN	P04209 homo sapien
45	325	24.5	111	1 LV2G_HUMAN	P01710 homo sapien

ALIGNMENTS

```
RESULT 1
LV3A_HUMAN
ID LV3A_HUMAN STANDARD; PRT; 108 AA.
AC P01714;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-III region SH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70166723; PubMed=4909564;
RA Titani K., Wikier M., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT complete amino acid sequence and the location of the disulfide
RT bridges."
RL J. Biol. Chem. 245:2171-2176(1970).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01980; L3HUSH.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 21 86
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11392 MW; E7E1229586411A56 CRC64;
```

Query Match 39.2%; Score 521; DB 1; Length 108;
Best Local Similarity 92.5%; Pred. No. 2e-32;
Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
QY 143 SELTODPAVSVALGQTVRTTCQDLSRSYASWYQKPGQAPVLVIYGNRPSPGIDRF 202
Db 1 SELTODPAVSVALGQTVRTTCQDLSRGLRQYDAAMYQKPGQAPLLVIYGNRPSPGIDRF 60
QY 203 SGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHVVFGGTKLTVL 249
Db 61 SGSSSGHTASLTITGAQAEDADYYCNSRDSSGKHVLFGGTKLTVL 107
```

```
RESULT 2
HV1G_HUMAN
ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=28411108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBL J. 7:1047-1051(1988).
CC -----
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CC -----
CC EMBL: X07448; -; NOT_ANNOTATED_CDS.
DR PIR: S00476; HVH035.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CB63F8CE97BD CRC64;

Query Match 36.3%; Score 483; DB 1; Length 117;
Best Local Similarity 92.9%; Pred. No. 1.4e-29;
Matches 91; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVOLVOSGAEVKKPGASVKVSKASGYFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 60
Db 20 QQLVQSGAEVKKPGASVKVSKASGYFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 79
QY 61 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCAR 98
Db 80 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCAR 117
QY 61 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCAR 98
Db 80 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCAR 117

RESULT 3
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.

DR PIR: A02026; ELHUND.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 36.1%; Score 479.5; DB 1; Length 147;
Best Local Similarity 69.5%; Pred. No. 3.3e-29;
Matches 89; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 1 EVOLVOSGAEVKKPGASVKVSKASGYFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 60
Db 20 QQLVQSGAEVKKPGASVKVSKASGYFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 79
QY 61 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCARDYSSAYHRG-SYMDVMWGR 119
Db 80 AQKFGRTVTMTDTSIGTAYMELSLRSDDTAVYYCARDYSSAYHRG-SYMDVMWGR 139
QY 120 GTLVTVSS 127
Db 140 GTTVTVSS 147

RESULT 4
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region Hg3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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CC -----
CC EMBL: J00240; AAA52988.1; -.
DR PIR: A02024; HVH0HG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.

```

FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 33.3%; Score 443; DB 1; Length 117;
Best Local Similarity 84.7%; Pred. No. 1.3e-26;
Matches 83; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVOLVQSGAEVKKPKASVKVSKASGYFTGYMYWVRQAPQGGLWGMWINPNPNSGGTNY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVOLVQSGAEVKKPKASVKVSKASGYFTNSYMYWVRQAPQGGLWGMWINPNPNSGGTNY 79
QY 61 AQKFGQVMTDRDTSIGTAYMELSLSSDDTAVYYCAR 98
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 AQKFGQVMTDRDTSVYMYELSLSSDDTAVYYCAR 117

RESULT 5
HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 32.7%; Score 434; DB 1; Length 117;
Best Local Similarity 64.6%; Pred. No. 6.1e-26;
Matches 82; Conservative 17; Mismatches 18; Indels 10; Gaps 1;

QY 1 EVOLVQSGAEVKKPKASVKVSKASGYFTGYMYWVRQAPQGGLWGMWINPNPNSGGTNY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLVQSGELVKKPKASVKVSKASGYFTDYMKVWKQSHGKSLWGDINPNNGGTSY 60.
QY 61 AQKFGQVMTDRDTSIGTAYMELSLSSDDTAVYYCARDRYYGSSAYHRGYSYMDVWGRG 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYYCARDRY-----WYFDVWGAG 110
QY 121 TLVTYSS 127
Db :|||||
111 TTVTVSS 117

RESULT 6
HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bochkwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 32.3%; Score 429.5; DB 1; Length 139;
Best Local Similarity 63.0%; Pred. No. 1.6e-25;
Matches 80; Conservative 19; Mismatches 21; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVKKPKASVKVSKASGYFTGYMYWVRQAPQGGLWGMWINPNPNSGGTNY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVOLVQSGAEVKKPKASVKVSKASGYFTSYMHVWKQRPGRGLEWIGRIDPNSGGTNY 79
QY 61 AQKFGQVMTDRDTSIGTAYMELSLSSDDTAVYYCARDRYYGSSAYHRGYSYMDVWGRG 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFKSKATLTVDKPSSTAYMQLNSLTSDSAVYYCARDYYGSS-----YFDYWGQG 132
QY 121 TLVTYSS 127
Db :|||||
133 TTVTVSS 139

RESULT 7
HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RX MEDLINE=83075344; PubMed=6816276;
RA Kehy M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT *Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.*;
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MMS4E.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE47E41 CRC64;

Query Match 31.6%; Score 420; DB 1; Length 117;
Best Local Similarity 63.0%; Pred. No. 6.7e-25;
Matches 80; Conservative 17; Mismatches 20; Indels 10; Gaps 1;

QY 1 EVLVQSGAEVKKPGASVKVKSCASGYFTFTGYMYWVRQAPQGQLEWGMWINPNSGGTNY 60
DB 1 EVLVQSGPELVKPGASVKMKSCASGYFTFTDYMKWKQSHGKSLWIGDINPNNGGTSY 60

QY 61 AQKFGQRTMTDTSIGTAYMELSLSSDDTAVYYCARDRYVYSSAYHRGSYYMDVWGKG 120
DB 61 NQKFGKATLTVDKSSSTAYMQLNSLTSDSAVYYCARDY-----DWYFDVWGAG 110

QY 121 TLTVYSS 127
DB 111 TTVTVSS 117

RESULT 8
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geiter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT *The genetic basis of antibody production: the dominant anti-arsonate
RT idotype response of the strain A mouse.*;
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC PIR: A02028; HVMSG7.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```

```
DR Pfam; PF00047; Igv; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 31.2%; Score 415; DB 1; Length 120;
Best Local Similarity 61.1%; Pred. No. 1.6e-24;
Matches 77; Conservative 20; Mismatches 23; Indels 6; Gaps 1;

QY 2 VOLVQSGAEVKKPGASVKVKSCASGYFTFTGYMYWVRQAPQGQLEWGMWINPNSGGTNYA 61
DB 1 VOLVQSGAEVLVAGSVKMSCKASGYFTFTSYGINVVKQRPQGQLEWIGYINFGNGYTRYN 60

QY 62 OKFGQRTMTDTSIGTAYMELSLSSDDTAVYYCARDRYVYSSAYHRGSYYMDVWGKG 121
DB 61 EKFGKATLTVDKSSSTAYMQLNSLTSDSAVYFCARSYYIG-----GSYYFDVWGQGT 114

QY 122 LVTVSS 127
DB 115 TLTVSS 120

RESULT 9
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 93g7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT *Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.*;
RL Science 216:309-311(1982).
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DR EMBL; J00493; AAA38128.1; -.
DR PIR; A02028; HVMSG7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Igv; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 30.9%; Score 411; DB 1; Length 140;
Best Local Similarity 60.6%; Pred. No. 3.8e-24;
Matches 77; Conservative 20; Mismatches 24; Indels 6; Gaps 1;

QY 1 EVLVQSGAEVKKPGASVKVKSCASGYFTFTGYMYWVRQAPQGQLEWGMWINPNSGGTNY 60
DB 1 EVLVQSGAEVKKPGASVKVKSCASGYFTFTGYMYWVRQAPQGQLEWGMWINPNSGGTNY 60
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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 54 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 122 D SEGMENT.  
FT DOMAIN 123 137 JH2 SEGMENT.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON_TER 137 137  
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;  
  
Query Match 29.8%; Score 395.5; DB 1; Length 137;  
Best Local Similarity 59.8%; Pred. No. 5.2e-23;  
Matches 76; Conservative 17; Mismatches 25; Indels 9; Gaps 2;  
  
QY 1 EVLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQGLEWGMWINPNSGGTNY 60  
DB 20 QVQLQQPGAERFYKPGASVKLSCKASGYTFTSYLMHWVNRQPGRGLEWIGRIDPNSGGTY 79  
QY 61 AOKFOGRVTMTSDTSIGTAYMELSLRLSDDTAVYYCARDRIYGSAYHRGSYYMDVWGRG 120  
DB 80 NEHFRSKATLTIDKPSSTAYMQLSLTSEDSAYYYCAR-----YRLGRYF-DYWQGG 130  
QY 121 TLVTYSS 127  
DB 131 TTLTVSS 137  
  
RESULT 13  
HV01_MOUSE  
ID HV01_MOUSE STANDARD; PRT; 121 AA.  
AC P01745;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region MPC 11.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81053741; PubMed=6253904;  
RA Zakut R., Cohen J., Givol D.;  
RT "Cloning and sequence of the cDNA corresponding to the variable  
RT region of immunoglobulin heavy chain MPC11.";  
RL Nucleic Acids Res. 8:3591-3601(1980).  
RN [2]  
RP REVISTONS.  
RA Zakut R., Cohen J., Givol D.;  
RL Nucleic Acids Res. 8:4839-4840(1980).  
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED  
CC FROM A MYELOMA THAT SECRETES IGG2B.  
DR PIR; A02027; GVMS11.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT NON_TER 121 121  
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;  
  
Query Match 29.0%; Score 385; DB 1; Length 121;  
Best Local Similarity 55.9%; Pred. No. 2.7e-22;  
Matches 71; Conservative 21; Mismatches 29; Indels 6; Gaps 1;  
  
QY 1 EVLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQGLEWGMWINPNSGGTNY 60  
DB 20 QVQLQQPGAERFYKPGASVKLSCKASGYTFTSYLMHWVNRQPGRGLEWIGRIDPNSGGTY 79  
QY 61 AOKFOGRVTMTSDTSIGTAYMELSLRLSDDTAVYYCARDRIYGSAYHRGSYYMDVWGRG 120  
DB 80 NEHFRSKATLTIDKPSSTAYMQLSLTSEDSAYYYCAR-----YRLGRYF-DYWQGG 130  
QY 121 TLVTYSS 127  
DB 131 TTLTVSS 137  
  
RESULT 14  
HV48_MOUSE  
ID HV48_MOUSE STANDARD; PRT; 138 AA.  
AC P03980;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region TEPC 1017 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84248078; PubMed=6429663;  
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,  
RA Tucker P.W.;  
RT "Illegitimate recombination generates a class switch from C mu to C  
RT delta in an IgD-secreting plasmacytoma";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).  
DR PIR; A02033; HYMS77.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.  
FT DOMAIN 21 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 128 138 FRAMEWORK-4.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON_TER 138 138  
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;  
  
Query Match 28.7%; Score 381; DB 1; Length 138;  
Best Local Similarity 57.0%; Pred. No. 6.2e-22;  
Matches 73; Conservative 21; Mismatches 24; Indels 10; Gaps 2;  
  
QY 1 EVLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQGLEWGMWINPNSGGTNY 60  
DB 20 QVQLQQPGAERFYKPGASVKLSCKASGYTFTSYLMHWVNRQPGRGLEWIGRIDPNSGGTY 79  
QY 61 AOKFOGRVTMTSDTSIGTAYMELSLRLSDDTAVYYCARDRIYGSAYHRGSYYMDVWGRG 119  
DB 80 NEHFRSKATLTIDKPSSTAYMQLSLTSEDSAYYYCAR-----YRLGRYF-DYWQGG 130  
QY 120 GTLVTVSS 127  
DB 131 GTLVTVSS 138  
  
RESULT 15  
HV00_MOUSE
```



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ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Ig heavy chain V region (Anti-arsonate antibody).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid-10090;
RN [1]
RP SEQUENCE.
RC STRAIN-A/J;
RX MEDLINE-79195438; PubMed-109536;
RA Capra J.D.; Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype."
RL J. Immunol. 123:279-284(1979).
CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC PIR; A02022; GIMSA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 28.6%; Score 380.5; DB 1; Length 114;
Best Local Similarity 62.6%; Pred. No. 5.5e-22;
Matches 77; Conservative 14; Mismatches 23; Indels 9; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYMTWVRQAPCGGLEWGMWINPNSGGTNY 60
DB 1 EVOLQSGAEVKKPGASVKVSCKASGYTFTGYMTWVRQAPCGGLEWGMWINPNSGGTNY 60
QY 61 AQKFGQRTVMTDTSIGTAYMELSLRLSDDTAVYICARDRYGSSAYHGRGYSYMDVWGRG 120
DB 61 AQKFGQRTVMTDTSIGTAYMELSLRLSDDTAVYICARDRYGSSAYHGRGYSYMDVWGRG 120
QY 121 TLV 123
DB 112 TLV 114

```

Search completed: August 15, 2002, 16:36:09
Job time: 719 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	635	47.8	268	2	A56446	Ig heavy chain v r
2	619.5	46.6	249	2	S41374	single chain Fv an
3	602	45.3	129	2	A56593	Ig heavy chain v r
4	569.5	42.9	233	2	JC5322	p53 specific singl
5	562	42.8	108	2	S47184	lambda chain -
6	562	42.3	109	2	I19663	Ig lambda chain v
7	561	42.2	123	2	D33548	Ig heavy chain v-1
8	547.5	41.2	118	2	S35265	Ig heavy chain v r
9	546.5	41.1	135	2	S49530	anti-Sm antibody v
10	546	41.1	127	2	S70444	Ig lambda chain pr
11	545.5	41.0	110	2	S36272	Ig lambda chain v
12	535	40.3	108	2	S38498	Ig lambda chain -
13	533	40.1	109	2	S38496	Ig lambda chain -
14	531	40.0	171	2	S23623	Ig heavy chain v r
15	524	39.4	233	2	S25748	Ig lambda chain -
16	521	39.2	108	1	L3H0SH	Ig lambda chain v-
17	517.5	38.9	146	2	S20083	Ig lambda chain v-
18	512.5	38.6	110	2	I19672	Ig lambda chain v
19	507	38.1	98	2	S26938	Ig heavy chain v r
20	507	38.1	109	2	PH1668	Ig heavy chain v r
21	507	38.1	117	2	S18551	Ig heavy chain v r
22	503	37.8	96	2	S36060	Ig lambda chain -
23	503	37.8	115	2	S13726	Ig lambda chain v
24	502	37.8	233	2	S25741	Ig lambda chain -
25	499	37.5	98	2	S26912	Ig heavy chain v r
26	497	37.4	117	2	S31680	Ig heavy chain v r
27	495	37.2	142	2	A34483	Ig heavy chain v r
28	493.5	37.1	110	2	PH1669	Ig heavy chain v r
29	493	37.1	129	2	S36260	Ig heavy chain v r

A:Description: Construction and functional characterization of a single chain Fv anti-

S19663
Ig lambda chain V region (clone alpha-BSA3) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19663
R:Marks, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:Reference number: S19663; MUID:92085276
A:Accession: S19663
A:Molecule type: mRNA
A:Residues: 1-109 <MAR>
A:Cross-references: EMBL:X61640; NID:g29492; PTDN:CAA43821.1; PID:g1340166
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-89/Domain: immunoglobulin homology <IMM>

```
Query Match      42.3%; Score 562; DB 2; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.7e-33;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	142	SSELTQDPAVSVALGQTVRTTCQGSLSRYASYWQQKPGQAPVLVIYGNRRSGIDPR	201
Dd	1	SSELTQDPAVSVALGQTVRTTCQGSLSRYASWTQKPGQAPVLVIYGNRRSGIDPR	60
QY	202	FSSGSSCNTASLTTTGAQAEDADYYCNSRDSNGHHVVFGGGTKLTVL	249
Dd	61	FSSGSSCNTASLTTTGAQAEDADYYCNSRDSNGHHVVFGGGTKLTVL	108

RESULT 7
D33548
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expressed in B-1 cells
A:Reference number: A33548; MUID:89345575
A:Accession: D33548
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	42.2%;	Score 561;	DB 2;	Length 123;
Best Local Similarity	82.7%;	Pred. No. 3.6e-33;		
Matches 105;	Conservative 8;	Mismatches 10;	Indels 4;	Gaps 1;
QY	1	EVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMYWVRQAPQGQGLWMGWLNPNNSGGTNY	60	
	:			
	:			
Db	1	QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHVVRQAPQGQGLWMGWLNPNNSGGTNY	60	
QY	61	AQKQFQGRVTWTRDTSIGTAYMELSRLSDDTAVYTCARDRYGSSAYIRGSGFYMDVWGRC	120	
	:			
	:			
Db	61	AEKQFQGRVTITRDTSINTAYMELSRLSRDDTAVYTCARASVCGYDVCY---YFFDYWGQC	116	

Qy 121 TLVTVSS 127
| | | | |
Db 117 TLVTVSS 123

RESULT 8
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:date: 03-feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, E.MBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries
A:Reference number: S36256; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>
A:Cross-references: EMBL:Z18846; NID:933121; PIDN:CAA79298.1; PID:g939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 547.5; DB 2; Length 118;
Best Local Similarity 81.9%; Pred. No. 3.1e-32;
Matches 104; Conservative 6; Mismatches 8; Indels 9; Gaps 1;

[illegible]

Qy 121 TLVTVSS 127
 111111
 Db 112 TLVTVSS 118

```

RESULT          9
S49530
anti-Sm antibody VH chain (VHL/DK1 or DML/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies .
A:Reference number: S48797
A:Accession: S49530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Dom40: immunoglobulin homology <IMM>

```

Query Match 41.1%; Score 546.5; DB 2; Length 135;
Best Local Similarity 83.5%; Pred. No. 4.2e-32;
Matches 106; Conservative 5; Mismatches 5; Indels 11; Gaps 2

[illegible]

QY	121	TLVTVSS	127
D _b	129	TLVTVSS	135

```

RESULT 10
S70444
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000
C:Accession: S70444; S70426

```

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A:Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe

A:Reference number: S70442; MUID:93024508

A:Accession: S70444

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-127 <GUI>

A:Experimental source: clone E29.1

R:Tonnelle, C.

submitted to the EMBL Data Library, May 1990

A:Reference number: S70426

A:Accession: S70426

A:Molecule type: mRNA

A:Residues: 1-90 <TON>

A:Cross-references: EMBL:X53070

A:Experimental source: cell line E29.1, clone VL 29-1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-127/Product: Ig lambda chain V region (fragment) #status predicted <MAT>

F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 41.1%; Score 546; DB 2; Length 127;

Best Local Similarity 97.2%; Pred. No. 4.3e-32;

Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 142 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 201

Db 20 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 79

QY 202 FSGSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGGKTLTVL 249

Db 80 FSGSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGTGNKTVL 127

RESULT 11

S36272

Ig lambda chain V region (clone alpha-THY-29) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C:Accession: S36272

R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A:Title: Human anti-self antibodies with high specificity from phage display libraries.

A:Reference number: S36256; MUID:93178448

A:Accession: S36272

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-110 <GRI>

A:Cross-references: EMBL:218833; NID:g33419; PIDN:CAA79285.1; PID:g939912

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 545.5; DB 2; Length 110;

Best Local Similarity 98.2%; Pred. No. 4e-32;

Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 142 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 201

Db 1 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 60

QY 202 FSGSSGNTASLTITGAQAEDADYCNRRDSSGN-HVFGGKTLTVL 249

Db 61 FSGSSGNTASLTITGAQAEDADYCNRRDSSGNLYVFGGKTLTVL 109

RESULT 12

S38498

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S38498

R:Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from

A:Reference number: S38488

A:Accession: S38498

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <MAR>

A:Cross-references: EMBL:Z23035; NID:g414043; PIDN:CAA80570.1; PID:g414044

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 40.3%; Score 535; DB 2; Length 108;

Best Local Similarity 97.2%; Pred. No. 2.2e-31;

Matches 104; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 143 SELTODPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 202

Db 1 SELTODPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDRF 60

QY 203 SGSSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGGKTLTVL 249

Db 61 SGSSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGGKTLTVL 107

RESULT 13

S38496

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S38496

R:Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe

submitted to the EMBL Data Library, June 1993

A:Description: Human antibody fragments specific for human blood group antigens from

A:Reference number: S38488

A:Accession: S38496

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-109 <MAR>

A:Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-89/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 533; DB 2; Length 109;

Best Local Similarity 93.5%; Pred. No. 3.1e-31;

Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 142 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 201

Db 1 SSELTPAVSVAGTGTVRITCGDSLRSYASWYQKPGQAPVLVIYGNRRPSGIPDR 60

QY 202 FSGSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGGKTLTVL 249

Db 61 FSGSSGNTASLTITGAQAEDADYCNRRDSSGNHVFGGKTLTVL 108

RESULT 14

S23623

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S23623

R:Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro

A:Reference number: S23623; MUID:92156804

A:Accession: S23623
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-171 <OLE>
A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 531; DB 2; Length 171;
Best Local Similarity 68.8%; Pred. No. 6.8e-31;
Matches 106; Conservative 12; Mismatches 24; Indels 12; Gaps 3;

QY 1 EVLVQSGAEVKKPGASVKVSCKASQYTFGYYMYVROAPGQGLEWMGWINPNSGGTNY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QVLVQSGAEVKKPGASVKVSCKGSGTFTAYQMHWVRQAPGQGLEWMGWINPNSGGTGY 79

QY 61 AOKFQGRVTMTDRTSTGTAYMELSLSSDDTAVYCYCARDYRGSSAYHRGSYYMDYNGRG 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 GQKFGQGRVLTTRDTSITAYMELSLRSDDTAVYCAIEFYFDGSDL-KPSDVFDIWGQG 138

QY 121 TLTVSSGGGGTGG-----GSGGGGGSSEL 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 139 TMTVTSS--ASTKGPSVFPLAPSSKSTSGGTAAL 170

RESULT 15
S25748
Ig lambda chain - human
C:Species: Homo sapiens (nan)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25748
R:Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162
A:Accession: S25748
A>Status: Preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-233 <COM>
A:Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 524; DB 2; Length 233;
Best Local Similarity 91.7%; Pred. No. 2.9e-30;
Matches 99; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 142 SSELTDPAVSVVALGQTVRTTCGDSLSRSYASWYQKPGQAPVLYYKNNRPSGIPDR 201
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 SSELTDPAVSVVALGQTVRTTCGDSLSRAYASWYQKPGQAPILVYGENRPSGIPDR 79

QY 202 FSGSSGNTASLTITGAQAEDADYYCNSRDSSGNHWVFGGTKLTVL 249
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 FSGSSGNTASFAITGAQAEDADYYCNSRDSSGDDQVLFGGTKLTVL 127

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:21:20 ; Search time 410.32 Seconds
(without alignments)
999.360 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFYIVT.....QTCTQTHKIMENKMDLTV 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Listing first 45 summaries

Database : Pending Patents AA_Main.*
1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
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14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
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21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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24: /cgn2_6/ptodata/2/paa/US100_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6254	100.0	1165	9 US-08-570-142D-4	Sequence 4, Appli
2	6254	100.0	1165	9 US-08-583-153A-4	Sequence 4, Appli
3	6254	100.0	1165	9 US-08-585-005-2	Sequence 2, Appli
4	6254	100.0	1165	10 US-08-638-524B-4	Sequence 4, Appli
5	6254	100.0	1165	10 US-08-667-197-2	Sequence 2, Appli
6	6254	100.0	1165	11 US-08-708-123D-4	Sequence 4, Appli
7	6254	100.0	1165	11 US-08-779-457-2	Sequence 2, Appli

8	6254	100.0	1165	11	US-08-780-562-2	Sequence 2, Appli
9	6254	100.0	1165	14	US-09-094-410-4	Sequence 4, Appli
10	6254	100.0	1165	15	US-09-137-132-4	Sequence 4, Appli
11	6254	100.0	1165	23	US-09-950-149-4	Sequence 4, Appli
12	6254	100.0	1216	11	US-08-774-414-7	Sequence 7, Appli
13	6254	100.0	1216	20	US-09-671-049-7	Sequence 7, Appli
14	6247	99.9	1167	23	US-09-948-333-284	Sequence 284, Appl
15	6247	99.9	1167	23	US-09-948-947-87	Sequence 87, Appl
16	6246	99.9	1165	9	US-08-599-974C-56	Sequence 56, Appl
17	6246	99.9	1165	11	US-08-713-296-11	Sequence 11, Appl
18	6246	99.9	1165	13	US-08-961-809-4	Sequence 4, Appli
19	6246	99.9	1165	15	US-09-178-891-4	Sequence 4, Appli
20	6246	99.9	1165	21	US-09-700-813-10	Sequence 10, Appl
21	6246	99.9	1165	23	US-09-948-933-256	Sequence 256, App
22	6246	99.9	1165	23	US-09-948-947-73	Sequence 73, Appl
23	6246	99.9	1165	24	US-10-095-929-11	Sequence 11, Appl
24	6240	99.8	1165	9	US-08-583-153-4	Sequence 4, Appli
25	6240	99.8	1165	9	US-08-599-455A-4	Sequence 4, Appli
26	6240	99.8	1165	10	US-08-638-524A-4	Sequence 4, Appli
27	6240	99.8	1165	11	US-08-708-123C-4	Sequence 4, Appli
28	6240	99.8	1165	12	US-08-864-564A-4	Sequence 4, Appli
29	6240	99.8	1165	24	US-10-079-625-4	Sequence 4, Appli
30	6236	99.7	1165	9	US-08-570-142B-4	Sequence 4, Appli
31	6236	99.7	1165	9	US-08-570-142C-4	Sequence 4, Appli
32	6172	98.7	1165	9	US-08-589-915A-11	Sequence 11, Appl
33	6032	96.5	1137	9	US-08-569-485-4	Sequence 2, Appli
34	5809	92.9	1221	13	US-08-982-430-2	Sequence 5, Appli
35	4831.5	77.3	969	9	US-08-582-825-5	Sequence 5, Appli
36	4831.5	77.3	969	9	US-08-582-825A-5	Sequence 5, Appli
37	4831.5	77.3	969	11	US-08-774-414-5	Sequence 6, Appli
38	4831.5	77.3	969	11	US-08-774-414-6	Sequence 6, Appli
39	4831.5	77.3	969	20	US-09-671-049-5	Sequence 5, Appli
40	4831.5	77.3	969	20	US-09-671-049-6	Sequence 6, Appli
41	4826	77.2	896	9	US-08-582-825-1	Sequence 1, Appli
42	4826	77.2	896	9	US-08-582-825A-1	Sequence 1, Appli
43	4826	77.2	896	9	US-08-585-005-3	Sequence 3, Appli
44	4826	77.2	896	10	US-08-667-197-3	Sequence 3, Appli
45	4826	77.2	896	11	US-08-779-457-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-570-142D-4
; Sequence 4, Application US/08570142D
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Cupepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,142D
; FILING DATE: 11-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622

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; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-08-570-142D-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVITAFNLSPYITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFYIVITAFNLSPYITPWRFKLSCLMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEPKNSGTFHSCFNLSKTFHCCFRSEDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAPEPKNSGTFHSCFNLSKTFHCCFRSEDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNITQCKLKGDLKLFICYVESLKNLFRNNYKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 QOIDANNITQCKLKGDLKLFICYVESLKNLFRNNYKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHCECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSYQPINMVKPDPP 240
Db 181 FQWVHCNCSVHCECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSYQPINMVKPDPP 240
QY 241 LGLHWEITDDGNLKSWSPPPLPQYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHWEITDDGNLKSWSPPPLPQYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GGSYEYQVRGKRLDGPGLNSDSTPRVFTTQDVIYFPPPKILTSVGSNVSFHCYIKKENKI 360
Db 301 GGSYEYQVRGKRLDGPGLNSDSTPRVFTTQDVIYFPPPKILTSVGSNVSFHCYIKKENKI 360
QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPNNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFPNNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEYLVIVDNNINISCTDGYLTMTKCRWSTSTIQSLAESTLQRYHRSLSYCSDIPTSH 480
Db 421 RYAEYLVIVDNNINISCTDGYLTMTKCRWSTSTIQSLAESTLQRYHRSLSYCSDIPTSH 480
QY 481 PISEPKDCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFEYECIFQIFLLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSYSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSYSVSLPV 600
QY 601 PDLCAVAYQVRCRKLGLGYSNNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
Db 601 PDLCAVAYQVRCRKLGLGYSNNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
QY 661 TLLWKLPMKNDSLCSVQRVVIINHHTSCNGTWSVDVGNHHTKFTPLWTEQAHVTYVLAINSI 720
Db 661 TLLWKLPMKNDSLCSVQRVVIINHHTSCNGTWSVDVGNHHTKFTPLWTEQAHVTYVLAINSI 720
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QY 721 GASVANFNLTFSWPMKSNVINQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLND 780
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QY 781 GEIKWLRISSSVKXYIHDHFPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKXYIHDHFPIEKYQFSLYPIFMEGVGPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQKPTFEHLFI 900
Db 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVPNPKNCSSWAQGLNFQKPTFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWNKDEMPPTVVSLSTDTDLKSGSVCSIDQFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWNKDEMPPTVVSLSTDTDLKSGSVCSIDQFN 960
QY 961 SYNFEAECTEVTYDEDSORQPFVKYATLINSKPKSETGEOGLINSVTKCFSSKNSPL 1020
Db 961 SYNFEAECTEVTYDEDSORQPFVKYATLINSKPKSETGEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSYYL 1080
Db 1021 KDSFNSSSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSYYL 1080
QY 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKMENKMCIDLTV 1165
Db 1141 YMPQFQTCSTQTHKMENKMCIDLTV 1165

RESULT 2
US-08-583-153A-4
; Sequence 4, Application US/08583153A
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,153A
; FILING DATE: 28-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/016001
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-583-153A-4

Query Match 100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MICQFCVLLHWEFTYVITAFNLSPYTPWRFKLSCMPNSTDYDFLLPAGLSKNTS 60

QY 61 NGHETAVEPKFNSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHETAVEPKFNSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QOIDANWNTQCHLKGDLKLFICYVESLFLNLFNRYKVHLLYVLPVLEDSPLVPQKS 180
DB 121 QOIDANWNTQCHLKGDLKLFICYVESLFLNLFNRYKVHLLYVLPVLEDSPLVPQKS 180

QY 181 FQWVHCNCSVHECCCLVPPVPAKNDTLMLCKLITSGGVIFQSPVMSVQPINWVKPDP 240
DB 181 FQWVHCNCSVHECCCLVPPVPAKNDTLMLCKLITSGGVIFQSPVMSVQPINWVKPDP 240

QY 241 LGLHMEITDDGNLKIWSPPPLVPPLOQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSPPPLVPPLOQVYKYSNSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVOVRGKRLDGPINSWDSSTPRVFTQDVIFPPKILTSVGSNSVHFCHYKKNKI 360
DB 301 GSSYEVOVRGKRLDGPINSWDSSTPRVFTQDVIFPPKILTSVGSNSVHFCHYKKNKI 360

QY 361 VPSKEIVWMNLAEKIPQSOYDVSHVSKVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVWMNLAEKIPQSOYDVSHVSKVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIVDIVNINISCTDGYITKMTCRNSTSTIOSLAESTLQLRVHRSLSYCSDIPI 480
DB 421 RYAEIVDIVNINISCTDGYITKMTCRNSTSTIOSLAESTLQLRVHRSLSYCSDIPI 480

QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMTIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMTIRINHSLGSLDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKTSWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKTSWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDKSKSVSLPV 600

QY 601 PDLCAVAVQVRCKRDLGLGYNNSNPNAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCKRDLGLGYNNSNPNAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 660

QY 661 TLLWKPMLKNDSLCSQVRYVINHHSTSCNCTWSDVGNHHTKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLWKPMLKNDSLCSQVRYVINHHSTSCNCTWSDVGNHHTKFTFLWTEQAHVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIENKLNED 780
DB 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIENKLNED 780

QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSTQDDIERHQSDA 840
DB 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMEGVGKPKIINSTQDDIERHQSDA 840

QY 841 GLYVIVPVIISSILLGLTLLISHORMKKLFWEDVPNPKNCNWAQGLNFKQKPTTEHLFI 900
DB 841 GLYVIVPVIISSILLGLTLLISHORMKKLFWEDVPNPKNCNWAQGLNFKQKPTTEHLFI 900

QY 901 KHTASVTCGPILEPETISEDLSVDTSWKNKDEMPTTVVSLSTTDLKSGVCISDQFN 960
DB 901 KHTASVTCGPILEPETISEDLSVDTSWKNKDEMPTTVVSLSTTDLKSGVCISDQFN 960

QY 961 SYNFEAEGETVYEDESQRPVYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020
DB 961 SYNFEAEGETVYEDESQRPVYATLISNSKPSSETGEEGLINSSVTKCFSSKNSPL 1020

QY 1021 KDSFNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPENNDDKSIYVL 1080
DB 1021 KDSFNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPENNDDKSIYVL 1080

QY 1081 GYTSIKKRESGVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 GYTSIKKRESGVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140

QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 3
US-08-585-005-2
Sequence 2, Application US/08585005
GENERAL INFORMATION:
APPLICANT: Matthews, William
APPLICANT: Bennett, Brian
TITLE OF INVENTION: WSX RECEPTOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,005
FILING DATE: 08-Jan-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-585-005-2

Query Match 100.0%; Score 6254; DB 9; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFTYVITAFNLSPYTPWRFKLSCMPNSTDYDFLLPAGLSKNTS 60
DB 1 MICQFCVLLHWEFTYVITAFNLSPYTPWRFKLSCMPNSTDYDFLLPAGLSKNTS 60

QY 61 NGHYETA VEPKFNSSGTHFSNLKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETA VEPKFNSSGTHFSNLKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNITQWLKGDGLKFLICYVESLFLNLFNRYNYKVHLLYVLPVLESDSLVPQKGS 180
DB 121 QOIDANNITQWLKGDGLKFLICYVESLFLNLFNRYNYKVHLLYVLPVLESDSLVPQKGS 180
QY 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINWVKPDP 240
DB 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINWVKPDP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPPFLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSWSPPLVPPFLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRGKRLDGGIWSNDSTPRVFTQDVIYPPPKILTSVGSNVSFHCIYKKNKI 360
DB 301 GSSYEVQVRGKRLDGGIWSNDSTPRVFTQDVIYPPPKILTSVGSNVSFHCIYKKNKI 360
QY 361 VPSKEIVWMNLAETIPQSOYDVSDHVSQVTFPNNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVWMNLAETIPQSOYDVSDHVSQVTFPNNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNNISCTDYLTKMTCRWSTSTIQSLAESTLQRLYHRSLLYCSDDIPSIIH 480
DB 421 RYAEIYVIDVNNISCTDYLTKMTCRWSTSTIQSLAESTLQRLYHRSLLYCSDDIPSIIH 480
QY 481 PISEPKDCYLOSDGFECIFQFIFLLSGYTMIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDGFECIFQFIFLLSGYTMIRINHSILGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
DB 601 PDLCAVYAVQVRKRLDGLGYSNWSNPAYTVVMDIKVPMRGPEFWRINGDTMKKEKNV 660
QY 661 TLLWKLPMKNDLSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLLWKLPMKNDLSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFLTFWPMPSKVNIVOSLSAYPLNSSCVIYVSWILSPSDYKLMYFIIEWKNLND 780
DB 721 GASVANFLTFWPMPSKVNIVOSLSAYPLNSSCVIYVSWILSPSDYKLMYFIIEWKNLND 780
QY 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVTISSLGTLTLLSHOBKMLFVEDVNPKNCSWAQGLNFQKPTFEHLFI 900
DB 841 GLYVIVPVTISSLGTLTLLSHOBKMLFVEDVNPKNCSWAQGLNFQKPTFEHLFI 900
QY 901 KHTASVTCGPLLEPTTISEDIVSDTSMKNKDEMMPTTVVSLSTTDLEKSGVCSIDQFN 960
DB 901 KHTASVTCGPLLEPTTISEDIVSDTSMKNKDEMMPTTVVSLSTTDLEKSGVCSIDQFN 960
QY 961 SVNFSAEGETVYEDESORQPFVKATLISNSKSETGEEOGLNSSVTKCFSSKNSPL 1020
DB 961 SVNFSAEGETVYEDESORQPFVKATLISNSKSETGEEOGLNSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPLTFSEGLDELLKLEGNFPENNDDKKSIIYL 1080
DB 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPLTFSEGLDELLKLEGNFPENNDDKKSIIYL 1080
QY 1081 GVTSTIKKRESGVLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
DB 1081 GVTSTIKKRESGVLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKWCOLDTV 1165

DB 1141 YMPQFOTCSTQTHKIMENKWCOLDTV 1165
RESULT 4
US-08-638-524B-4
; Sequence 4, Application US/08638524B
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert L.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING
; TITLE OF INVENTION: CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,524B
; FILING DATE: 26-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meikiejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/018001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-638-524B-4

Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWERTYVITAENLSYPTTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQFCVLLHWERTYVITAENLSYPTTPWRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETA VEPKFNSSGTHFSNLKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETA VEPKFNSSGTHFSNLKTTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQIDANNIOCLWGLKGLDLCFICVYESLFKNLFRNYNKKVHLLVYLPEVLEDSPLVPQKGS 180
DB 121 QQIDANNIOCLWGLKGLDLCFICVYESLFKNLFRNYNKKVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FOMVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVOPINMVKPDPP 240
DB 181 FOMVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVOPINMVKPDPP 240
QY 241 LGLHMETDDGNLKIWSNPPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLDVDSILP 300
DB 241 LGLHMETDDGNLKIWSNPPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLDVDSILP 300
QY 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSFHCIIYKKNKI 360
DB 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSFHCIIYKKNKI 360
QY 361 VPSKEIWMNNLAEKIPQSOYDVVSDHVSKVTFENLNETPRGKFTYDAYVCCNEHCHH 420
DB 361 VPSKEIWMNNLAEKIPQSOYDVVSDHVSKVTFENLNETPRGKFTYDAYVCCNEHCHH 420
QY 421 RYABLYVDVNNISCTDGYLTKMTCRWSTSTIQSLAESTLQLYRHSRLYCSIDPSIH 480
DB 421 RYABLYVDVNNISCTDGYLTKMTCRWSTSTIQSLAESTLQLYRHSRLYCSIDPSIH 480
QY 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKRPLPP 540
DB 481 PISEPKCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKRPLPP 540
QY 541 SSVKAEITINIGLLKISWEPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRKRLDGLGWSNWSNAPYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRKRLDGLGWSNWSNAPYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLCSQVRYVYNNHSTCNGTWSGVDGHNKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLWKPLMKNDLCSQVRYVYNNHSTCNGTWSGVDGHNKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANENLTFSPWMSKVNTVQSLAYSAYPLNSCCVIVSWILSPSDYKLMYFIEMKNLNE 780
DB 721 GASVANENLTFSPWMSKVNTVQSLAYSAYPLNSCCVIVSWILSPSDYKLMYFIEMKNLNE 780
QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYOFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSVKKYYIHDHFIPIEKYOFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVISSSTLLGLTLLISHORMKLFWEVDPNPKNCWAQGLNFQKPFTEHLFI 900
DB 841 GLYVIVPVISSSTLLGLTLLISHORMKLFWEVDPNPKNCWAQGLNFQKPFTEHLFI 900
QY 901 KHTASVTCGPIILLPEPTEISEDIVSTSWKNKDEMMPTTVVSLSTTDLEKSGVCISDOFN 960
DB 901 KHTASVTCGPIILLPEPTEISEDIVSTSWKNKDEMMPTTVVSLSTTDLEKSGVCISDOFN 960
QY 961 SVNFSEAGTEVTVYEDSQRPQFVKYATLISNSKPSSETGEEQGLINSVTKCFSSKNSPL 1020
DB 961 SVNFSEAGTEVTVYEDSQRPQFVKYATLISNSKPSSETGEEQGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFSNSWEIEAQAFTILSDOHPNIIISPHLTFSEGDELKLGPNPEENNDKSIYLL 1080
DB 1021 KDSFSNSWEIEAQAFTILSDOHPNIIISPHLTFSEGDELKLGPNPEENNDKSIYLL 1080
QY 1081 GVTGIKRRESGVLLTDKRSVCPPPAPCLFTDIRVLQSDCSHFVENNINLGTSSKKTFFAS 1140
DB 1081 GVTGIKRRESGVLLTDKRSVCPPPAPCLFTDIRVLQSDCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165

RESULT 5
US-08-667-197-2
; Sequence 2, Application US/08667197
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; TITLE OF INVENTION: USES FOR WAX LIGANDS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,197
; FILING DATE: 20-Jun-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: P-40,378
; REFERENCE/DOCKET NUMBER: P0986P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-667-197-2

Query Match 100.0%; Score 6254; DB 10; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSMPPNSTYDYFLPAGLSKNTSNS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSMPPNSTYDYFLPAGLSKNTSNS 60
QY 61 NGHYTEAVEPKFNSSGTHFSNLSKTTTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYTEAVEPKFNSSGTHFSNLSKTTTHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANNIOCLWGLKGLDLCFICVYESLFKNLFRNYNKKVHLLVYLPEVLEDSPLVPQKGS 180
DB 121 QQIDANNIOCLWGLKGLDLCFICVYESLFKNLFRNYNKKVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FOMVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVOPINMVKPDPP 240
DB 181 FOMVHCNCSVHECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPPLMSVOPINMVKPDPP 240
QY 241 LGLHMETDDGNLKIWSNPPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLDVDSILP 300
DB 241 LGLHMETDDGNLKIWSNPPPLVPFPLOYQVYKSENSTTVIREADKIVSATSLLDVDSILP 300
QY 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSFHCIIYKKNKI 360
DB 301 GSSYEVOVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSFHCIIYKKNKI 360
QY 361 VPSKEIWMNNLAEKIPQSOYDVVSDHVSKVTFENLNETPRGKFTYDAYVCCNEHCHH 420

Db 361 VPSKEIYMMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAEIYVIVDYNINISCTDGLTKMTCRWSTSTIQSLAESTLOLRVHRSSLYCSDIPSIH 480
Db 421 RYAEIYVIVDYNINISCTDGLTKMTCRWSTSTIQSLAESTLOLRVHRSSLYCSDIPSIH 480
Qy 481 PISPKDCYLQSDGFCYICFQPIPLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 481 PISPKDCYLQSDGFCYICFQPIPLSGYTMWIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Qy 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGEKVQWKMVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGEKVQWKMVEYDAKSKSVSLPV 600
Qy 601 PDLCAVAVOVRCKRDLGLGWSNWSNPAYTVVMDIKVPMRGPEFRIINGDITMKKEKNV 660
Db 601 PDLCAVAVOVRCKRDLGLGWSNWSNPAYTVVMDIKVPMRGPEFRIINGDITMKKEKNV 660
Qy 661 TLLWKPLMKNDLSCSVORYVINHHTSCNGTWSEDEVGNHRTKFTFLWTRQAHTVTVIATNSI 720
Db 661 TLLWKPLMKNDLSCSVORYVINHHTSCNGTWSEDEVGNHRTKFTFLWTRQAHTVTVIATNSI 720
Qy 721 GASVANLFTSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
Db 721 GASVANLFTSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
Qy 781 GEIKWLRISSVKYIYTHDHFPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSDA 840
Db 781 GEIKWLRISSVKYIYTHDHFPIEKYQFSLYPIFMEGVGPKIINSFTODDIEKHOSDA 840
Qy 841 GLYVIVPVIISSILLGLTLLISHQRMKILFWEDVPNPKNCNAQAQGLNFKQPTFEHLFI 900
Db 841 GLYVIVPVIISSILLGLTLLISHQRMKILFWEDVPNPKNCNAQAQGLNFKQPTFEHLFI 900
Qy 901 KHTASVTCGPLLLEPEFISDVSITSWKKNKDEMPPTVYVLSITDLEKSGVCISIDQFN 960
Db 901 KHTASVTCGPLLLEPEFISDVSITSWKKNKDEMPPTVYVLSITDLEKSGVCISIDQFN 960
Qy 961 SVNFSEAGTEVYDEDSRQPFVKYATLISNPKSPTEGEEGLINSVTKCFSSKNSPL 1020
Db 961 SVNFSEAGTEVYDEDSRQPFVKYATLISNPKSPTEGEEGLINSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSWIEIAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNPPEENNDDKSIYYL 1080
Db 1021 KDSFNSWIEIAQAFFILSDQHPNIIISPHLTSEGLDELKLEGNPPEENNDDKSIYYL 1080
Qy 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GVTSIKKRESGVLLTDKRSVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Qy 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165
Db 1141 YMPQFOTCSTQTHKIMENKMCIDLTV 1165

RESULT 6
US-08-708-123D-4
; Sequence 4, Application US/08708123D
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; CITY: Boston
; STATE: MA
; COUNTRY: US

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,123D
FILING DATE: 03-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-708-123D-4

Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MICQKFCVLLHWEFIYVITAFNLISVPIPTWRFKLSGMPNPNSTYDYFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFIYVITAFNLISVPIPTWRFKLSGMPNPNSTYDYFLLPAGLSKNTS 60
Qy 61 NGHYETAVERPKFNSGTHFNSLKTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVERPKFNSGTHFNSLKTTHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Qy 121 QQIDANNIQCWLKGLKLFICYVESLFKNLFNRYNKKVHLLVYLPEVLEDSPLVPQKGS 180
Db 121 QQIDANNIQCWLKGLKLFICYVESLFKNLFNRYNKKVHLLVYLPEVLEDSPLVPQKGS 180
Qy 181 FQMVHCNCSVHECCCECLVPVPTAKLNDLMLCKLTSGGVIFOSPLMSVOPINWKPDP 240
Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDLMLCKLTSGGVIFOSPLMSVOPINWKPDP 240
Qy 241 LGLHMEITDDGNLKIWSSSPPLVPFPIQYQVYKYSNSTTIVREADKIVSATSLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSSSPPLVPFPIQYQVYKYSNSTTIVREADKIVSATSLVDSILP 300
Qy 301 GSSYEVOVRKRLDGGIWSDSWTPTVFTTQDVIYPPPKILTSGVSNVSPHCYIKKENKI 360
Db 301 GSSYEVOVRKRLDGGIWSDSWTPTVFTTQDVIYPPPKILTSGVSNVSPHCYIKKENKI 360
Qy 361 VPSKEIYMMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYMMNLAEKIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420

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QY 421 RYAEYVIVDININISCTDGYLTGKTCRWSTSTIOSLAESTLQLYHRSSLYCSDIPSH 480
Db 421 RYAEYVIVDININISCTDGYLTGKTCRWSTSTIOSLAESTLQLYHRSSLYCSDIPSH 480
QY 481 PISEPKDCYLOSDGFEYECIFQIFLLSGYTMWIRINHSLGSLDSDPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFEYECIFQIFLLSGYTMWIRINHSLGSLDSDPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVAVOVCKRLDGLGYWNSNFPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVAVOVCKRLDGLGYWNSNFPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWPKLKNDSVQRYVINHHTSCTGWSDEDVGNHTKFTFLWTEQAHTTVVLAINSI 720
Db 661 TLLWPKLKNDSVQRYVINHHTSCTGWSDEDVGNHTKFTFLWTEQAHTTVVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPDYKLYFIIWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPDYKLYFIIWKNLNED 780
QY 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLYPIWEGVGKPKIINSFTODDIEKHSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFTPIEKYQFSLYPIWEGVGKPKIINSFTODDIEKHSDA 840
QY 841 GLYVIVPVPIISSILLGLTLLSHORMKLFWEDVPNPKNCWSAOGNLFQKPEFELFI 900
Db 841 GLYVIVPVPIISSILLGLTLLSHORMKLFWEDVPNPKNCWSAOGNLFQKPEFELFI 900
QY 901 KHTASVTCGPLLEPETISEDLSVDTSWKNKDEMMPTTVVSLSTDLKSGVCISDQFN 960
Db 901 KHTASVTCGPLLEPETISEDLSVDTSWKNKDEMMPTTVVSLSTDLKSGVCISDQFN 960
QY 961 SYNFEAEGETEYDESORQPFVYATLINSKPSKSEGEGLINSVTKCFSSKNNSPL 1020
Db 961 SYNFEAEGETEYDESORQPFVYATLINSKPSKSEGEGLINSVTKCFSSKNNSPL 1020
QY 1021 KDSFNSWEIEAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNFPENNDRKSIYVL 1080
Db 1021 KDSFNSWEIEAQAFFILSDQHPIIISPHLTFSEGLDELKLEGNFPENNDRKSIYVL 1080
QY 1081 GVTSTKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
Db 1081 GVTSTKKRESGVLITDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

```

RESULT 7

US-08-779-457-2

; Sequence 2, Application US/08779457

; GENERAL INFORMATION:

; APPLICANT: Carter, Paul J.

; APPLICANT: Chiang, Nancy Y.

; APPLICANT: Kyung, Jin Kim

; APPLICANT: Matthews, William

; APPLICANT: Rodrigues, Maria L.

; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,457

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/667197

; FILING DATE: 06/20/96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585005

; FILING DATE: 01/08/96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0986P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1165 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-779-457-2

Query Match 100.0%; Score 6254; DB 11; Length 1165;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSMCPNPNSTYDYFLLPAGLSKNTNS 60

Db 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSMCPNPNSTYDYFLLPAGLSKNTNS 60

QY 61 NGHYTAVPEKPNSSGTHFSNLKTTFFHCCFRSEQDRNCSLADNIEGKTFSTVNSLVF 120

Db 61 NGHYTAVPEKPNSSGTHFSNLKTTFFHCCFRSEQDRNCSLADNIEGKTFSTVNSLVF 120

QY 121 QOIDANWNIQCKLGDGLKLFICYVESLFKNLFRNNYKVVHLLYVLPVLEDSPLVPKGS 180

Db 121 QOIDANWNIQCKLGDGLKLFICYVESLFKNLFRNNYKVVHLLYVLPVLEDSPLVPKGS 180

QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240

Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINMVKPDP 240

QY 241 LGLHWEITDDGNLKITSWSSPPLVPPLQVQVYSENSTTVIREADKIVSATSLLVDSILP 300

Db 241 LGLHWEITDDGNLKITSWSSPPLVPPLQVQVYSENSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVQVRGKRLDGPVTSWDSMTFRVFTTQDVIVFPKILTSGVSNVSFHCITYKKENKI 360

Db 301 GSSYEVQVRGKRLDGPVTSWDSMTFRVFTTQDVIVFPKILTSGVSNVSFHCITYKKENKI 360

QY 361 VPSKEITVMMNLAEKIPQSOYDVSDHVSKVTFNNLNETKPKGKFTYDAVYCCNEHECHH 420

Db 361 VPSKEITVMMNLAEKIPQSOYDVSDHVSKVTFNNLNETKPKGKFTYDAVYCCNEHECHH 420

QY 421 RYAEYVIVDININISCTDGYLTGKTCRWSTSTIOSLAESTLQLYHRSSLYCSDIPSH 480

Db 421 RYAEYVIVDININISCTDGYLTGKTCRWSTSTIOSLAESTLQLYHRSSLYCSDIPSH 480

QY 481 PISEPKDCYLOSDGFEYECIFQIFLLSGYTMWIRINHSLGSLDSDPTCVLPDSVVKPLPP 540

Db 481 PISEPKDCYLOSDGFEYECIFQIFLLSGYTMWIRINHSLGSLDSDPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600

601 PDLCAVAVQVRCKRLDGLGYSWNSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
601 PDLCAVAVQVRCKRLDGLGYSWNSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
661 TLLWPKLAKNDLSCSVQRYVVIINHRTSCNGTWSGDEYVGNHTKFTFLWTEQAHTTVVLAINSI 720
661 TLLWPKLAKNDLSCSVQRYVVIINHRTSCNGTWSGDEYVGNHTKFTFLWTEQAHTTVVLAINSI 720
721 GASVANFNLTFSWPMKSNIVQSLGYSAYPLNSSCVIVSWILSPDSYKLMYFIIWKLNLED 780
721 GASVANFNLTFSWPMKSNIVQSLGYSAYPLNSSCVIVSWILSPDSYKLMYFIIWKLNLED 780
781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
841 GLYVIVPVIISSIIILLGTLIIHQRMKLFWEDEVNPNKNCWSAOGLNPKQKPEFHLFI 900
841 GLYVIVPVIISSIIILLGTLIIHQRMKLFWEDEVNPNKNCWSAOGLNPKQKPEFHLFI 900
901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTTVVSLSTDLEKSGVCISDQFN 960
901 KHTASVTCGPLLEPETISEDISVDTSWKNKDEMPPTTVVSLSTDLEKSGVCISDQFN 960
961 SYNFEAEGETEYDESQRPVYATLISNSKPSKETGEEQGLINSSVTKCFSSKNSPL 1020
961 SYNFEAEGETEYDESQRPVYATLISNSKPSKETGEEQGLINSSVTKCFSSKNSPL 1020
1021 KDSFNSWEIEBAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYVL 1080
1021 KDSFNSWEIEBAQAFILSDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYVL 1080
1081 GYTSIKKRESGVLLTDKSRVSCPEFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAAS 1140
1081 GYTSIKKRESGVLLTDKSRVSCPEFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFAAS 1140
1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165

RESULT 8

US-08-780-562-2
; Sequence 2, Application US/08780562
; GENERAL INFORMATION:
; APPLICANT: Matthews, William
; APPLICANT: Bennett, Brian
; TITLE OF INVENTION: WSX RECEPTOR
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,562
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/
; FILING DATE: 01/08/97
; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-562-2

Query Match 100.0%; Score 6254; DB 11; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVVLLHWEIYVITAFNLSPITPWRFKLSCHMPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVVLLHWEIYVITAFNLSPITPWRFKLSCHMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPKPNSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHETAVEPKPNSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNIQCKLGDGLKLFICYVESLPKFLFRNYKVHLLYVLPEVLEDSPLVPQKGS 180
DB 121 QOIDANWNIQCKLGDGLKLFICYVESLPKFLFRNYKVHLLYVLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHCECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPILMSVQPINMVKPDP 240
DB 181 FQMVHCNCSVHCECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPILMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPPLQYQVYKSENSTTVIREADKIYSATSLLDVSLP 300
DB 241 LGLHMEITDDGNLKIWSWSPPLVPPLQYQVYKSENSTTVIREADKIYSATSLLDVSLP 300
QY 301 GSSYEVQVRGKRLDGPGLWSDMSTPRVFTQDVIYFPPKILTSVGSNSFHCIIYKKNKI 360
DB 301 GSSYEVQVRGKRLDGPGLWSDMSTPRVFTQDVIYFPPKILTSVGSNSFHCIIYKKNKI 360
QY 361 VPSKEIVMMNLAEKIPQSYDVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIVMMNLAEKIPQSYDVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQLRYHRSSLYCSDIPSIH 480
DB 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQLRYHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDFYECIFQPIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSDFYECIFQPIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYVYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMYEYVYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCKRLDGLGYSWNSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCKRLDGLGYSWNSNPNAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWPKLAKNDLSCSVQRYVVIINHRTSCNGTWSGDEYVGNHTKFTFLWTEQAHTTVVLAINSI 720
DB 661 TLLWPKLAKNDLSCSVQRYVVIINHRTSCNGTWSGDEYVGNHTKFTFLWTEQAHTTVVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLGYSAYPLNSSCVIVSWILSPDSYKLMYFIIWKLNLED 780
DB 721 GASVANFNLTFSWPMKSNIVQSLGYSAYPLNSSCVIVSWILSPDSYKLMYFIIWKLNLED 780
QY 781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840
DB 781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMGVGKPKIINSFTODDIEKHQSDA 840

Db 781 GEIKWLRISSVKKYIIHDFIPIEKYQFSLYPIPMGVGPKPIINSTQDDIEKHQSDA 840
Qy 841 GLYVIVPVISSILLGLTLLISHQRMKKLFWEDVPNPKNCWSAQLNFKQKPEFHLFI 900
Db 841 GLYVIVPVISSILLGLTLLISHQRMKKLFWEDVPNPKNCWSAQLNFKQKPEFHLFI 900
Qy 901 KHTASVTCGPIILPETISEDIVTSKNDKEMPTTVVSLTSTDLKSGVCISDQFN 960
Db 901 KHTASVTCGPIILPETISEDIVTSKNDKEMPTTVVSLTSTDLKSGVCISDQFN 960
Qy 961 SVNFSEAECTEVTYDESRQRPVFKYATLISNKSPPSETGEOGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSEAECTEVTYDESRQRPVFKYATLISNKSPPSETGEOGLINSSVTKCFSSKNSPL 1020
Qy 1021 KDSFNSNSWEIEAQAFFILSDQHPIIISPHLTFSBGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSNSWEIEAQAFFILSDQHPIIISPHLTFSBGLDELLKLEGNFPEENNDKKSIIYL 1080
Qy 1081 GVTSTKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
Db 1081 GVTSTKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
Qy 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 9
US-09-094-410-4
; Sequence 4, Application US/09094410
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,410
; FILING DATE: 09-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-094-410-4

Query Match 100.0%; Score 6254; DB 14; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MICQKFCVVLHWEIYVITAFNLSPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVVLHWEIYVITAFNLSPITPWRFKLSCHMPPNSTYDYFLLPAGLSKNTSNS 60
Qy 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVEPKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Qy 121 QOIDANNIOCLWKGDLKLFICYVESLFPKNLFRNRYKVHLLYVLPVELEDSPVPQKGS 180
Db 121 QOIDANNIOCLWKGDLKLFICYVESLFPKNLFRNRYKVHLLYVLPVELEDSPVPQKGS 180
Qy 181 FQMVHCNCSVHECCCLVPVPTAKLNDTILMCLKITSGVIFQSPILMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTILMCLKITSGVIFQSPILMSVQPINMVKPDP 240
Qy 241 LGLHMEITDDGNLKITSWSSPPLVPFLQYQVKYSNSTTVIREADKIYSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKITSWSSPPLVPFLQYQVKYSNSTTVIREADKIYSATSLLVDSILP 300
Qy 301 GSSYEYQVGRKLDGPGIWSDMSTPRVFTQDVIYFPKILTVSGSNVSFHCIIYKKNKI 360
Db 301 GSSYEYQVGRKLDGPGIWSDMSTPRVFTQDVIYFPKILTVSGSNVSFHCIIYKKNKI 360
Qy 361 VPSKEIVVMNLAEKIPQSDYVSDHVSQVTFVFFNLNETKPRGKFTYDAVYCCNEBEC 420
Db 361 VPSKEIVVMNLAEKIPQSDYVSDHVSQVTFVFFNLNETKPRGKFTYDAVYCCNEBEC 420
Qy 421 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSTIOSLAESTLQRLYHRSLSYCSIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSTIOSLAESTLQRLYHRSLSYCSIPSIH 480
Qy 481 PISEPKDCYLOSDGFYECIFQIFLLSGYTMIRINHSLGSLDSPPTCVLPVSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQIFLLSGYTMIRINHSLGSLDSPPTCVLPVSVVKPLPP 540
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKVEYVYDAKSYSVLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKVEYVYDAKSYSVLPV 600
Qy 601 PDLCAVAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
Db 601 PDLCAVAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
Qy 661 TLLWKLPMKNDSLCSVQRYVINHHTSCNCTWSEDVGNHTKFTFLWTEQAHVTYVLAINSI 720
Db 661 TLLWKLPMKNDSLCSVQRYVINHHTSCNCTWSEDVGNHTKFTFLWTEQAHVTYVLAINSI 720
Qy 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNNSCVIVSWILSPSDYKLYMFIIEWKNLND 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNNSCVIVSWILSPSDYKLYMFIIEWKNLND 780

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QY 781 GEIKWLRISSVKKYIIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDDIERHQSDA 840
|||||
Db 781 GEIKWLRISSVKKYIIHDHFIPIEKYQFSLYPIEMEGVGKPKIINSFTQDDIERHQSDA 840
QY 841 GUYIVPVISSIIILLGTLISHORMKKLFWEDVPNPKNCNSWAQGLNFQKPTPEHLFI 900
|||||
Db 841 GUYIVPVISSIIILLGTLISHORMKKLFWEDVPNPKNCNSWAQGLNFQKPTPEHLFI 900
QY 901 KHTASVTCGPLLEPETTISEDIVSTSMKNKDEMPPTTVSLLSTTDLKSGVCISDOFN 960
|||||
Db 901 KHTASVTCGPLLEPETTISEDIVSTSMKNKDEMPPTTVSLLSTTDLKSGVCISDOFN 960
QY 961 SVNFSEAEETEYVEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKN SPL 1020
|||||
Db 961 SVNFSEAEETEYVEDESORQPFVKYATLISNSKPSSETGEEGLINSSVTKCFSSKN SPL 1020
QY 1021 KDSFNSNSWEIPAQAFILSDQHPNIIISPHLTFSGLDLLEKLNFEENNNDKKSIIYL 1080
|||||
Db 1021 KDSFNSNSWEIPAQAFILSDQHPNIIISPHLTFSGLDLLEKLNFEENNNDKKSIIYL 1080
QY 1081 GYTSIKKRESGVLLTDKSRVSCPPFPACLFDTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
|||||
Db 1081 GYTSIKKRESGVLLTDKSRVSCPPFPACLFDTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
QY 1141 YMPQFQTCSTQTHKIENKMCDLTV 1165
|||||
Db 1141 YMPQFQTCSTQTHKIENKMCDLTV 1165

RESULT 10
US-09-137-132-4
; Sequence 4, Application US/09137132
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: White, David W.
; TITLE OF INVENTION: THE O RECEPTOR AND METHODS FOR
; TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
; TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,132
; FILING DATE: 18-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/864,564
; FILING DATE: 28-MAY-1997
; APPLICATION NUMBER: 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
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;
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/019004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-137-132-4

Query Match          100.0%; Score 6254; DB 15; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKILSCMPNPSTYDYFLLPAGLSKNTSNS 60
|||||
Db 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRFKILSCMPNPSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHETAVEPKFNSGTHFSNLSTKTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120
|||||
Db 61 NGHETAVEPKFNSGTHFSNLSTKTFHCCFRSEODRNCSCADNIEGKTFVSTVNSLVF 120

QY 121 QOIDANNIQCWLKGLDLKLCYVESLEFKNLFRNNYVHLLYVLPEVLEDSPLVPQKGS 180
|||||
Db 121 QOIDANNIQCWLKGLDLKLCYVESLEFKNLFRNNYVHLLYVLPEVLEDSPLVPQKGS 180

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINMYKPDPP 240
|||||
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINMYKPDPP 240

QY 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVYKYSNSTTVI READKIVSATSLLVDSILP 300
|||||
Db 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVYKYSNSTTVI READKIVSATSLLVDSILP 300

QY 301 GSSYEVQVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCIIYKKENKI 360
|||||
Db 301 GSSYEVQVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSVGSNVSFHCIIYKKENKI 360

QY 361 VPSKEIVVMNLAEKIPQSQYDWDVSDHYSKVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420
|||||
Db 361 VPSKEIVVMNLAEKIPQSQYDWDVSDHYSKVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIDVAINISCTDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLYCSIPSIH 480
|||||
Db 421 RYAEIYVIDVAINISCTDGYLTMTKCRWSTSTIQSLAESTLQLRHYRSSLYCSIPSIH 480

QY 481 PTSEPKDCYLOSDFYECIFQPIFLLSGYTWIRINHSILGSLDSPPTCVLPDSVVVKPLPP 540
|||||
Db 481 PTSEPKDCYLOSDFYECIFQPIFLLSGYTWIRINHSILGSLDSPPTCVLPDSVVVKPLPP 540

QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVOWKNMYEYVDKSKSVSLPV 600
|||||
Db 541 SSVKAEITINIGLKLISWEKVPFPENNLOFQIRYGLSGKEVOWKNMYEYVDKSKSVSLPV 600

QY 601 PDLCAVAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGCPPEWRILNGDTMKKEKNV 660
|||||
Db 601 PDLCAVAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGCPPEWRILNGDTMKKEKNV 660

QY 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
|||||
Db 661 TLLWKPLMKNDSLCSVQRYVINHHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
```

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QY 721 GASVANFLTESWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLYMFIIEWKNLNED 780
;
Db 721 GASVANFLTESWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLYMFIIEWKNLNED 780
;
QY 781 GEIKWLRISSSVKKYYIHDFPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
;
Db 781 GEIKWLRISSSVKKYYIHDFPIEKYQSLPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
;
QY 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCWAQGLNFQKPTFHLFI 900
;
Db 841 GLYVIVPVISSILLGLTLLISHQRMKLFWEDEVNPNKNCWAQGLNFQKPTFHLFI 900
;
QY 901 KHTASVTCGPLLEPETISEDIVSDTSWKNKDEMMPTTVVSLSTTDLKGSVCISDOFN 960
;
Db 901 KHTASVTCGPLLEPETISEDIVSDTSWKNKDEMMPTTVVSLSTTDLKGSVCISDOFN 960
;
QY 961 SVNFSAEGTEVYDESORQPFVKYATLISNKPSETGEOGLINSVTKCFSSKNSPL 1020
;
Db 961 SVNFSAEGTEVYDESORQPFVKYATLISNKPSETGEOGLINSVTKCFSSKNSPL 1020
;
QY 1021 KDSFSSWEIEAQAFFILSDQHPNIIISHLTFSEGLDELLKLEGNFPENNDKKSIYIL 1080
;
Db 1021 KDSFSSWEIEAQAFFILSDQHPNIIISHLTFSEGLDELLKLEGNFPENNDKKSIYIL 1080
;
QY 1081 GVTSIKKREGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHEVENNINLTSSKKTFAS 1140
;
Db 1081 GVTSIKKREGVLLTDKSRVSCPPAPCLFTDIRVLQDSCSHEVENNINLTSSKKTFAS 1140
;
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
;
Db 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
;
RESULT 11
US-09-950-149-4
; Sequence 4, Application US/09950149
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
;           Tepper, Robert I.
;           Culpepper, Janice A.
;           White, David W.
; TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
;                   THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
;                   INCLUDING OBESITY AND CACHEXIA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; City: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/950,149
; FILING DATE: 10-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,781
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 08/708,123
; FILING DATE: 03-SEP-1996
; APPLICATION NUMBER: US 08/638,524
; FILING DATE: 26-APR-1996
; APPLICATION NUMBER: US 08/599,455
; FILING DATE: 22-JAN-1996
; APPLICATION NUMBER: US 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: US 08/570,142
; FILING DATE: 11-DEC-1995
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; APPLICATION NUMBER: US 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: US 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: US 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Melkielejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/082001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-950-149-4

Query Match      100.0%; Score 6254; DB 23; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYVITAFNLSYPIPTWRFKLSGMPNPNSTYDFLLPAGLSKNTSNS 60
;
Db 1 MICQKFCVLLHWEFYVITAFNLSYPIPTWRFKLSGMPNPNSTYDFLLPAGLSKNTSNS 60
;
QY 61 NGHETAVEPKFNSSGTHFSNLKTTFHCCFRSEQRNCSLCADNIEGKTFVTVNSLVF 120
;
Db 61 NGHETAVEPKFNSSGTHFSNLKTTFHCCFRSEQRNCSLCADNIEGKTFVTVNSLVF 120
;
QY 121 QOIDANNITOCWLKGLKLFICYVESLFLKLNFRNFKVHLLVYLVEVLEDSPLVPQKGS 180
;
Db 121 QOIDANNITOCWLKGLKLFICYVESLFLKLNFRNFKVHLLVYLVEVLEDSPLVPQKGS 180
;
QY 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
;
Db 181 FQMVHCNCSVHECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
;
QY 241 LGLHMEITDDGNLKIWSNPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLIVDSILP 300
;
Db 241 LGLHMEITDDGNLKIWSNPPPLVPPFLOQYQVYKYSNSTTVIREADKIVSATSLIVDSILP 300
;
QY 301 GSSYEYQVGRKLDGPGCINSDWSTPRVFTTQDVIYPPPKILTSGVSNVSPHCYKKNKI 360
;
Db 301 GSSYEYQVGRKLDGPGCINSDWSTPRVFTTQDVIYPPPKILTSGVSNVSPHCYKKNKI 360
;
QY 361 VPSKEIWWWNNLAEKIPQSOYDVVSDHVSQVTFPNNETKPRGKFTYDAYVCCNEHECHH 420
;
Db 361 VPSKEIWWWNNLAEKIPQSOYDVVSDHVSQVTFPNNETKPRGKFTYDAYVCCNEHECHH 420
;
QY 421 RYAEIYVDVNIINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCDIPSIIH 480
;
Db 421 RYAEIYVDVNIINISCTDGYLTKMTCRWSTSTIQSLAESTLQLRHRSLSYCDIPSIIH 480
;
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540
;
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540
;
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQWKNYEVYDAKSKVSLPV 600
;
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQWKNYEVYDAKSKVSLPV 600
;
QY 601 PDLCAVYAVQVRCRDLGLGYSWNSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
;
Db 601 PDLCAVYAVQVRCRDLGLGYSWNSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
;
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Db 961 SYNFSEAEGETVYEDSORQPVKYATLISNSKPSETGEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFILSDQHPIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSNSWEIEAQAFILSDQHPIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
QY 1081 GYTSIKKREGSVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GYTSIKKREGSVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

RESULT 13
US-09-671-049-7
; Sequence 7, Application US/09671049
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; FLETCHER, FREDERICK A.
; TITLE OF INVENTION: OB PROTEIN RECEPTOR AND RELATED
; COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/671,049
; FILING DATE: 27-Sep-2000
; PRIOR APPLICATION DATA:
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-382-A
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-671-049-7

Query Match 100.0%; Score 6254; DB 20; Length 1216;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFFIVYVTAFLNSLPTIPWRFKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFFIVYVTAFLNSLPTIPWRFKLSCMPNPNSTYDFLLPAGLSKNTSNS 60
QY 61 NGHYTEAVPEKFNSSCTHFSNLKSTTFHCCFRSEQDRNCSLCAADNEGKTFVSTVNSLVF 120
Db 61 NGHYTEAVPEKFNSSCTHFSNLKSTTFHCCFRSEQDRNCSLCAADNEGKTFVSTVNSLVF 120
QY 121 QQIDANNIQCWLKGLDKLFICYVESLFLKFLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANNIQCWLKGLDKLFICYVESLFLKFLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180

RESULT 14

US-09-948-933-284

; Sequence 284, Application US/09948933

; GENERAL INFORMATION:

QY 181 FQVHHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDP 240
Db 181 FQVHHCNCSVHECCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPMLSVQPINMVKPDP 240
QY 241 LGLHMEITDGNLKITSWSSPPLVPFPLOQVQKYSNSTVIRADKIVSATSLVDSILP 300
Db 241 LGLHMEITDGNLKITSWSSPPLVPFPLOQVQKYSNSTVIRADKIVSATSLVDSILP 300
QY 301 GSSYEVQVGRKRLDGPINSDMSTPRVFTQDVIYPPPKILTSVGSNSVGFHCIIYKKNKI 360
Db 301 GSSYEVQVGRKRLDGPINSDMSTPRVFTQDVIYPPPKILTSVGSNSVGFHCIIYKKNKI 360
QY 361 VPSKEIYVMMNLAELIPQSOYDVVSDHVSQVTFENLNKPKRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVMMNLAELIPQSOYDVVSDHVSQVTFENLNKPKRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIVDNNINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRVHRSLSYCDIPSIH 480
Db 421 RYAEIYVIVDNNINISCTDGYLTMTKTCRWSTSTIQSLAESTLQLRVHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVRPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVRPLPP 540
QY 541 SSVKAEITINIGLLKITSWEKPVPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKITSWEKPVPENNLOFOIRYGLSGKEVQMKYEVYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCKRLDGLGYNSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCKRLDGLGYNSNWSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDLSLCSVQRYVINHHTSCNGTWSEDVGNHKTFTPLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPLMKNDLSLCSVQRYVINHHTSCNGTWSEDVGNHKTFTPLWTEQAHTVTVLAINSI 720
QY 721 GASVANFLNTEFWPMKSKVNIQVLSAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNED 780
Db 721 GASVANFLNTEFWPMKSKVNIQVLSAYPLNSSCVIVSWILSPSDYKLMYFLIEMKNLNED 780
QY 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKWLRISSVKKYIYHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVIISSILLGLTLLISHQRMKKLFWEDEVNPNKNCSWAQLNFKOKPTFEHLFI 900
Db 841 GLYVIVPVIISSILLGLTLLISHQRMKKLFWEDEVNPNKNCSWAQLNFKOKPTFEHLFI 900
QY 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDOFN 960
Db 901 KHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVVSLSTTDLEKGSVCISDOFN 960
QY 961 SYNFSAEAGTEVYDEDSORQPVKYATLISNSKPSETGEOGLINSVTKCFSSKNSPL 1020
Db 961 SYNFSAEAGTEVYDEDSORQPVKYATLISNSKPSETGEOGLINSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEAQAFILSDQHPIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1021 KDSFNSNSWEIEAQAFILSDQHPIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
QY 1081 GYTSIKKREGSVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
Db 1081 GYTSIKKREGSVLLTDKSRVSCFPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; PRIOR FILING DATE: 2001-09-10
; CURRENT APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
US-09-948-933-284

Query Match 99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFTYVITAFNLSYPTIPWRFKLSKMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHWEFTYVITAFNLSYPTIPWRFKLSKMPNPNSTYDYFLLPAGLSKNTSNS 62

QY 61 NGHYETAPEPKFNSSGTHFNSLKTTHFCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHYETAPEPKFNSSGTHFNSLKTTHFCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 122

QY 121 QQIDANNIQCWLKGDGLKLFICVSVESLFKNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
Db 123 QQIDANNIQCWLKGDGLKLFICVSVESLFKNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 182

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 183 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 242

QY 241 LGLHMEITDDGNLIKISWSSPPLVPFPFLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
Db 243 LGLHMEITDDGNLIKISWSSPPLVPFPFLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 302

QY 301 GSSYEVQVGRKLDGKISWSDNSTPRVFTTQDVYIYPPPKILTSVGSNVSFHCYIKKENKI 360
Db 303 GSSYEVQVGRKLDGKISWSDNSTPRVFTTQDVYIYPPPKILTSVGSNVSFHCYIKKENKI 362

QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 420
Db 363 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFNLFNETKPRGKFTYDAVYCCNEHECHH 422

QY 421 RYAEYVIDVNIINISCTDGYLTMTKRCWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 423 RYAEYVIDVNIINISCTDGYLTMTKRCWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 482

QY 481 PIPEPKDCYLOSDGFECIFQPIFLLSGTWTWIRINHSIGLSDSPPTCVLPDSVWKLPP 540
Db 483 PIPEPKDCYLOSDGFECIFQPIFLLSGTWTWIRINHSIGLSDSPPTCVLPDSVWKLPP 542

QY 541 SSVKAEITINIGLLKISWEKVPFPPENLOFOIRYGLSGKEVQWMEYVDKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKVPFPPENLOFOIRYGLSGKEVQWMEYVDKSKSVSLPV 602

QY 601 PDLCAVAYQVRCRKLDDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
Db 603 PDLCAVAYQVRCRKLDDGLGYNSWNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 662

QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSVDGNGHHTKFTFLWTEQARTVTVLAINSI 720
Db 663 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSVDGNGHHTKFTFLWTEQARTVTVLAINSI 722

QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFILLEWKNLNE 780
Db 723 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFILLEWKNLNE 782

QY 781 GEIKWLRISSSVKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 783 GEIKWLRISSSVKYIYHDFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 842

QY 841 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPTFEHLFI 900
Db 843 GLYVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQKPTFEHLFI 902

QY 901 KHTASVTCGPPLLEPETISEDISVDTSWKNKDEMPTTVVYSLSTTDLEKGSVCISDOFN 960
Db 903 KHTASVTCGPPLLEPETISEDISVDTSWKNKDEMPTTVVYSLSTTDLEKGSVCISDOFN 962

QY 961 SVNFSEAGTEVTYDEDSQRPVFKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1020
Db 963 SVNFSEAGTEVTYDEDSQRPVFKYATLISNSKPSSETGEOGLINSVTKCFSSKNSPL 1022

QY 1021 KOSFSNSSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELLKLEGNFPENNNDKSIYYL 1080
Db 1023 KOSFSNSSWEIEAQAFFILSDQHPNIIISPHLTSEGLDELLKLEGNFPENNNDKSIYYL 1082

QY 1081 GYTSIKKRESGVLLTOKSRVSCPPAPCLFTDIRVLQDSCSHEVENNINLTSSKKTFFAS 1140
Db 1083 GYTSIKKRESGVLLTOKSRVSCPPAPCLFTDIRVLQDSCSHEVENNINLTSSKKTFFAS 1142

QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

RESULT 15
US-09-948-947-87
; Sequence 87, Application US/09948947
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; FILE REFERENCE: CL000786
; CURRENT APPLICATION NUMBER: US/09/948,947
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1167
; TYPE: PRT
; ORGANISM: Human
US-09-948-947-87

Query Match 99.9%; Score 6247; DB 23; Length 1167;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFTYVITAFNLSYPTIPWRFKLSKMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 3 MICQKFCVLLHWEFTYVITAFNLSYPTIPWRFKLSKMPNPNSTYDYFLLPAGLSKNTSNS 62

QY 61 NGHYETAPEPKFNSSGTHFNSLKTTHFCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHYETAPEPKFNSSGTHFNSLKTTHFCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 122

QY 121 QQIDANNIQCWLKGDGLKLFICVSVESLFKNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
Db 123 QQIDANNIQCWLKGDGLKLFICVSVESLFKNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 182

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 183 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINNVKPDPP 242

QY 241 LGLHMEITDDGNLIKISWSSPPLVPFPFLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300

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Db 243 LGLHMEITDDGNLKSWSPPPLVPPLOVQVYSENSVTVIREADKIYVATSLLVDSILP 302
QY 301 GSSYEVQVRGKRLDQPGIWSDMSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 360
Db 303 GSSYEVQVRGKRLDQPGIWSDMSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 362
QY 361 VPSKETVMMNLAEKIPQSOYDVVDHVSKVTFNLTNETKPRGKETYDAVYCCNEHECHH 420
Db 363 VPSKETVMMNLAEKIPQSOYDVVDHVSKVTFNLTNETKPRGKETYDAVYCCNEHECHH 422
QY 421 RYAEIYVIVDNININISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 480
Db 423 RYAEIYVIVDNININISCEITDGYLTMTKCRWSTSTIQSLAESTLQLRYHRSSLYCSDIPSIIH 482
QY 481 PISEPKDCYLOSDGFEYECIFQIFILLSGYTMWIRINHSLGSLDSDPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFEYECIFQIFILLSGYTMWIRINHSLGSLDSDPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYNSNNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 660
Db 603 PDLCAVYAVQVRCKRLDGLGYNSNNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKNV 662
QY 661 TLLWKPLMKNDSLCSVQRYVINNHHTSCNGTSEDYGNHTKFTFLMTEQAHTVTVLAINSI 720
Db 663 TLLWKPLMKNDSLCSVQRYVINNHHTSCNGTSEDYGNHTKFTFLMTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLND 780
Db 723 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLND 782
QY 781 GRIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 783 GRIKWLRISSSVKKYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 842
QY 841 GLYVIVPVISSIIILLGPTLLISHORMKLFWEDEVNPNKNCSWAOGNLFQKPTFEHLFI 900
Db 843 GLYVIVPVISSIIILLGPTLLISHORMKLFWEDEVNPNKNCSWAOGNLFQKPTFEHLFI 902
QY 901 KHTASVTCGPLLEPETISEDLSVDTSMKNKDEMPTTVVSLSTDLKSGVCISDQFN 960
Db 903 KHTASVTCGPLLEPETISEDLSVDTSMKNKDEMPTTVVSLSTDLKSGVCISDQFN 962
QY 961 SYNFEAEGETVYDESORQPFVKYATLINSKPSSETGEOGLINSSVTKCFSSKNSPL 1020
Db 963 SYNFEAEGETVYDESORQPFVKYATLINSKPSSETGEOGLINSSVTKCFSSKNSPL 1022
QY 1021 KDSFNSNSWEIEBAQAFPIISDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1080
Db 1023 KDSFNSNSWEIEBAQAFPIISDQHPNIIISPHLTFSEGLDELLKLEGNFPEENNDKKSIIYL 1082
QY 1081 GVTSLIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1140
Db 1083 GVTSLIKKRESGVLLTDKSRVSCPPFAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTAS 1142
QY 1141 YMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1143 YMPQFOTCSTQTHKIMENKMDLTV 1167

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Search completed: August 15, 2002, 16:34:03
Job time: 763 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:20:55 ; Search time 111.01 Seconds
(without alignments)
2425.061 Million cell updates/sec

Title: US-08-779-457-2
Perfect score: 6254
Sequence: 1 MICQKFCVLLHWEFIYVIT.....QTCSTQTHKINMKCDLTV 1165

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6254	100.0	1165	5	US-09-791-537-95040
2	6246	99.9	1165	5	US-09-791-537-120058
3	5967	95.4	1163	5	US-09-791-537-14096
4	5941.5	95.0	1194	5	US-09-791-537-75134
5	4831.5	77.3	958	5	US-09-791-537-95039
6	4826	77.2	896	5	US-09-791-537-95038
7	4819.5	77.1	958	5	US-09-791-537-114050
8	4816	77.0	906	5	US-09-791-537-114052
9	4814	77.0	896	5	US-09-791-537-114053
10	4786.5	76.5	1162	5	US-09-791-537-128089
11	4778.5	76.4	1162	5	US-09-791-537-57257
12	4766.5	76.2	1162	5	US-09-791-537-65061
13	4766.5	76.2	1174	5	US-09-791-537-26913
14	4761.5	76.1	1162	5	US-09-791-537-53431
15	4760.5	76.1	1162	5	US-09-791-537-45617
16	4757.5	76.1	1162	5	US-09-791-537-91206
17	4591	73.4	925	5	US-09-791-537-75138
18	4590	73.4	894	5	US-09-791-537-75131
19	3787	60.6	894	5	US-09-791-537-76191
20	3781	60.5	894	5	US-09-791-537-11623
21	3779	60.4	894	5	US-09-791-537-144499
22	3340	53.4	805	5	US-09-791-537-144103
23	3337	53.4	805	5	US-09-791-537-144369
24	2775	44.4	1148	5	US-09-791-537-8198
25	2693	43.1	1146	5	US-09-791-537-126327
26	1620	25.9	308	6	US-10-038-010-46

27	934	14.9	179	6	US-10-038-010-44	Sequence 44, Appl
28	703	11.2	133	6	US-10-038-010-42	Sequence 42, Appl
29	444	7.1	881	5	US-09-791-537-142984	Sequence 142984, A
30	409.5	6.5	918	5	US-09-791-537-56948	Sequence 56948, A
31	384	6.1	1158	5	US-09-935-868-26	Sequence 26, Appl
32	376	6.0	1168	5	US-09-935-868-24	Sequence 24, Appl
33	354	5.7	710	5	US-09-791-537-143846	Sequence 143846, A
34	345.5	5.5	918	1	PCT-US02-19669-230	Sequence 230, App
35	345.5	5.5	918	5	US-09-853-180-4	Sequence 4, Appl
36	345.5	5.5	918	5	US-09-829-472A-9	Sequence 9, Appl
37	345.5	5.5	918	6	US-09-791-537-118267	Sequence 118267, A
38	345.5	5.5	918	6	US-10-177-293-230	Sequence 230, App
39	313	5.0	837	5	US-09-791-537-99945	Sequence 99945, A
40	303.5	4.9	859	5	US-09-935-868-7	Sequence 7, Appl
41	308.5	4.9	951	5	US-09-935-868-9	Sequence 9, Appl
42	295.5	4.7	1078	5	US-09-791-537-21626	Sequence 21626, A
43	294.5	4.7	1078	5	US-09-791-537-120086	Sequence 120086, A
44	288.5	4.6	863	5	US-09-791-537-5078	Sequence 5078, Ap
45	284	4.5	783	5	US-09-791-537-78448	Sequence 78448, A

ALIGNMENTS

RESULT 1

US-09-791-537-95040
; Sequence 95040, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95040
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-95040

Query Match 100.0%; Score 6254; DB 5; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPNSTYDYFLLPAGLSKNTS	60
Db	1	MICQKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPNSTYDYFLLPAGLSKNTS	60
Qy	61	NGHYETAPEPKNSGTHFSNLSKTTFHCCFRSEQRNCSLCADNIEGKTFVTSNLSVF	120
Db	61	NGHYETAPEPKNSGTHFSNLSKTTFHCCFRSEQRNCSLCADNIEGKTFVTSNLSVF	120
Qy	121	QOIDANNITOCWLKGLKLFICYVESLFKNLFNRYKVVHLLYVLDEVLEDSPLVPQKS	180
Db	121	QOIDANNITOCWLKGLKLFICYVESLFKNLFNRYKVVHLLYVLDEVLEDSPLVPQKS	180
Qy	181	FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITISGGVIFQSPMLSVQPINNVKPDPP	240
Db	181	FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITISGGVIFQSPMLSVQPINNVKPDPP	240
Qy	241	LGHLMEITDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP	300
Db	241	LGHLMEITDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP	300
Qy	301	GSSYEYQVRGKRLDGPINSDNSTPRVFTTQDVIYFPFKILTSVGSNVSPHCYKKNKI	360
Db	301	GSSYEYQVRGKRLDGPINSDNSTPRVFTTQDVIYFPFKILTSVGSNVSPHCYKKNKI	360

:	TYPE: PRT
:	ORGANISM: Homo sapiens
us-09-791-537-120058	
Query Match	99.9%; Score 6246; DB 5; Length 1165;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1164; Conservative	0; Mismatches 1; Indels 0; Gaps
Qy	1 MICQKFCVLLHWEFIVITAFNLSPYIPTRWRFKLSCMPNSTDYDFLLPAGLSKNTS 60
Db	1 MICQKFCVLLHWEFIVITAFNLSPYIPTRWRFKLSCMPNSTDYDFLLPAGLSKNTS 60
Qy	61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCFCFRSEQDRNSCLCADNIETGKTFTSVTNLSLV 120
Db	61 NGHYETAVEPKFNSSGTHFSNLSKTTFHCFCFRSEQDRNSCLCADNIETGKTFTSVTNLSLV 120
Qy	121 QQIDANNIQCWLKGDLKLFICVESLFKNLFRNYNKVHLHLYVLPEVLEDSPLVPQKS 180
Db	121 QQIDANNIQCWLKGDLKLFICVESLFKNLFRNYNKVHLHLYVLPEVLEDSPLVPQKS 180
Qy	181 FQMWHCNCSEHECECLVPVPTAKLNDTLMLCKLIITSGGVIFOSPLMSVQPINMKPDPP 240
Db	181 FQMWHCNCSEHECECLVPVPTAKLNDTLMLCKLIITSGGVIFOSPLMSVQPINMKPDPP 240
Qy	241 LGLHMEITDGNLIKISWSSPPLVPFPLOYQVKYSNSTTVIRADKIIVSATSLVDSDILP 300
Db	241 LGLHMEITDGNLIKISWSSPPLVPFPLOYQVKYSNSTTVIRADKIIVSATSLVDSDILP 300
Qy	301 GSSYEVOVRKRRLDGPQIWSDWSTPRVTTQDVVIYFPFKILTSGVSNVSFHCIYKKENKI 360
Db	301 GSSYEVOVRKRRLDGPQIWSDWSTPRVTTQDVVIYFPFKILTSGVSNVSFHCIYKKENKI 360
Qy	361 VPSKEIYVMWNLAEKIPQSODYVVSDHVSKVTFFNLNETKPRGKFYTDVAYCCNEHECHH 420
Db	361 VPSKEIYVMWNLAEKIPQSODYVVSDHVSKVTFFNLNETKPRGKFYTDVAYCCNEHECHH 420
Qy	421 RYABEYYIDVNNINISCTDGYLKMTCRWSTSIQSLAESTQLRYHRSSLXCSDIPSITH 480
Db	421 RYABEYYIDVNNINISCTDGYLKMTCRWSTSIQSLAESTQLRYHRSSLXCSDIPSITH 480
Qy	481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRIHNSLGSDSPCTCVLPDSVVKPLPP 540
Db	481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRIHNSLGSDSPCTCVLPDSVVKPLPP 540
Qy	541 SSVKAETITIGLLKTIWEKPVPENNLOFIQIRYGLSGKEVOMKYEVYDAKSYSVSLPV 600
Db	541 SSVKAETITIGLLKTIWEKPVPENNLOFIQIRYGLSGKEVOMKYEVYDAKSYSVSLPV 600
Qy	601 PDLCAVTAVOVRKRRLDGLGYSWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db	601 PDLCAVTAVOVRKRRLDGLGYSWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Qy	661 TLLWKPLMKNDSLCSVORYVINNHSTSCNGTWSEDVGNNHTKFTPLWTEQAHTVTVLAINSI 720
Db	661 TLLWKPLMKNDSLCSVORYVINNHSTSCNGTWSEDVGNNHTKFTPLWTEQAHTVTVLAINSI 720
Qy	721 GASVANPNLTFSWPMKSVNTIQSLSAYPALNSSCVIVSWILSPSDYKLMFYIEWKMLNED 780
Db	721 GASVANPNLTFSWPMKSVNTIQSLSAYPALNSSCVIVSWILSPSDYKLMFYIEWKMLNED 780
Qy	781 GEIKWLRISSVKXXYYIHDHFPIPEKVQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDA 840
Db	781 GEIKWLRISSVKXXYYIHDHFPIPEKVQFSLYPIFMEGVGKPKIINSFTQDDIEKHOSDA 840
Qy	841 GLYIVIVPIIISSILLGTLLISHQRMKKLFWDENVPNKNCSWAOGLNLFQKPTFPHLFI 900
Db	841 GLYIVIVPIIISSILLGTLLISHQRMKKLFWDENVPNKNCSWAOGLNLFQKPTFPHLFI 900
Qy	901 KHTASVTCGPLLLEPETIISEDIVSDTSWKNKDEMMPTTVVSLSTTDLLEGGSVCISDQFN 960
Db	901 KHTASVTCGPLLLEPETIISEDIVSDTSWKNKDEMMPTTVVSLSTTDLLEGGSVCISDQFN 960

[illegible]

QY 961 SYNFSAEAGTEVTYEDSQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
DB 961 SYNFSAEAGTEVTYEAESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPENNDKSIYYL 1080
DB 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPENNDKSIYYL 1080
QY 1081 GVTISIKKRESGVLITDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1140
DB 1081 GVTISIKKRESGVLITDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1140
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
RESULT 3
US-09-791-537-14096
; Sequence 14096, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14096
; LENGTH: 1163
; TYPE: PRP
; ORGANISM: Macaca mulatta
US-09-791-537-14096
Query Match 95.4%; Score 5967; DB 5; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;
QY 1 MICOKFCVLLHWEFICVITAFNLSPITPWREKLSKMPNPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICOKFCVLLHWEFICVITAFNLSPITPWREKLSKMPNPNSTYDFLLPAGLSKNTSNL 60
QY 61 NGHYTEAVPEKFNSSGTHFNSLKTTHFCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYTEAVE--FNSSDTHFNSLKTTHFCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 118
QY 121 QOIDANNITOCWLKGDILKLFICYVESLFKNLFRNYKYVHLLVLPVLEDSPLVPQKS 180
DB 119 QOMGANNITOCWLKGDILKLFICYVESLFKNLFRNYKYVHLLVLPVLEDSPLVPQKS 178
QY 181 FQMVHNCNSVHECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINNVKPDPP 240
DB 179 FQMVHNCNSVHECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDCNLKSWSPPVFPFLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 300
DB 239 LGLHMEITDDCNLKSWSPPVFPFLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 298
QY 301 GSSYEVOVRKRLDGPICGWSMDSTPRVFTTQDVIYFPKPLITSVGSNVSFHCYKKNKI 360
DB 299 GSSYEVOVRKRLDGPICGWSMDSTPRVFTTQDVIYFPKPLITSVGSNVSFHCYKKNKI 358
QY 361 VPSKEIYVWNNLAEKIPQSOYDQVSVSHVSKVTFPNLNETKPRGKFTYDAYCCNEHECHH 420
DB 359 VSSKKIYVWNNLAEKIPQSOYDQVSVSHVSKVTFPNLNETKPRGKFTYDAYCCNEHECHH 418
QY 421 RYAEIYVIDVNIINISCTDGLTKMTCRWSTSTIQSLAESTLOLRHRSLSLYCSDIPSIH 480
DB 419 RYAEIYVIDVNIINISCTDGLTKMTCRWSTSTIQSLAESTLOLRHRSLSLYCSDIPSIH 478

QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVWKPLPP 540
DB 479 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVWKPLPP 538
QY 541 SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEVOMKMYEYDADAKSKSYSLPV 600
DB 539 SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEVOMKMYEYDADAKSKSYSLPV 598
QY 601 PDICAYAVQVRCRDLGLGYWNSNPNPAYTVVMDIKVPMRGPEFWIRITNGDTMKKEKNV 660
DB 599 PDICAYAVQVRCRDLGLGYWNSNPNPAYTVVMDIKVPMRGPEFWIRITNGDTMKKEKNV 658
QY 661 TLLWKPLMKNDLSCSVQRYVINHHTSCNGTWSEDVGNHRTFTFLWTEQAHTVTVLAINSI 720
DB 659 TLLWKPLMKNDLSCSVQRYVINHHTSCNGTWSEDVGNHRTFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKVNIVQSLSAVPLNSSCVIVSWILSPDYSKLMYFIIEWKNLNED 780
DB 719 GASVANFNLTFSWPMKVNIVQSLSAVPLNSSCVIVSWILSPDYSKLMYFIIEWKNLNED 778
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMVGVGKPKIINSFTODDIEKHQSDA 840
DB 779 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMVGVGKPKIINSFTODDIEKHQSDA 838
QY 841 GLYVIVPVISSSILLGLTLLISHORMKCLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 900
DB 839 GLYVIVPVISSSILLGLTLLISHORMKCLFWEDVNPKNCSWAQGLNFQKPFTEHLFI 898
QY 901 KHTASVTCGPLELLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKSGVCISDQFN 960
DB 899 KHTASVTCGPLELLEPETISEDIVSDTSWKNKDEMPTTVVSLSTTDLEKSGVCISDQFN 958
QY 961 SYNFSAEAGTEVTYEDSQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1020
DB 959 SYNFSAEAGTEVTCEDESQRPVVKYATLISNSKPSSETGEEQGLINSSVTKCFSSKNSPL 1018
QY 1021 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPENNDKSIYYL 1080
DB 1019 KDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSEGLDELLKLEGFPENNDKSIYYL 1078
QY 1081 GVTISIKKRESGVLITDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1140
DB 1079 GVTISIKKRESGVLITDKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFAS 1138
QY 1141 YMPQFQTCSTQTHKIMENKMDLTV 1165
DB 1139 YMPQFQTCSTQTHKIMENKMDLTV 1163
RESULT 4
US-09-791-537-75134
; Sequence 75134, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75134
; LENGTH: 1194
; TYPE: PRP
; ORGANISM: Macaca mulatta
US-09-791-537-75134
Query Match 95.0%; Score 5941.5; DB 5; Length 1194;
Best Local Similarity 93.1%; Pred. No. 0;

Matches 1114; Conservative 18; Mismatches 31; Indels 33; Gaps 2;

Qy 1 MICOKFCVLLHWFYIVITAFNLSYPTWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICOKFCVLLHWFYIVITAFNLSYPTWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
Qy 61 NGHETAVEPKFNSSGTHFNSLKTTHFCFRSQDRNCSLCADNIEGKTFVSVNSLVF 120
Db 61 NGHETAVE--FNSSDTHFNSLKTTHFCFRSQDRNCSLCADNIEGKTFVSVNSLVF 118
Qy 121 QOIDANNIQCWLKGLKLFICYVESLFKNLFRNYKVKHLLYVLPVEDESPVLPOKGS 180
Db 119 QOIGANNIQCWLKGLKLFICYVESLFKNLFRNYKVKHLLYVLPVEDESPVLPOKGS 178
Qy 181 FQVHCNCSVHECECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPVPLSVQPINNVKDPDP 240
Db 179 FQVHCNCSVHECECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPVPLSVQPINNVKDPDP 238
Qy 241 LGLHMEITDDGNLKSWSPPPLPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKSWSPPPLPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 298
Qy 301 GSSYEVOVRKRLDGPICGWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
Db 299 GSSYEVOVRKRLDGPICGWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 358
Qy 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIYVWNNLAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 418
Qy 421 RYAEIYVIVDNNINISCTDGYLTWKTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIH 480
Db 419 RYAEIYVIVDNNINISCTDGYLTWKTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIH 478
Qy 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKPLPP 538
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEQVQWKEVYDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEQVQWKEVYDAKSKSVSLPV 598
Qy 601 PDLCAVAVQVRCRDLGLGWSNWSNPATVVMIDKVPMPGPEFRIINGDTMKKEKNV 660
Db 599 PDLCAVAVQVRCRDLGLGWSNWSNPATVVMIDKVPMPGPEFRIINGDTMKKEKNV 658
Qy 661 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTWSDEVDGHTKFTPLWTEQAHVTVVLANSI 720
Db 659 TLLMKPLMKNDLSLCSVQRYVINHTSCNGTWSDEVDGHTKFTPLWTEQAHVTVVLANSI 718
Qy 721 GASVANFLTFSPMKSQVNIQSLSAYPLNSCIVSVILSPSDYKLMYFIIENKLNED 780
Db 719 GASVANFLTFSPMKSQVNIQSLSAYPLNSCIVSVILSPSDYKLMYFIIENKLNED 778
Qy 781 GEIKWLRISSVKYIYTHDPIEYKQFSLPIFPMGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 GEIKWLRISSVKYIYTHDPIEYKQFSLPIFPMGVGKPKIINSFTQDDIEKHQSDA 838
Qy 841 GLYIVVPVILSSSTLLGTLTLLSHORMKLFWEVDPNPKNSAQGLNFQK----- 891
Db 839 GLYIVVPVILSSSTLLGTLTLLSHORMKLFWEVDPNPKNSAQGLNFQKIRFVMLPR 898
Qy 892 -----PETFHELFKHTASVTCGPFLLLEPETISEDIVSDTSWK 929
Db 899 LVLSNQAOVIHPPRPKVLQEPETFHELFKHTASVTCGPFLLLEPETISEDIVSDTSWK 958
Qy 930 NKDEMPPTVYVLSLSTTDLEKGSVCISDQNSVNFSAEGTEVTEYDESORQPVKYATL 989
Db 959 NKDEMPPTVYVLSLSTTDLEKGSVCISDQNSVNFSAEGTEVTEYDESORQPVKYATL 1018
Qy 990 ISNSKPSGTGEQGLINSSVTKCFSSKNSPLKDSFNSNWEIEAQAFILLSDQHPNLIIS 1049
Db 1019 ISNSKPSGTGEQGLINSSVTKCFSSKNSPLKDSFNSNWEIEAQAFILLSDQHPNLIIS 1078

Qy 1050 HLTFSEGLDELLKLEGNFPENNDKSIYYLGVTSIKKRESGVLLTOKSRVSCFPAPCL 1109
Db 1079 HLTFSEGLDELLKLEGNFPENNDKSIYYLGVTSIKKRESGVLLTOKSRVSCFPAPCL 1138
Qy 1110 FTDIRVLQDSCSHFVENNINLGTSSKKTFFASYMPQFQCTQTQTHKIMENKMDLTV 1165
Db 1139 FTDIRVLQDSCSHFVENNINLGTSSKKTFFASYMPQFQCTQTQTHKIMENKMDLTV 1194
RESULT 5
US-09-791-537-95039
; Sequence 95039, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95039
; LENGTH: 958
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-95039

Query Match 77.3%; Score 4831.5; DB 5; Length 958;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps 3;

Qy 1 MICOKFCVLLHWFYIVITAFNLSYPTWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICOKFCVLLHWFYIVITAFNLSYPTWRFKLSKMPNSTYDYFLLPAGLSKNTSNS 60
Qy 61 NGHETAVEPKFNSSGTHFNSLKTTHFCFRSQDRNCSLCADNIEGKTFVSVNSLVF 120
Db 61 NGHETAVEPKFNSSGTHFNSLKTTHFCFRSQDRNCSLCADNIEGKTFVSVNSLVF 120
Qy 121 QOIDANNIQCWLKGLKLFICYVESLFKNLFRNYKVKHLLYVLPVEDESPVLPOKGS 180
Db 121 QOIDANNIQCWLKGLKLFICYVESLFKNLFRNYKVKHLLYVLPVEDESPVLPOKGS 180
Qy 181 FQVHCNCSVHECECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPVPLSVQPINNVKDPDP 240
Db 181 FQVHCNCSVHECECECLVPVPTAKLNDTLLMCLKITSGGVIFQSPVPLSVQPINNVKDPDP 240
Qy 241 LGLHMEITDDGNLKSWSPPPLPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKSWSPPPLPFPLOYQVYKSENSTTVIREADKIVSATSLLVDSILP 300
Qy 301 GSSYEVOVRKRLDGPICGWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEVOVRKRLDGPICGWSDMSTPRVFTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
Qy 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFPNLNETKPRGKFTYDAVYCCNEHECHH 420
Qy 421 RYAEIYVIVDNNINISCTDGYLTWKTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVIVDNNINISCTDGYLTWKTCRWSTSTIQSLAESTLQRYHRSSLYCSDIPSIIH 480
Qy 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEQVQWKEVYDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEQVQWKEVYDAKSKSVSLPV 598

Dbb 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRKRLDGLGYWNSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Dbb 601 PDLCAVAVQVRKRLDGLGYWNSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKKPLMKNDLSVCVORYVINHHITSCNGTWSDEVDGNHKTFTLWTEQAHTVTVLAINSI 720
Dbb 661 TLLWKKPLMKNDLSVCVORYVINHHITSCNGTWSDEVDGNHKTFTLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Dbb 721 GASVANFNLTFSWPMKSNIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMGEVQKPKIINSFTQDDIEKHQSDA 840
Dbb 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMGEVQKPKIINSFTQDDIEKHQSDA 840
QY 841 GLXVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK-----PE 893
Dbb 841 GLXVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK-----PE 893
QY 894 TFEHLFIKHT-ASVTCGP-----LILEPETISEDISVDTSWKNKDE 933
Dbb 901 SHHSLISSTQGHKHCGRQGPGLHRKTRDLCSLVYLLTLPPLLSYDPAKSPSVNTQOE 958

RESULT 6

US-09-791-537-95038
; Sequence 95038, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95038
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-95038

Query Match 77.2%; Score 4826; DB 5; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTSNS 60
Dbb 1 MICQKFCVLLHWEFIVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSLVF 120
Dbb 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANNIQCWLKGDILKFCVYVESLFLKFNRYNKHVLLVYLPVLEDSPLVPQKGS 180
Dbb 121 QQIDANNIQCWLKGDILKFCVYVESLFLKFNRYNKHVLLVYLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSHECCCLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMSVQPINNVKPDPP 240
Dbb 181 FQMVHCNCSHECCCLVPPVPTAKLNDTLMLCKLITSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMEITDGNLKIWSHSSPPLVPPFLOQYQVKYSENSTTVIREADKIVSATSLVDSILP 300
Dbb 241 LGLHMEITDGNLKIWSHSSPPLVPPFLOQYQVKYSENSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRKRLDGLGPGIWSDNSTPRVFTTQDVIYPPPKILTSVGSNVSFHCYKKNKI 360

Dbb 301 GSSYEVOVRKRLDGLGPGIWSDNSTPRVFTTQDVIYPPPKILTSVGSNVSFHCYKKNKI 360
QY 361 VPSKEIYVWMNLAEKIPQSQDYDVSVSHVSKTFEFLNLMETPRGKFTYDAYCYCNEHECHH 420
Dbb 361 VPSKEIYVWMNLAEKIPQSQDYDVSVSHVSKTFEFLNLMETPRGKFTYDAYCYCNEHECHH 420
QY 421 RYAEIYVIVDYNINISCTDGYLTKMTCRWSTSIQSLAESTLOLRHRSLSLYSDPSIH 480
Dbb 421 RYAEIYVIVDYNINISCTDGYLTKMTCRWSTSIQSLAESTLOLRHRSLSLYSDPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540
Dbb 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
Dbb 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRKRLDGLGYWNSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Dbb 601 PDLCAVAVQVRKRLDGLGYWNSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKKPLMKNDLSVCVORYVINHHITSCNGTWSDEVDGNHKTFTLWTEQAHTVTVLAINSI 720
Dbb 661 TLLWKKPLMKNDLSVCVORYVINHHITSCNGTWSDEVDGNHKTFTLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Dbb 721 GASVANFNLTFSWPMKSNIVQSLSAIPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMGEVQKPKIINSFTQDDIEKHQSDA 840
Dbb 781 GEIKWLRISSVKKYYIHDHFIPIEKYQSLYPIFMGEVQKPKIINSFTQDDIEKHQSDA 840
QY 841 GLXVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK 891
Dbb 841 GLXVIVPVISSSILLGLTLLISHQRMKKLFWEDVNPKNCSWAQGLNFQK 891

RESULT 7

US-09-791-537-114050
; Sequence 114050, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114050
; LENGTH: 958
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-114050

Query Match 77.1%; Score 4819.5; DB 5; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;
QY 1 MICQKFCVLLHWEFIVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTSNS 60
Dbb 1 MICQKFCVLLHWEFIVITAFNLSPITPWRFKLSCMPNPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSLVF 120
Dbb 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSLVF 120

QY 121 QQDANNNIOCWLGKDLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQDANNNIOCWLGKDLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 181 FQMVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVQKYSNSTTVIREADKIYSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVQKYSNSTTVIREADKIYSATSLLVDSILP 300
QY 301 GSSYEVOVQVGRKLDGPGIWSDMSTPRVFTTQDVYIPPPKILTSVGSNVSPHCYKKNKI 360
Db 301 GSSYEVOVQVGRKLDGPGIWSDMSTPRVFTTQDVYIPPPKILTSVGSNVSPHCYKKNKI 360
QY 361 VPSKEIIVMMNLAEPKIQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDVCNEHECHH 420
Db 361 VPSKEIIVMMNLAEPKIQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDVCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIPQIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIPQIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQMKVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQMKVEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPMLKNDSCSVQRYVINHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPMLKNDSCSVQRYVINHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWAQGLNFQK-----PE 893
Db 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWAQGLNFQKMLEGSMFVK 900
QY 894 TFEHLFTKHT-ASVTCGP-----LLLLPETISEDISVDTSWKNKDE 933
Db 901 SHHSLISSTQGHKHCGRPOGPHRKTRDCLSLVLLTLPPLLSYDPAKSPSVRNTOE 958

RESULT 8
US-09-791-537-114052
; Sequence 114052, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 114052
; LENGTH: 906

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-114052

Query Match 77.0%; Score 4816; DB 5; Length 906;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 892; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 MICQKFCVLLHWEFTYVITAENLSYPITPWRFKLSMPNPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFTYVITAENLSYPITPWRFKLSMPNPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAVERPKFNSGTHFSNLKTTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHYETAVERPKFNSGTHFSNLKTTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQDANNNIOCWLGKDLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQDANNNIOCWLGKDLKLFICYVESLFKNLFRNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 181 FQMVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVQKYSNSTTVIREADKIYSATSLLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSSSPPLVPFPLOYQVQKYSNSTTVIREADKIYSATSLLVDSILP 300
QY 301 GSSYEVOVQVGRKLDGPGIWSDMSTPRVFTTQDVYIPPPKILTSVGSNVSPHCYKKNKI 360
Db 301 GSSYEVOVQVGRKLDGPGIWSDMSTPRVFTTQDVYIPPPKILTSVGSNVSPHCYKKNKI 360
QY 361 VPSKEIIVMMNLAEPKIQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDVCNEHECHH 420
Db 361 VPSKEIIVMMNLAEPKIQSOYDVVSDHVSQVTFEFLNETKPRGKFTYDVCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTAKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIPQIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIPQIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQMKVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLTKISWEKVPENNLOFOIRYGLSGKEVQMKVEYDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPMLKNDSCSVQRYVINHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPMLKNDSCSVQRYVINHHTSCNGTWSEDVGNHKTFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAAYPLNSSCVIVSWILSPSDYKLMYFIEWKNNLNE 780
QY 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHQSDA 840
QY 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWAQGLNFQK--PETFEHL 898
Db 841 GLYVIVPVIISSSILLGLTLLISHQRMKKLFWEDEVNPNKNCWAQGLNFQKMPGTKELL 900

RESULT 9
US-09-791-537-114053
; Sequence 114053, Application US/09791537

; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114053
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-114053

Query Match 77.0%; Score 4814; DB 5; Length 896;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 888; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFYVITAFNLSPYIPWRFKLSMPNSTDYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFYVITAFNLSPYIPWRFKLSMPNSTDYDFLLPAGLSKNTS 60
QY 61 NGHETAVPEKFNSSGTHFSNLKSTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVPEKFNSSGTHFSNLKSTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANWNTQCKLGDGLKFCYVESLFKNLFRNRYKVHLLVYLVEVLEDSPLVPQKGS 180
Db 121 QOIDANWNTQCKLGDGLKFCYVESLFKNLFRNRYKVHLLVYLVEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMSVQPINMVKPDP 240
Db 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKIWSGSPPLVPFPLOQVYKSENSTTVIREADKIVSATSLLDVSI 300
Db 241 LGLHMEITDDGNLKIWSGSPPLVPFPLOQVYKSENSTTVIREADKIVSATSLLDVSI 300
QY 301 GSSYEQVQGRKLDGPGIWSNDSSTPRVFTQDVYIPPKILTSGVSNVSHFCHYKKNKI 360
Db 301 GSSYEQVQGRKLDGPGIWSNDSSTPRVFTQDVYIPPKILTSGVSNVSHFCHYKKNKI 360
QY 361 VPSKEIYVWNNLAETIPQSOYDVSVDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHCH 420
Db 361 VPSKEIYVWNNLAETIPQSOYDVSVDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHCH 420
QY 421 RYAELVVIDVNNISCTDGYLTQVYKSENSTTVIREADKIVSATSLLDVSI 480
Db 421 RYAELVVIDVNNISCTDGYLTQVYKSENSTTVIREADKIVSATSLLDVSI 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCVLPDSVVKPL 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCVLPDSVVKPL 540
QY 541 SSVKAEITINIGLLKISWEPKPPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEPKPPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCKRLDGLGYNSNWPAYTVVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
Db 601 PDLCAVAVQVRCKRLDGLGYNSNWPAYTVVMDIKVPMRGPEFWRILNGDTMKKEKNV 660
QY 661 TLWPKMLKNDLSLCSVQRYVINHTSCNGTWSVDGNHTKFTPLWTEQAHTVTVLAINSI 720
Db 661 TLWPKMLKNDLSLCSVQRYVINHTSCNGTWSVDGNHTKFTPLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVQVSLASAYPLNSSCVIYSWILSPSDYKLMFYIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVQVSLASAYPLNSSCVIYSWILSPSDYKLMFYIEWKNLNED 780

QY 781 GEIKWLRISSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKKYYIHDHFPIPIEKYQFSLYPIFMGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVLISSILLGLTLLSHQMKKLFWEDEVNPNKNCWQAQGLNFK 891
Db 841 GLYVIVPVLISSILLGLTLLSHQMKKLFWEDEVNPNKNCWQAQGLNFK 891
RESULT 10
US-09-791-537-128089
; Sequence 128089, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128089
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-128089

Query Match 76.5%; Score 4786.5; DB 5; Length 1162;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 882; Conservative 119; Mismatches 160; Indels 5; Gaps 5;
QY 1 MICQKFCVLLHWEFYVITAFNLSPYIPWRFKLSMPNSTDYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFYVITAFNLSPYIPWRFKLSMPNSTDYDFLLPAGLSKNTS 60
QY 61 NGHETAVPEKFNSSGTHFSNLKSTFHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFGEQNGCSALTGTGTEGKTLASVWKPLV 120
QY 121 QOIDANWNTQCKLGDGLKFCYVESLFKNLFRNRYKVHLLVYLVEVLEDSPLVPQKGS 180
Db 121 RQLGVNNDIECMWKGDLTFLFICHEPMLLPKNPKNDYKSVHLLYDLDEVLDLPLPKDS 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPMSVQPINMVKPDP 240
Db 181 FQTVQCNCSVRE-CECHVPVPRAKVYALLMYLEITSAGVSFQSPMSLQPLMVKPDP 239
QY 241 LGLHMEITDDGNLKIWSGSPPLVPFPLOQVYKSENSTTVIREADKIVSATSLLDVSI 300
Db 240 LGLHMEITDDGNLKIWSGSPPLVPFPLOQVYKLEN-TIVREAAEIVSDTSLLDVSI 298
QY 301 GSSYEQVQGRKLDGPGIWSNDSSTPRVFTQDVYIPPKILTSGVSNVSHFCHYKKNKI 360
Db 299 GSSYEQVQGRKLDGPGIWSNDSSTPRVFTQDVYIPPKILTSGVSNVSHFCHYKKNKI 358
QY 361 VPSKEIYVWNNLAETIPQSOYDVSVDHVSQVTFNLTNETKPRGKFTYDAVYCCNEHCH 420
Db 359 ISSKQIYVWNNLAETIPQYNTVSDHISKVTFNLTNETKPRGKFTYDAVYCCNEHCH 418
QY 421 RYAELVVIDVNNISCTDGYLTQVYKSENSTTVIREADKIVSATSLLDVSI 480
Db 419 RYAELVVIDVNNISCTDGYLTQVYKSENSTTVIREADKIVSATSLLDVSI 478
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCVLPDSVVKPL 540
Db 479 PISEPKDCYLOSDGFYECIFQPIFLLSGTYMIRINHSLSGLSDSPPTCVLPDSVVKPL 538
QY 541 SSVKAEITINIGLLKISWEPKPPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEPKPPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600

Db 539 SNNKAEITINTGLLKYSWEKVPENNLOFQIRYGLNGKEIQWKTHEVFDKSKSASLPV 598
QY 601 POLCAVAVQVRCKRDLGGLGYSNWNPNAYTVVMDIKVPMRGPEFRIINGDTMKKEKNV 660
Db 599 SDCAVYVQVRCKRDLGGLGYSNWNPNAYTVVMDIKVPMRGPEFRIINGDTMKKEKNV 658
QY 661 TLLWPKPLMKNDLSLCSVQRYVYINHHTSCNGTWSBDVGNHKTFTFLMTEQAHTVTVLAINSI 720
Db 659 TLLWPKPLMKNDLSLCSVQRYVYINHHTSCNGTWSBDVGNHKTFTFLMTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIVSWILSPDSYKLMYFIEWKLNED 780
Db 719 GASLVNFNLTFSWPMKSNIVQSLAYPLNSSCVIVSWILSPDSYKLMYFIEWKLNED 778
QY 781 GEIKWLRISSVKKYIYHDFPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRISSVKKYIYHDFPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHQSDA 838
QY 841 GLYVIVPVIISSSVLLGLTLLSHQRMKLFWDVDPNPKNCWAQGLNFQKPTFELHFI 900
Db 839 GLYVIVPVIISSSVLLGLTLLSHQRMKLFWDVDPNPKNCWAQGLNFQKPTFELHFI 898
QY 901 KHTASVTCGPLLLEPETISEDVSVDTSWKNKDEMPFTTVVLSLSTT-DLEKGSVCISDOF 959
Db 899 KHAESVIFGPLLLEPETISEDVSVDTSWKNKDEMPFTTVVLSLSTT-DLEKGSVCISDOF 958
QY 960 NSVNFSEAGTEVTVYDESDQRPVYKATLINSKPSKSETGEQGLINSVTKCFSSKNSP 1019
Db 959 NSANFSGAOSTGTCDEQCQSPSVKATLVSNVKTETDEEQGAIHSSVQSCIAKHKSP 1018
QY 1020 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSBGLDELKLEGNFPENNNDKKSIIY 1079
Db 1019 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSBGLDELKLEGNFPENNNDKKSIIY 1077
QY 1080 LGVTSIKKRESGVLLTDRKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFA 1139
Db 1078 LGVSSGNKRENDMLLTDEAGVLCPPAHCLFSDIRILQSCSHFVENNINLGTSK-KNEV 1136
QY 1140 SYMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1137 PYMPQFOTCSTQTHKIMENKMDLTV 1162

RESULT 11
US-09-791-537-57257
; Sequence 57257, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dancer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57257
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-57257

Query Match 76.4%; Score 4778.5; DB 5; Length 1162;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 881; Conservative 118; Mismatches 162; Indels 5; Gaps 5;

QY 1 MTCQKFCVLLHWEFYVITAFNLSYPIPTWRFKLSMCPNPNYDYFLLPAGLSKNTS 60
1 MTCQKFCVLLHWEFYVITAFNLSYPIPTWRFKLSMCPNPNYDYFLLPAGLSKNTS 60
Db 1 MTCQKFCVLLHWEFYVITAFNLSYPIPTWRFKLSMCPNPNYDYFLLPAGLSKNTS 60
QY 61 NGHYETAPEKPNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 120

Db 61 KGASEALVEAKFNSTGIYVSELSKTIHFHCCFQNEQONCSALTNGTEGKTLASVWKPLVF 120
QY 121 QOILDANNIQCWLKGLDKLFCVVESELEKFNLPNNYKVKHLLVYLPEVLEDSPLVPKQGS 180
Db 121 RQJGVNWDIECWNKGLDTLFIHMEPLLNKPNFYKNDYKSKVHLLDDEVLDDPLPLPKUS 180
QY 181 FQMVHCNCSVHBCCECLVPVPTAKLNDTLLMCLKITSGGVIFQSPLMSVQPINMKVPDP 240
Db 181 FQVQCNCVSRE-CECHVFPVPRAKVNYALLMYLEITSAGVSFQSPLMSLQPLMLVKVPDP 239
QY 241 LGHMEITDGNLKIWSVSPPLVPFPLOYQVYKSENNSTTVIREADKIVSATSLLVDSILP 300
Db 240 LGLRMEVTDGNLKIWSVSPPLVPFPLOYQVYKSENNSTTVIREADKIVSATSLLVDSILP 298
QY 301 GSSYEVOVQGRKLDGPGIWSNDSTPRVFTTODVIEPPPKILTSVGSNVSHFCHIKKENKI 360
Db 299 GSSYEVOVQGRKLDGPGIWSNDSTPRVFTTODVIEPPPKILTSVGSNVSHFCHIKKENKI 358
QY 361 VPSKEIYVWNNLAETIPOSQYDVVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECH 420
Db 359 ISKQIYVWNNLAETIPOSQYDVVSDHVSQVTFNFNLNETKPRGKFTYDAVYCCNEHECH 418
QY 421 RYAEIYVIVNINISCTDGYLTMTKTCRWSSTSTIOSLAESTLQLRVHRSLSYCSIDPSIH 480
Db 419 RYAEIYVIVNINISCTDGYLTMTKTCRWSSTSTIOSLAESTLQLRVHRSLSYCSIDPSIH 478
QY 481 PISEPKDCYQSDGFEVCFQFIEFLLSGYTMIRINHSLGSLDSDPPTCVLPDSVWKPLPP 540
Db 479 PISEPKDCYQSDGFEVCFQFIEFLLSGYTMIRINHSLGSLDSDPPTCVLPDSVWKPLPP 538
QY 541 SSVKABITINIGILLKTSWEKVPENNLOFQIRYGLNGKEIQWKTHEVFDKSKSASLPV 600
Db 539 SSVKABITINIGILLKTSWEKVPENNLOFQIRYGLNGKEIQWKTHEVFDKSKSASLPV 598
QY 601 PDLCAVAVQVRCKRDLGGLGYSNWNPNAYTVVMDIKVPMRGPEFRIINGDTMKKEKNV 660
Db 599 SDCAVYVQVRCKRDLGGLGYSNWNPNAYTVVMDIKVPMRGPEFRIINGDTMKKEKNV 658
QY 661 TLLWPKPLMKNDLSLCSVQRYVYINHHTSCNGTWSBDVGNHKTFTFLMTEQAHTVTVLAINSI 720
Db 659 TLLWPKPLMKNDLSLCSVQRYVYINHHTSCNGTWSBDVGNHKTFTFLMTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNIVQSLAYPLNSSCVIVSWILSPDSYKLMYFIEWKLNED 780
Db 719 GASLVNFNLTFSWPMKSNIVQSLAYPLNSSCVIVSWILSPDSYKLMYFIEWKLNED 778
QY 781 GEIKWLRISSVKKYIYHDFPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 779 DGMKWLRISSVKKYIYHDFPIEKYQFSLYPFMEGVGKPKIINSFTQDDIEKHQSDA 838
QY 841 GLYVIVPVIISSSVLLGLTLLSHQRMKLFWDVDPNPKNCWAQGLNFQKPTFELHFI 900
Db 839 GLYVIVPVIISSSVLLGLTLLSHQRMKLFWDVDPNPKNCWAQGLNFQKPTFELHFI 898
QY 901 KHTASVTCGPLLLEPETISEDVSVDTSWKNKDEMPFTTVVLSLSTT-DLEKGSVCISDOF 959
Db 899 KHAESVIFGPLLLEPETISEDVSVDTSWKNKDEMPFTTVVLSLSTT-DLEKGSVCISDOF 958
QY 960 NSVNFSEAGTEVTVYDESDQRPVYKATLINSKPSKSETGEQGLINSVTKCFSSKNSP 1019
Db 959 NSANFSGAOSTGTCDEQCQSPSVKATLVSNVKTETDEEQGAIHSSVQSCIAKHKSP 1018
QY 1020 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSBGLDELKLEGNFPENNNDKKSIIY 1079
Db 1019 LKDSFSSNSWEIEAQAFFILSDQHPNIIISPHLTFSBGLDELKLEGNFPENNNDKKSIIY 1077
QY 1080 LGVTSIKKRESGVLLTDRKSRVSCPPAPCLFTDIRVLQDSCSHFVENNINLGTSKKTFA 1139
Db 1078 LGVSSGNKRENDMLLTDEAGVLCPPAHCLFSDIRILQSCSHFVENNINLGTSK-KNEV 1136
QY 1140 SYMPQFOTCSTQTHKIMENKMDLTV 1165
Db 1137 PYMPQFOTCSTQTHKIMENKMDLTV 1162

Db 1137 PYMPQFQSCSTSHKIIENKMCIDLTV 1162

RESULT 12

US-09-791-537-65061

; Sequence 65061, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791.537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 65061

; LENGTH: 1162

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-791-537-65061

Query Match 76.2%; Score 4766.5; DB 5; Length 1162;

Best Local Similarity 75.4%; Pred. No. 0;

Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

Qy 1 MICQFCVYVLLHWEFYVITAFNLSYPTPMRFKLSCHMPNSTYDYFLPAGLSKNTS 60

Db 1 MMCQFYVYVLLHWEFLYVIAALNLAYIPSPWKEFLFCGPPNTTDDSFSPAGAPNNASAL 60

Qy 61 NGHYETAVEPKFNSTGTHFSNLKTTFFHCCRSERSEODRNCSLCADNIEGKTFVSTVNSLVF 120

Db 61 KGASAIVEAKFNSSGIVYVPELSKTFVHCCFNEQGNCSALTDTNTEGKTLASVYKASVF 120

Qy 121 QOIDANNWIOCKLGDGLKFLICYVESLFKFNRYNYKVHLLYVLPVEYDLSPLVPQKGS 180

Db 121 RQLGVNWDIECKMGDLTLFICHMEPLPKNPKNYDSKVHLLYDLPEVIDDSPLPLKDS 180

Qy 181 FQVHCNCSVHECCCLVPVPTAKLNDLLMCKLTSGGVIFQSPMSVQPINMYKPPDP 240

Db 181 FQVHCNCSVHECCCLVPVPTAKLNDLLMCKLTSGGVIFQSPMSVQPINMYKPPDP 240

Qy 241 LGLHMEITDDGNLKSWSPLVPPLOQYQYKYSNSTVITREADKIYSATSLVDSILP 300

Db 241 LGLHMEITDDGNLKSWSPLVPPLOQYQYKYSNSTVITREADKIYSATSLVDSILP 300

Qy 301 GSSYEVQVGRKLDGPGTWSWSTPRVFTTODVYFPPKILTSVGSNYSFHCYKKNKI 360

Db 301 GSSYEVQVGRKLDGPGTWSWSTPRVFTTODVYFPPKILTSVGSNYSFHCYKKNKI 360

Qy 361 VPSKEIVWMNLAEKIPQSDYDVSVDHYSKYVTFNNLNETKPRGFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSVDHYSKYVTFNNLNETKPRGFTYDAVYCCNEHCCH 420

Qy 421 RYAEIYVIVDWINISCTEDGYLTMTCTCRWSTSTQSLAESTLQLRHRSLSYCSIPS 480

Db 421 RYAEIYVIVDWINISCTEDGYLTMTCTCRWSTSTQSLAESTLQLRHRSLSYCSIPS 480

Qy 481 PISEPKDCYLOSDGFEYICFOPIFLLSGYTWIRLNHLSGLSDSPPTCVLPDVSVPKPLPP 540

Db 481 PISEPKDCYLOSDGFEYICFOPIFLLSGYTWIRLNHLSGLSDSPPTCVLPDVSVPKPLPP 540

Qy 541 SSVKAEITINTIGLLKISWEKVPFPENNLFQFIRYGLSKEVQWKMYEYDAKSKSVSLPV 600

Db 541 SSVKAEITINTIGLLKISWEKVPFPENNLFQFIRYGLSKEVQWKMYEYDAKSKSVSLPV 600

Qy 601 PDLCAVAVQVRCRKLGLGWTWNSNPAFTVYVMDIKVPMRGPEFWRIINGDTMKKKNV 660

Db 601 PDLCAVAVQVRCRKLGLGWTWNSNPAFTVYVMDIKVPMRGPEFWRIINGDTMKKKNV 660

Qy 661 TLLWKPMLKNDLSLCSQYRVVINHHTSCNGTWSDEGVNHTKFTFLWTEQAHTVTVLA 720

Db 659 TLLWKPMLKNDLSLCSQYRVVINHHTSCNGTWSDEGVNHTKFTFLWTEQAHTVTVLA 718

Qy 721 GASVANFNLTFSWPMKSNVYVITAFNLSYPTPMRFKLSCHMPNSTYDYFLPAGLSKNTS 780

Db 721 GASVANFNLTFSWPMKSNVYVITAFNLSYPTPMRFKLSCHMPNSTYDYFLPAGLSKNTS 780

Qy 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIWEGVGRKPIINFTQDDIEKHQSDA 840

Db 781 GEIKWLRISSSVKYYIHDHFIPIEKYQFSLYPIWEGVGRKPIINFTQDDIEKHQSDA 840

Qy 841 GLYVIVPIVLISSILLGTLISHORMKFLPWEDVPNPKNCMAOGLNAPKQKPTETHEHLFI 900

Db 841 GLYVIVPIVLISSILLGTLISHORMKFLPWEDVPNPKNCMAOGLNAPKQKPTETHEHLFI 900

Qy 901 KHTASVTCGPLEPETISEDISVDTSMKNKDNEMPTTVVYSLTST-DLEKSGVCSIDQF 959

Db 901 KHTASVTCGPLEPETISEDISVDTSMKNKDNEMPTTVVYSLTST-DLEKSGVCSIDQF 959

Qy 959 NSVNFSEAEAGTEVYDESEORQPFVKYATLINSKPSETGEOGLINSVTKCFSKNSP 1019

Db 959 NSVNFSEAEAGTEVYDESEORQPFVKYATLINSKPSETGEOGLINSVTKCFSKNSP 1019

Qy 1019 LRQSFSSSWETEATQFPFLSDQPTMTISPOLSPS-GLDELLELGSFPPEENHREKSVCY 1077

Db 1019 LRQSFSSSWETEATQFPFLSDQPTMTISPOLSPS-GLDELLELGSFPPEENHREKSVCY 1077

Qy 1078 LGVTSIKKRESGVLLTDSRVSCPPAPCLFTDIRVLODSCSHFVENNINLTGTSKKTFA 1139

Db 1078 LGVTSIKKRESGVLLTDSRVSCPPAPCLFTDIRVLODSCSHFVENNINLTGTSKKTFA 1139

Qy 1139 LGVTSIKKRESGVLLTDSRVSCPPAPCLFTDIRVLODSCSHFVENNINLTGTSKKTFA 1139

Db 1139 LGVTSIKKRESGVLLTDSRVSCPPAPCLFTDIRVLODSCSHFVENNINLTGTSKKTFA 1139

Qy 1140 SYMPOFQTCSTOHTKIMENKMCIDLTV 1165

Db 1140 SYMPOFQTCSTOHTKIMENKMCIDLTV 1165

Qy 1165 SYMPOFQTCSTOHTKIMENKMCIDLTV 1165

Db 1165 SYMPOFQTCSTOHTKIMENKMCIDLTV 1165

RESULT 13

US-09-791-537-26913

; Sequence 26913, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791.537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 26913

; LENGTH: 1174

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-791-537-26913

Query Match 76.2%; Score 4766.5; DB 5; Length 1174;

Best Local Similarity 75.4%; Pred. No. 0;

Matches 879; Conservative 115; Mismatches 167; Indels 5; Gaps 5;

Qy 1 MICQFCVYVLLHWEFYVITAFNLSYPTPMRFKLSCHMPNSTYDYFLPAGLSKNTS 60

Db 1 MMCQFYVYVLLHWEFLYVIAALNLAYIPSPWKEFLFCGPPNTTDDSFSPAGAPNNASAL 60

Qy 61 NGHYETAVEPKFNSTGTHFSNLKTTFFHCCRSERSEODRNCSLCADNIEGKTFVSTVNSLVF 120

Db 61 KGASAIVEAKFNSSGIVYVPELSKTFVHCCFNEQGNCSALTDTNTEGKTLASVYKASVF 120

Qy 121 QOIDANNWIOCKLGDGLKFLICYVESLFKFNRYNYKVHLLYVLPVEYDLSPLVPQKGS 180

Db 121 RQLGVNWDIECKMGDLTLFICHMEPLPKNPKNYDSKVHLLYDLPEVIDDSPLPLKDS 180

Qy 181 FQVHCNCSVHECCCLVPVPTAKLNDLLMCKLTSGGVIFQSPMSVQPINMYKPPDP 240

Db 181 FQVHCNCSVHECCCLVPVPTAKLNDLLMCKLTSGGVIFQSPMSVQPINMYKPPDP 240

Qy 241 LGLHMEITDDGNLKSWSPLVPPLOQYQYKYSNSTVITREADKIYSATSLVDSILP 300

Db 241 LGLHMEITDDGNLKSWSPLVPPLOQYQYKYSNSTVITREADKIYSATSLVDSILP 300

Qy 301 GSSYEVQVGRKLDGPGTWSWSTPRVFTTODVYFPPKILTSVGSNYSFHCYKKNKI 360

Db 301 GSSYEVQVGRKLDGPGTWSWSTPRVFTTODVYFPPKILTSVGSNYSFHCYKKNKI 360

Qy 361 VPSKEIVWMNLAEKIPQSDYDVSVDHYSKYVTFNNLNETKPRGFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSVDHYSKYVTFNNLNETKPRGFTYDAVYCCNEHCCH 420

Qy 421 RYAEIYVIVDWINISCTEDGYLTMTCTCRWSTSTQSLAESTLQLRHRSLSYCSIPS 480

Db 421 RYAEIYVIVDWINISCTEDGYLTMTCTCRWSTSTQSLAESTLQLRHRSLSYCSIPS 480

Qy 481 PISEPKDCYLOSDGFEYICFOPIFLLSGYTWIRLNHLSGLSDSPPTCVLPDVSVPKPLPP 540

Db 481 PISEPKDCYLOSDGFEYICFOPIFLLSGYTWIRLNHLSGLSDSPPTCVLPDVSVPKPLPP 540

Qy 541 SSVKAEITINTIGLLKISWEKVPFPENNLFQFIRYGLSKEVQWKMYEYDAKSKSVSLPV 600

Db 541 SSVKAEITINTIGLLKISWEKVPFPENNLFQFIRYGLSKEVQWKMYEYDAKSKSVSLPV 600

Qy 601 PDLCAVAVQVRCRKLGLGWTWNSNPAFTVYVMDIKVPMRGPEFWRIINGDTMKKKNV 660

Db 601 PDLCAVAVQVRCRKLGLGWTWNSNPAFTVYVMDIKVPMRGPEFWRIINGDTMKKKNV 660

Qy 661 TLLWKPMLKNDLSLCSQYRVVINHHTSCNGTWSDEGVNHTKFTFLWTEQAHTVTVLA 720

Qy 181 FQWVHCNGSVHCCBCLVPVPTAKNDTLMLCKLITSGVIFQSPMLSVQPINMVKPDP 240
Db 181 FQWVHCNGSVHCCBCLVPVPTAKNDTLMLCKLITSGVIFQSPMLSVQPINMVKPDP 239
Qy 241 LGLHMEITDDGNLKTISWSPPPLVPPLOQVQVYKNSNTTVIREADKIYVATSLLVDSILP 300
Db 240 LGLHMEITDDGNLKTISWSPPPLVPPLOQVQVYKNSNTTVIREADKIYVATSLLVDSILP 298
Qy 301 GSSVEVQVGRKLDGPGIWSDMSTPRVFTQDVVIFPPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSVEVQVGRKLDGPGIWSDMSTPRVFTQDVVIFPPKILTSVGSNVSFHCIIYKKNKI 358
Qy 361 VPSKEIVVMNLAERKIPQSDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 ISSKQIIVWNRNLAEKIPQSDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 418
Qy 421 RYAEILYVIVDNNINISCEFDGYLTMTKCRWSTSTIOSLAESTLQLRHRSLLYCSIPSIH 480
Db 419 RYAEILYVIVDNNINISCEFDGYLTMTKCRWSTSTIOSLAESTLQLRHRSLLYCSIPSIH 478
Qy 481 PISEPKDCVLOSDGPFYECIFQIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCVLOSDGPFYECIFQIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 538
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQVMKYEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQVMKYEYVDAKSKSVSLPV 598
Qy 601 PDLCAVYAVQVRCKRLDGLGYNSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVQVRCKRLDGLGYNSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
Qy 661 TLLWKPLMKNDLSCSVQRYVVIINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTTVVLAINSI 720
Db 659 TLLWKPLMKNDLSCSVQRYVVIINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTTVVLAINSI 718
Qy 721 GASVANFNLTFSWPMKSKVINIVOSLSAYPLNNSCIVSWTILSPSDYKLMYFIIEWKNLND 780
Db 719 GASVANFNLTFSWPMKSKVINIVOSLSAYPLNNSCIVSWTILSPSDYKLMYFIIEWKNLND 778
Qy 781 GFIKWLRTSSSVKYYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHSDA 840
Db 779 GFIKWLRTSSSVKYYIHDHFTPIEKYQFSLYPIFMEGVGKPKIINSFTODDIEKHSDA 838
Qy 841 GLYIVPVIISIISSVLLGLTLLSHQRMKFLPVEDVNPKNCSWAQGLNFKPETFELHFI 900
Db 839 GLYIVPVIISIISSVLLGLTLLSHQRMKFLPVEDVNPKNCSWAQGLNFKPETFELHFI 898
Qy 901 KITASVTCGPLLEPETISEDIVSTSWKNKDEMPPTTVVLSLST-DLEKSGVCSIDQF 959
Db 899 KITASVTCGPLLEPETISEDIVSTSWKNKDEMPPTTVVLSLST-DLEKSGVCSIDQF 958
Qy 960 NSVNFSEAGTBTWYDEDSOROPFYKYATLISNKPSETGEQGLINSSVTKCFSSKNSP 1019
Db 959 NSVNFSEAGTBTWYDEDSOROPFYKYATLISNKPSETGEQGLINSSVTKCFSSKNSP 1018
Qy 1020 LKDSFSNKSWEIEAQAFFTLSDQHPNIIISPHLTFSEGLDELLKLEGPNFPEENNDKKSIIY 1079
Db 1019 LKDSFSNKSWEIEAQAFFTLSDQHPNIIISPHLTFSEGLDELLKLEGPNFPEENNDKKSIIY 1077
Qy 1080 LGVTSIKKRESGVLLTDRSRVSCPPAPCLFTWDIRVLQDSCSHFVFNENNLNLTSSKKKFA 1139
Db 1078 LGVTSIKKRESGVLLTDRSRVSCPPAPCLFTWDIRVLQDSCSHFVFNENNLNLTSSKKKFA 1136
Qy 1140 SYMPOFOTCSTOCHKIMENKMDLTV 1165
Db 1137 SYMPOFOTCSTOCHKIMENKMDLTV 1162

; APPLICANT: Biomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dazer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53431
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-53431

Query Match 76.1%; Score 4761.5; DB 5; Length 1162;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 878; Conservative 116; Mismatches 167; Indels 5; Gaps 5;
Qy 1 MICQKFCVLLHWEIYVITAENLSPITPWRFKLSMPPNSTYDFYLLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEIYVITAENLSPITPWRFKLSMPPNSTYDFYLLPAGLSKNTNS 60
Qy 61 NGHETAVEPEKNSGTHFSNLKTTFHCCFRSEQDRNCSLADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPEKNSGTHFSNLKTTFHCCFRSEQDRNCSLADNIEGKTFVSTVNSLVF 120
Qy 121 QOIDANWITQWLKDGKLFIYCVESLTKNLFNRYKVHLLVYLVPEVLEDSPLVPKQGS 180
Db 121 QOIDANWITQWLKDGKLFIYCVESLTKNLFNRYKVHLLVYLVPEVLEDSPLVPKQGS 180
Qy 181 FQWVHCNGSVHCCBCLVPVPTAKNDTLMLCKLITSGVIFQSPMLSVQPINMVKPDP 240
Db 181 FQWVHCNGSVHCCBCLVPVPTAKNDTLMLCKLITSGVIFQSPMLSVQPINMVKPDP 239
Qy 241 LGLHMEITDDGNLKTISWSPPPLVPPLOQVQVYKNSNTTVIREADKIYVATSLLVDSILP 300
Db 240 LGLHMEITDDGNLKTISWSPPPLVPPLOQVQVYKNSNTTVIREADKIYVATSLLVDSILP 298
Qy 301 GSSVEVQVGRKLDGPGIWSDMSTPRVFTQDVVIFPPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSVEVQVGRKLDGPGIWSDMSTPRVFTQDVVIFPPKILTSVGSNVSFHCIIYKKNKI 358
Qy 361 VPSKEIVVMNLAERKIPQSDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 ISSKQIIVWNRNLAEKIPQSDVSDHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 418
Qy 421 RYAEILYVIVDNNINISCEFDGYLTMTKCRWSTSTIOSLAESTLQLRHRSLLYCSIPSIH 480
Db 419 RYAEILYVIVDNNINISCEFDGYLTMTKCRWSTSTIOSLAESTLQLRHRSLLYCSIPSIH 478
Qy 481 PISEPKDCVLOSDGPFYECIFQIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCVLOSDGPFYECIFQIFLLSGVTMIRINHSLGSLDSPPTCVLPDSVVKPLPP 538
Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQVMKYEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOQFQIRYGLSGKEVQVMKYEYVDAKSKSVSLPV 598
Qy 601 PDLCAVYAVQVRCKRLDGLGYNSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 599 PDLCAVYAVQVRCKRLDGLGYNSNNSPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 658
Qy 661 TLLWKPLMKNDLSCSVQRYVVIINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTTVVLAINSI 720
Db 659 TLLWKPLMKNDLSCSVQRYVVIINHHTSCNGTWSDEDVGNHTKFTFLMTEQAHTTVVLAINSI 718
Qy 721 GASVANFNLTFSWPMKSKVINIVOSLSAYPLNNSCIVSWTILSPSDYKLMYFIIEWKNLND 780
Db 719 GASVANFNLTFSWPMKSKVINIVOSLSAYPLNNSCIVSWTILSPSDYKLMYFIIEWKNLND 778

Qy	781	GETKWLRISSSVKYYIHDHFTPIEKYQFSLYPIFMGVGPKPIINSFTQDDIEKHOSDA	840
Db	779	DKMKWLRIIPSNVKFYIHDHNFPIEKYQFSLYPVPMEGVGPKPIINGFTKDAIDKOONDA	838
Qy	841	GLXVIVPVIISSSILLGTLISHORMKKLEWEDVPNPKNSWAQGLNFQKPTFEHLFI	900
Db	839	GLXVIVPVIISCVLLGLTLISHORMKKLEWDDVPNPKNSWAQGLNFQKPTFEHLFT	898
Qy	901	KHTASVTCPLLEPETISEDISVDTSMKNKDEMPTTVSLLSTT-DLEKGSVCISDQF	959
Db	899	KHAESVIFGCPILLEPEISEEISVDTAMKNKDEMVPAAVLSLLTTPDPRESSICISDQC	958
Qy	960	NSVNFSEAGTEVYDEDSQROPVKYATLISNKPSTBEEQGLINSVTKCFSSKNSP	1019
Db	959	NSANFSGSOSTQCTCDEQORQSPVKYATLVNSDKLVTBEEQGFTHSPVSNCTISSNHSP	1018
Qy	1020	LKDSFNSSWETEAQAFFTLSDOHPNLTSPHLTSEGEIDELLKLEGNFPPENNDDKSIYY	1079
Db	1019	LKQSFSSSWETAQFTFLULSQOQTMISLPQLSFS-GLUDELULEGSPPEENHREKSVCY	1077
Qy	1080	LGVTSTKKRESGYLLTDKSRVCPFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFA	1139
Db	1078	LGVTSVNRRESGYLLTGEAGILCTPQAQCLFSDIRLQERCSHFVENNISLGTSG-ENFV	1136
Qy	1140	SYMPOFQTCSTQPHKIEMNKMCDLTV	1165
Db	1137	PYMPQFOTCTSHSHKIEMNKMCDLTV	1162

RESULT 15
US-09-791-537-45617
; Sequence 45617, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45617
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-45617

Query Match 76.1%; Score 4750.5; DB 5; Length 1162;
Best Local Similarity 75.3%; Pred. No. 0;
Matches 878; Conservative 115; Mismatches 168; Indels 5; Gaps 5;

Qy	1	MICQKFCVLLHWEFIYVITAFNLSYSPITPWRPKLSMCPNPNSTYDYFLLPAGLSKNTSNS	60
Db	1	MMCKFFVYVLLHWEFLYVITAFNLSYSPITPWRPKLSMCPNPNSTYDYFLLPAGLSKNTSNS	60
Qy	61	NGHYETAPEKFNSSGTHFSNLKSTTFHCCFEORNRCSLCADNTEGKTFYSTVNSLVF	120
Db	61	KGASEAIVEAKFNSSGIYVPELSKTFVHCCFGEQCNQCSALTDTEGKTLASVVKASF	120
Qy	121	QQIDANNIOCWLGDKDLKFCYVESLFKNLFRNYKYVHLYLYLPEVLEDSPLVPQKGS	180
Db	121	RLQGVNNDIECWMMKGDUTLIICHMEPLKPNPFKNYDSKVHLLYDLPEVITDDSPPLPKDS	180
Qy	181	FQWYHCHSCVHECECLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSYQPTNMYKPDPP	240
Db	181	FQTVQCNCSLRG-CECHVVPVRAKLYALLMYLEITISAGVSQSPMLSLQPMVLVYKPDPP	239
Qy	241	LGLHMETDDGNLKIUSWSSPPLVPFFPQYQVKYSENSTTVIREADKIVSATSLLVDSILP	300
Db	240	LGLHMETYDGNLKIUSWDSQTMAFFPQYQVKYSENS-TIVREAAIVSATSLLVDSVLP	298

Qy	301	GSSVEQVGRKRLDGGGINSWDSMTFRVFTTQDVYIYPFKLLITSVGSNVSFHCYIKKENKI	360
Dy	299	GSSYEQVRSKRLDGGGVMSWSSSQVFVTQDVYFPFKLLITSVGSNASFHCYIKKENQI	358
Qy	361	VPSKEIWWNNLAEKIPQSOYDWVSDHVSKVTFEFLNLTCKPRGFTYDAVVCNEHECHH	420
Dy	359	ISSKOIWWNRNLAEKIPETQYSIVSDRVSVKTFNSLNKATRPGRGFTYDAVVCNEQACHH	418
Qy	421	RYAELYYVIDVNIINISCTDGYITKMTFCRWSTSIQSIAESTLQJRYHRSSLYCSDIPSIIH	480
Dy	419	RYAELYYVIDVNIINISCTDGYITKMTFCRWSPTSIQSLVGSTVQLRYHRRSLYCSPDSPSIH	478
Qy	481	PISEPKCYLOSGDFECIFOPFIELLSGYTWMIRINHSLGSLSGDSPPTCVLPDSVVKKPLPP	540
Dy	479	PTSEPKNCVLQRDGFECEVFQPIFLLSGTWMIRINHSLGSLSGDSPPTCVLPDSVVKKPLPP	538
Qy	541	SSVKAETIINGILLKISWEKPVPENNLOFQIRYGLSGKEYOWKMYYEYDAKSXSPLPV	600
Dy	539	SNVKAETIVNTGLLVKSWEPVPENNLOFQIRYGLSGKEIQWKTHEYFDAKSASALIV	598
Qy	601	PDLCAYAVOVRCKRLDGLGYASNNSNPAYTVVMDIKYPMRGPEPWRILNGDTMKKEKNV	660
Dy	599	SDBCAYVVOVRCRLDGLGYSNSSSPAYTLVMDOVKYPMRGPEPFMRKMDGDVTKKERNV	658
Qy	661	TLLWKPLMKNDSCSVORYVIYNHHTSCNTWSEDVGNHTKFTFLWTQAHVTVTVAINSI	720
Dy	659	TLLWKPLTKNDSLCSVRRYVVKHRTAHNGTWSEDVGNRTNLTLFWTPAHTVTVLAVNSL	718
Qy	721	GASVANFNLTFSMPMKNVIGOSLAYPLANSSCVIVSMILSPSDYKMLFYIEWKNLNED	780
Dy	719	GASIVNFNLTSFMPMSKVASVESLSAYPLSSSCVILSWTLSPDDYSLLYLVIEWKLINED	778
Qy	781	GEIKWLRISSSVKKYVIHDHFPIEKYQPSLYPIFMEGVGPKLIINSTODIEKHOSDA	840
Dy	779	DGMKWLRIPNVAKKFITHDNFPIEKYQPSLYPIFMEGVGPKLIINGTFOADIKOQNDA	838
Qy	841	GLYIVYVPIISSLILGLTLLISHORMKLLFWDYVNPKNCSWAQGLNFQKPFTEHLFI	900
Dy	839	GLYIVYVPIISSLVLLGLTLLISHORMKLLFWDVDPKNCSWAQGLNFQKPFTEHLFT	898
Qy	901	KHTASVTCGPILLLEPETISHDISVDTSWNKDMMPTTVVSLLSITT-DLEKSGVICISDOF	959
Dy	899	KHAESVIFGPLLLEPEPISSEISVDTFANKNKDMWPAAWVSLUULTTPDPRESSICISIDQC	958
Qy	960	NSVNFSEAEGTEVYDESORQPFVKYATLLINSKXSPSETGBEOGLINSVTRKCFSSKNSP	1019
Dy	959	NSANFGSQSTQVTCEDBECORQSVKAYATLVNSDKLIVETDEOCQFIHSPVSNCLISNHSP	1018
Qy	1020	LKDSFSSNSWEIBAQAFFILSDQHPIIISPHUTTFSEGDELCLKLEGNPPEENNDKKSIIYY	1079
Dy	1019	LROQSFSSSWEETAQTAFLLSDQQPTMIISPQLSFS-GLDEELLEPGSPPEENHREKSVCY	1077
Qy	1080	LGVTISKRESGVLITDKSRVSCPFPAPCLFTDIRVLQDCSHFVENNINLGTSKKTFA	1139
Dy	1078	LGVTISVNRESGVLITCEAGILCTFPAQCLFSDIRILQERCSHFVENNISLGTSG-ENVF	1136
Qy	1140	SYMPQOTCSTQTHKIMENKMCDLTV	1165
Dy	1137	PYMPQOTCSTHSHKIMENKMCDLTV	1162

Search completed: August 15, 2002, 16:27:05
Job time: 370 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:20 ; Search time 91.6 Seconds

(without alignments)
2200.208 Million cell updates/sec

Title: US-08-779-457-2

Perfect score: 6254

Sequence: 1 MICQKFCVLLHWEFIVIT.....QTCTQTHKIMNKMDLTV 1165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL-197*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6254	100.0	1165	4 Q92921	Q92921 homo sapien
2	5967	95.4	1163	6 Q9MYL2	Q9MYL2 macaca mula
3	5941.5	95.0	1194	6 Q9MYL0	Q9MYL0 macaca mula
4	5269	84.3	1165	6 Q02671	Q02671 sus scrofa
5	4831.5	77.3	958	4 Q92920	Q92920 homo sapien
6	4826	77.2	896	4 Q92919	Q92919 homo sapien
7	4819.5	77.1	958	4 Q13592	Q13592 homo sapien
8	4816	77.0	906	4 Q13593	Q13593 homo sapien
9	4761.5	76.1	1162	11 Q13594	Q13594 homo sapien
10	4761.5	76.1	1162	11 Q9QWG3	Q9QWG3 mus musculu
11	4591	73.4	925	6 Q9MYK9	Q9MYK9 macaca mula
12	4590	73.4	894	6 Q9MYL1	Q9MYL1 macaca mula
13	3970.5	63.5	848	6 Q9MZS2	Q9MZS2 sus scrofa
14	3729	59.6	895	11 Q62960	Q62960 rattus norv
15	2790.5	44.6	1147	13 Q9DDK1	Q9DDK1 meleagris g
16	2775	44.4	1148	13 Q9IBA7	Q9IBA7 gallus gall

17	2693	43.1	1146	13 Q918V6	Q918V6 gallus gall
18	1074	17.2	246	11 Q35773	Q35773 rattus norv
19	981.5	15.7	273	11 Q9QWV5	Q9QWV5 mus musculu
20	801	12.8	203	6 Q28604	Q28604 ovies aries
21	683	10.9	161	6 Q28606	Q28606 ovies aries
22	660.5	10.6	173	6 Q9XSN9	Q9XSN9 sus scrofa
23	616	9.8	147	6 Q95257	Q95257 sus scrofa
24	588	9.4	152	6 P79115	P79115 bos taurus
25	497	7.9	123	6 Q9NIF9	Q9NIF9 sus taurus
26	477	7.6	121	6 Q18980	Q18980 bos taurus
27	456	7.3	145	13 Q91A32	Q91A32 gallus gall
28	444	7.1	881	13 Q57519	Q57519 xenopus lae
29	409.5	6.5	918	13 Q9W609	Q9W609 gallus gall
30	366	5.9	102	6 Q9XSH3	Q9XSH3 equus cabal
31	354	5.7	710	13 Q57520	Q57520 xenopus lae
32	325	5.2	74	11 Q9ER14	Q9ER14 rattus norv
33	312.5	5.0	1093	11 Q70535	Q70535 rattus norv
34	299	4.8	57	6 Q97778	Q97778 elephas max
35	299	4.8	57	6 Q97779	Q97779 loxodonta a
36	267	4.3	979	4 Q99650	Q99650 homo sapien
37	251.5	4.0	2302	11 Q88488	Q88488 rattus norv
38	232.5	3.7	970	11 Q88821	Q88821 mus musculu
39	228	3.6	971	11 Q70458	Q70458 mus musculu
40	213	3.4	57	13 Q90WY8	Q90WY8 gallus gall
41	197	3.1	861	6 Q9BEG2	Q9BEG2 bos taurus
42	195	3.1	1598	4 Q9P214	Q9P214 homo sapien
43	191.5	3.1	6875	6 Q28733	Q28733 oryctolagus
44	189.5	3.0	1114	5 Q9VSG6	Q9VSG6 drosophila
45	188	3.0	26926	4 Q10466	Q10466 homo sapien

ALIGNMENTS

RESULT 1

Q92921 PRELIMINARY; PRT; 1165 AA.
AC Q92921
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE LEPTIN RECEPTOR
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96398968; PubMed=8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis.";
RL Curr. Biol. 6:1170-1180(1996)
DR EMBL; U66497; AA807497.1;
DR HSP; P16471; IBP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 100.0%; Score 6254; DB 4; Length 1165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIVITAFNLSPITPWFKLSMPNSTDYFLPAGLSKNTSNS 60
|||||

Db 1 MICQKFCVLLHWEFYIVITAFNLSPYITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFYVTSNLSVF 120
Db 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFYVTSNLSVF 120
QY 121 QOIDANNNITOCWLKGLDLKLFICYVESLFRNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
Db 121 QOIDANNNITOCWLKGLDLKLFICYVESLFRNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLTSGGVIFQSPPLMSVQPINMYKPDPP 240
Db 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLTSGGVIFQSPPLMSVQPINMYKPDPP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 300
QY 301 GSSYEVOVRGKRLDGPFIWSDMSTPRVFTTQDVYIPPPKILTSGVNSVSHFHCYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPFIWSDMSTPRVFTTQDVYIPPPKILTSGVNSVSHFHCYKKNKI 360
QY 361 VPSKEIIVWNNLAETKIQSQDYVSDHVSQVTFNPNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIIVWNNLAETKIQSQDYVSDHVSQVTFNPNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIVVIDVNNISCTDGLTKMTCRWSTSTIQSLAESTLQLRVHRSLSYCDIPSTH 480
Db 421 RYAEIVVIDVNNISCTDGLTKMTCRWSTSTIQSLAESTLQLRVHRSLSYCDIPSTH 480
QY 481 PISEPKDCYLQSDGFEYCFQPIFLLSGYTWMIRINHSLGSLDSPPTCYLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFEYCFQPIFLLSGYTWMIRINHSLGSLDSPPTCYLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKTSWEKVPFPENNLOFQIRYGLSGKEVQWKMTEYDASKSVSLPV 600
Db 541 SSVKAEITINIGLLKTSWEKVPFPENNLOFQIRYGLSGKEVQWKMTEYDASKSVSLPV 600
QY 601 PDLCAVAYQVRCRDLGGLGKYSNNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKV 660
Db 601 PDLCAVAYQVRCRDLGGLGKYSNNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKV 660
QY 661 TLLWKPMLKNDLCSQVRYVVIINHHTSCNGTWSDEDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWKPMLKNDLCSQVRYVVIINHHTSCNGTWSDEDVGNHHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNTLFWPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKLNED 780
Db 721 GASVANFNTLFWPMSKVNIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEWKLNED 780
QY 781 GEIKWLRISSSVKYIYHDFHTPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
Db 781 GEIKWLRISSSVKYIYHDFHTPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
QY 841 GLYVIVPVIISSILLGTLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFKQPTFPHLFI 900
Db 841 GLYVIVPVIISSILLGTLTLLISHQRMKLLFWEDVNPKNCSWAQGLNFKQPTFPHLFI 900
QY 901 KHTASVTCGPLLLEPTI SEDISVDFSWKNKDEMPPTTVVLSLSTPDLKSGVCSIDQFN 960
Db 901 KHTASVTCGPLLLEPTI SEDISVDFSWKNKDEMPPTTVVLSLSTPDLKSGVCSIDQFN 960
QY 961 SVNFSAEGETVYEDESQRFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
Db 961 SVNFSAEGETVYEDESQRFVKYATLISNSKPSGTGEQGLINSSVTKCFSSKNSPL 1020
QY 1021 KDSFNSNSWEIEBAQAFILSDQHPNTIISPHLTFSEGLDELLKLEGNFPEENDKKSIIYVL 1080
Db 1021 KDSFNSNSWEIEBAQAFILSDQHPNTIISPHLTFSEGLDELLKLEGNFPEENDKKSIIYVL 1080
QY 1081 GVTISIKKRESGVLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSKKKTFAS 1140
Db 1081 GVTISIKKRESGVLTDKSRVSCPEPAPCLFTDIRVLQDSCSHFVENNINLGTSKKKTFAS 1140

QY 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
Db 1141 YMPQFQTCSTQTHKIMENKMCDLTV 1165
RESULT 2
Q9MYL2
ID Q9MYL2 PRELIMINARY; PRT; 1163 AA.
AC Q9MYL2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR LONG FORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
expression in the adipose tissue of normal, hyperinsulinemic, and type
2 diabetic rhesus monkeys.";
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222960; AAF34683.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;
Query Match 95.4%; Score 5967; DB 6; Length 1163;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1114; Conservative 18; Mismatches 31; Indels 2; Gaps 1;
QY 1 MICQKFCVLLHWEFYIVITAFNLSPYITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFYIVITAFNLSPYITPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFYVTSNLSVF 120
Db 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFYVTSNLSVF 120
QY 121 QOIDANNNITOCWLKGLDLKLFICYVESLFRNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
Db 121 QOIDANNNITOCWLKGLDLKLFICYVESLFRNLFNRYNYKVHLLYVLPVEVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLTSGGVIFQSPPLMSVQPINMYKPDPP 240
Db 181 FQWVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLTSGGVIFQSPPLMSVQPINMYKPDPP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOQYOVKYSNSTTVIREADKIVSATSLLDVDSILP 300
QY 301 GSSYEVOVRGKRLDGPFIWSDMSTPRVFTTQDVYIPPPKILTSGVNSVSHFHCYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPFIWSDMSTPRVFTTQDVYIPPPKILTSGVNSVSHFHCYKKNKI 360

QY	361	VPSKEIYVWNNLAEKIPQSOYDVSDHVSKVTFEFLNLTNETKPRCKFTYDAYVCCNEHECHH	420
Db	359	VSSKKIYVWNNLAEKIPQSOYDVSDHVSKVTFEFLNLTNETKPRCKFTYDAYVCCNEHECHH	418
QY	421	RYAELVYDVNINISCEITDGYLTKTCRWSTSTIQSLAESTLQLRVHRSSLYCSIDPSIH	480
Db	419	RYAELVYDVNINISCEITDGYLTKTCRWSTSTIQSLAESTLQLRVHRSSLYCFDIPSIH	478
QY	481	PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540
Db	479	PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	538
QY	541	SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKVEYVDAKSYSVLPV	600
Db	539	SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEIQWKMDVYVDAKSYSVLPV	598
QY	601	POLCAVYAVQVRCRDLGLGYVNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	599	PDFCAVYAVQVRCRDLGLGYVNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	658
QY	661	TLWPKPLMKNDLSVQRYVVIHHTSCNGTWSDEDVGNHTKFTFLTEQAHVTVVLAINSI	720
Db	659	TLWPKPLMKNESLCSVQRYVVIHHTSCNGTWSDEDVGNHTKFTFLTEQAHVTVVLAINSI	718
QY	721	GASVANFNLTFSWPKSKVNIQVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE	780
Db	719	GASVANFNLTFSWPKSKVNIQVOSLSAYPLNSSCVILSWILSPSDYKLMYFIIEWKNLNE	778
QY	781	GEIKWLRISSSVKKYIYHDFPIEIKYQSLYPIFMGVGKPKIINSFTQDDIEKHQSDA	840
Db	779	GEIKWLRISSSVKKYIYHDFPIEIKYQSLYPIFMGVGKPKIINSFAODNTERKHONDA	838
QY	841	GLYVIVPVLISSILLGLLISHQBMKKLFWEDVPNPKNCSSWAQGLNFKQKPTTEHLEFI	900
Db	839	GLYVIVPVLISSILLGLLISHQBMKKLFWEDVPNPKNCSSWAQGLNFKQKPTTEHLEFI	898
QY	901	KITASVTCGPLELPEITISEDIVSTWSKNKDEMPTTVVSLSTDLKSGVCISDQFN	960
Db	899	KITASVTCGPLELPEITISEDIVSTWSKNKDEMPTTVVSLSTDLKSGVCISDQFN	958
QY	961	SVNFSAEGETEYVDESORQPFVKYATILISNSKPSETGEQGLINSVYTKFSSKNSPL	1020
Db	959	SVNFSAEGETEYVDESORQPFVKYATILISNSKPSETDEEQGLINSVYTKFSSKNSPL	1018
QY	1021	KDSFNSNWEIEAQAFILLSDQHPNLIISPLTFSEGLDELLEKLEGNFPENNDDKSIYYL	1080
Db	1019	KDSFNSNWEIEAQAFILLSDQHPNLIISPLTFSEGLDELLEKLEGNFPENNDDKSIYYL	1078
QY	1081	GVTSTIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS	1140
Db	1079	GVTSTIKKRESGVLLTDKSRVSCFPAPCLFTDIRVLQDSCSHFVENNINLGTSSKKTFFAS	1138
QY	1141	YMPQFOTCSTQTHKIMENKMDLTV	1165
Db	1139	YMPQFOTCSTQTHKIMENKMDLTV	1163
RESULT	3		
Q9MYL0			
ID	Q9MYL0	PRELIMINARY;	PRT; 1194 AA.
AC	Q9MYL0;		
DT	01-OCT-2000 (TreeBLrel. 15, Created)		
DT	01-OCT-2000 (TreeBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TreeBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR LONG INSERT ISOFORM.		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;		
OC	Cercopitheciinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=ADIPOSE TISSUE;		

RX	MEDLINE=98408931; PubMed=9738551;		
RA	Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;		
RT	"Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA		
RT	expression in the adipose tissue of normal, hyperinsulinemic, and type		
RT	2 diabetic rhesus monkeys.";		
RL	Obes. Res. 6:353-360(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=ADIPOSE TISSUE;		
RA	Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF225874; AAF35388.1;		
DR	HSP: P16471; 1Bp3		
DR	InterPro; IPR002996; CRIA.		
DR	InterPro; IPR003961; FN_III.		
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.		
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.		
DR	Pfam: PF00041; fn3; 2.		
DR	SMART: SM00060; FN3; 1.		
DR	PROSITE; PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.		
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.		
KW	Receptor.		
SQ	SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;		
Query Match	95.0%; Score 5941.5; DB 6; Length 1194;		
Best Local Similarity	93.1%; Pred. No. 0;		
Matches 1114; Conservative 18; Mismatches 31; Indels 33; Gaps 2;			
QY	1	MICQKFCVLLHWEFTYVITAFNLISYPIPTWRPKLSCMPNPNSTYDFLLPAGLSKNTSNS	60
Db	1	MICQKFCVLLHWEFTYVITAFNLISYPIPTWRPKLSCMPNPNSTYDFLLPAGLSKNTSNL	60
QY	61	NGHYETAVPEKFNSSCTHFSNLSKTTFHCCFSEQDRNCSLCAADNIEGKTFVTVNSLVF	120
Db	61	NGHYETAVE--FNSSDTHFSNLSKTTFHCCFSEQDRNCSLCAADNIEGKTFVTVNSSVF	118
QY	121	QIDANNNTQCLWGLKLFICYVESLFLFNLYKVKVHLLVLEVLDSPLVPQKGS	180
Db	119	QQMGANNIQCWLKGLKLFICYVESLFLFNLYKVKVHLLVLEVLDSPLVPQKGS	178
QY	181	FQVHCHNCVHECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINNVKPDPP	240
Db	179	FQVHCHNCVHERCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMSVQPINNVKPDPP	238
QY	241	LGLHMEITDGNLKIWSVPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLLVDSILP	300
Db	239	LGLRMEITDGNLKIWSVPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLLVDSILP	298
QY	301	GSSYEYQVRGKRLDGPGLWSDNSTPRVFTTQDVVYPPPKILTSGVSNVSPHCYKKNKI	360
Db	299	GSSYEYQVRGKRLDGPGLWSDNSTPRVFTTQDVVYPPPKILTSGVSNVSPHCYKKNKI	358
QY	361	VPSKEIYVWNNLAEKIPQSOYDVSDHVSKVTFEFLNLTNETKPRCKFTYDAYVCCNEHECHH	420
Db	359	VSSKKIYVWNNLAEKIPQSOYDVSDHVSKVTFEFLNLTNETKPRCKFTYDAYVCCNEHECHH	418
QY	421	RYAELVYDVNINISCEITDGYLTKTCRWSTSTIQSLAESTLQLRVHRSSLYCSIDPSIH	480
Db	419	RYAELVYDVNINISCEITDGYLTKTCRWSTSTIQSLAESTLQLRVHRSSLYCFDIPSIH	478
QY	481	PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	540
Db	479	PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP	538
QY	541	SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKVEYVDAKSYSVLPV	600
Db	539	SSVKAETITNIGLLKISWEKPVFPENNLOFQIRYGLSGKEIQWKMDVYVDAKSYSVLPV	598
QY	601	POLCAVYAVQVRCRDLGLGYVNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	660
Db	599	PDFCAVYAVQVRCRDLGLGYVNSNPNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV	658

QY 661 TLLKKPLMKNDLSCSVQRYVINHTSCGTWSEDVGNHTKFTFLWTEQAHVTVLAINSI 720
DB 659 TLLKKPLMKNESLCSVQRYVINHTSCGTWSEDVGNHTKFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSPMSKVNIVQSLSAIPLNSNCVIVSWILSPSDYKLMYFIEWKNLNED 760
DB 719 GASVANFNLTFSPMSKVNIVQSLSAIPLNSNCVIVSWILSPSDYKLMYFIEWKNLNED 778
QY 781 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSDA 840
DB 779 GEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFPAQDNTEKHQSDA 838
QY 841 GLXVIVPVISSSILLGLTLLSHORMKLFWDVFNPKNCWAQGLNFQKIRGFVWLPR 898
DB 839 GLXVIVPVISSSILLGLTLLSHORMKLFWDVFNPKNCWAQGLNFQKIRGFVWLPR 898
QY 892 -----PETEHLPIKHTASVTCGPLLLEPETISEDISVDTSWK 929
DB 899 LVLSQAQVHPPRPKVLQLEPETEHLPIKHTASVTCGPLLLEPETISEDISVDTSWK 958
QY 930 NKDEMPPTVSVLLSTTDLEKGVCSIDQFNSVNFSEAEGETEVTYDESORQPFVAYATL 989
DB 959 NKDEMPPTVSVLLSTTDLEKGVCSIDQFNSVNFSEAEGETEVTYDESORQPFVAYATL 1018
QY 990 ISNKPSETGEEQGLINSSVTKCFSSKNPLKDFSNSSWEIEAQAFFILSDQHPNIIS 1049
DB 1019 ISNKPSETGEEQGLINSSVTKCFSSKNPLKDFSNSSWEIEAQAFFILSDQHPNIIS 1078
QY 1050 HLTFSEGLDELLKLEGNFENNDKSIYVLGVTSTKKRESGVLLTDKRSVCPFPAPCL 1109
DB 1079 HLTFSEGLDELLKLEGNFENNDKSIYVLGVTSTKKRESGVLLTDKRSVCPFPAPCL 1138
QY 1110 FTDIRVLQDSCSHFVNNILNLTSSKKTFTASYMPQFQTCSTQTHKMENKMDLTV 1165
DB 1139 FTDIRVLQDSCSHFVNNILNLTSSKKTFTASYMPQFQTCSTQTHKMENKMDLTV 1194
RESULT 4
002671 PRELIMINARY; PRT; 1165 AA.
AC 002671
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR.
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN TISSUE=LIVER;
RC SEQUENCE FROM N.A.
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.-F.,
RA Murphy B.D.;
RT *Porcine leptin (Ob) receptor complete coding sequence.*;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 408-470 FROM N.A.
RX MEDLINE=97222487; PubMed=9069130;
RA Ernst C.W., Kapke P.A., Yerie M., Rothschild M.F.;
RT *The leptin receptor gene (LEPR) maps to porcine chromosome 6.*;
RL Mamm. Genome 8:226-226(1997).
DR EMBL; AF092422; AAC61766.1; -.
DR EMBL; U72070; AAC48707.1; -.
DR HSSP; P16471; 1Bp3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR Pfam; PF00041; f03; 1.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F12 CRC64;
Query Match 84.3%; Score 5269; DB 6; Length 1165;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 980; Conservative 73; Mismatches 110; Indels 4; Gaps 4;
QY 1 MTCQKFCVLLHWEFTYVITAFNLSYPIPTWPKFLSCMPNPSTYDYFLPAGLSKWTNS 60
DB 1 MTCPKFSVALLHWEFTYVITAFDLAYIPITWPKFLSCMPNPNTYD-FLPAGISKNTSTL 59
QY 61 NGHETAVAPKNSCTHFSNL-SKTEHCCPSESDRNCSLCADNIECKTFVSTVNSLV 119
DB 60 NGDEAVTEINISCTIYLSNLSSTFHCCFSEEDKNCVHADNIAKAFVAVNSLV 119
QY 120 FOQIDANNIQCWLKGLKLFICYVESLEKFLFNRYNYKVHLLYLVLEVLEDSPLVPQK 179
DB 120 FOOTGANNIQCWMKEDLKFICYMESLFKNPFKNYDLKLVHLLYLVLEVLEGSPLLPQK 179
QY 180 SFQMVHCNCSVHECCBCLVPVPTAKLNDLLMCLKITSGVIFOSPLMSVQPINNVKPD 239
DB 180 SFQSVQCNCARSCECHVPVSAAKLNYLLMYKITSGAVFHPSPMSVQPINNVKPD 239
QY 240 PLGLHMEITDDGNLKSWSPPPLVPPLOQYQVYKYSNSTTVIREADKIVSATSLVDSIL 299
DB 240 PLGLHMEITDGNLKSWSPTLPVFPLOQYQVYKYSNSTTNMREADEIVSDTSLVDSVL 299
QY 300 PSSYEVQVGRKRLDGPGLWSDMSTPRVTTQDVIVFPKILTSVGSNVSFHCYKKNK 359
DB 300 PSSYEVQVGRKRLDGPGLWSDMSTPFTTQDVIVFPKILTSVGSNISFHCYKKNK 359
QY 360 IYPSKEIVWMNLAEKIPQSDVDVSDHVSQVYKVTFFNLNETKPRGKETYDAVYCCNHECH 419
DB 360 IYSSKKIVWMNLAEKIPQSDVDVGDHVSQVYKVTFFNNATKPRGKETYDAVYCCNHECH 419
QY 420 HRYAELYVIDVNIINISCETDGYLTMTCTWSTSTIOSLAESTLQLRYHRSSLYCSDIPSI 479
DB 420 HRYAELYVIDVNIINISCETDGYLTMTCTWSTNAIQSLVGLTQLRYHRSSLYCSDVPSV 479
QY 480 HPISPEKCYLQSDGFEYECIFQPIFLLSGYTWMIRINHSGLSDSPPTCVLSDVSVKPL 539
DB 480 HPISPEKDCQLQSDGFEYECIFQPIFLLSGYTWMIRINHPGLSDSPPTCVIPDSVVKPL 539
QY 540 PSSVRAEITINIGLKIWEKVPFENNLOFQIRYGLSGKEVQWKMYEYVDAKSKVSPL 599
DB 540 PSSVRAEITAKIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKIYEVYDTKLSTSL 599
QY 600 VPDLCAYAVQVRCRRLDGLGYSNMSNPAYTVYMDIKYPMRGPEFWRIINGDTMKKEN 659
DB 600 VPDLCAYAVQVRCRRLDGLGYSNMSNPAYTVYMDIKYPMRGPEFWRIINGDTMKKEN 659
QY 660 VTLWKPLMKNDLSCSVQRYVINHTSCGTWSEDVGNHTKFTFLWTEQAHVTVLAINSI 719
DB 660 ITLWKPLMKNDLSCSVRSYVYKHHSTSRGTWSEDVGNHTKFTFLWTEQAHVTVLAINSI 719
QY 720 IGASVANFNLTFSPMSKVNIVQSLSAIPLNSNCVIVSWILSPSDYKLMYFIEWKNLNE 779
DB 720 IGASSANFNLTFSPMSKVNIVQSLSAIPLNSNCVIVSWILSPSDYKLMYFIEWKNLNE 779
QY 780 DGEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSD 839
DB 780 DHEIKWLRISSSVKYYIHDHFPIEKYQFSLYPIFMEGVGKPKIINSFTQDDIEKHQSD 838
QY 840 AGLYVIVPVISSSILLGLTLLSHORMKLFWDVFNPKNCWAQGLNFQKIRGFVWLPR 899
DB 839 AGLYVIVPVISSSILLGLTLLSHORMKLFWDVFNPKNCWAQGLNFQKIRGFVWLPR 898
QY 900 IKHTASVTCGPLLLEPETISEDISVDTSWKNKDEMPTTVSVLLSTT-DLEKSGVCISDQ 958
DB 899 IKHTESVTCGPLLLEPETISEDISVDTSWKNKDEMVPPTTVSVLLTTPDLEKSSICISDQ 958

Qy	959	FNSVNFSEAGTEVTVEDSQRPQPKVYATILNSKPKSETGEQGLNSSVTKCFSSKNS	1010
Dy	959	SSAHFSEAESMEITREDENRRQPSIKYATILSSPKSGETEQEQLVSSLVSRCFSSNS	1018
Qy	1019	PLKDSFNSSWELRAQAFILSDQHNIISPHLTFSEGLDELLKLEGNFPEENNDKSIY	1078
Dy	1019	LPKESFNSSWELTAQAFILSDQHNMNTSPHLSFSEGLDELMKFEQPKHEHNDERSVY	1078
Qy	1079	YLGVTSTKKRESQVLLTDKSRVSCFPAPCLFTDTRVLQDSCSHFVENNTNLGTSKKTF	1138
Dy	1079	YLGVTSTKKRESQVLLTDKSRVSCFPAPCLFADIKIQLQESCShLVENNFNLGTSQKTF	1138
Qy	1139	ASTWPOFQTCSTQTHKIMENKMDLTV	1165
Dy	1139	VSYMPQFQTCSTQTKIMENKMYDLTV	1165
RESULT 5			
Q92920			
ID	Q92920	PRELIMINARY; PRT; 958 AA.	
AC	Q92920;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	LEPTIN RECEPTOR.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96398968; PubMed=8805376;		
RA	Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,		
RA	Matthews W.		
RT	"A role for leptin and its cognate receptor in hematopoiesis.";		
RL	EMBL. Biol. 6:11170-11180(1996).		
DR	CURL; U66496; AAB07496.1; -.		
DR	HSSP; P16471; LBP3.		
DR	InterPro; IPR002996; CRJA.		
DR	InterPro; IPR003961; FN.III.		
DR	InterPro; IPR003529; Hematopo_receptor_L_F2.		
DR	InterPro; IPR003531; Hematopo_receptor_S_F1.		
DR	Pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 1.		
DR	PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN1.		
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN1.		
KW	Receptor.		
SQ	SEQUENCE 958 AA; 109392 MW; 3F65BC5A187E803A CRC64;		
Query Match 77.3%; Score 4831.5; DB 4; Length 958;			
Best Local Similarity 94.4%; Pred No. 0;			
Matches 904; Conservative 5; Mismatches 24; Indels 25; Gaps			
Qy	1	MICOKFCVLLHWEFIVYITAFNLSPYTPMPWFKLSMPPNSTYDYFLLPAGLSKNTSNS	60
Dy	1	MICOKFCVLLHWEFIVYITAFNLSPYTPMPWFKLSMPPNSTYDYFLLPAGLSKNTSNS	60
Qy	61	NGHYETAPEKFNSSGTHPSNLSTKTFHCCFRSEQDRNCSLCADIENKGTFTVSTVNSLVF	120
Dy	61	NGHYETAPEKFNSSGTHPSNLSTKTFHCCFRSEQDRNCSLCADIENKGTFTVSTVNSLVF	120
Qy	121	QQIDANWNIQWLKGLDKLFCVPSLKNLPNNYKVHLLYVLPVLEDSPLVPQGS	180
Dy	121	QQIDANWNIQWLKGLDKLFCVPSLKNLPNNYKVHLLYVLPVLEDSPLVPQGS	180
Qy	181	QWVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPMLSVQPINNVKPDPP	240
Dy	181	QWVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGVIFQSPMLSVQPINNVKPDPP	240
Qy	241	LGHLMEITDGNLKIWSGSPPLVPPLQVQVYKYSNSTTVITREADKIVSATSLVDSILP	300
Dy	241	LGHLMEITDGNLKIWSGSPPLVPPLQVQVYKYSNSTTVITREADKIVSATSLVDSILP	300

Qy	301	GSSEVQVQRKRLDGP	PGTISDWSPTPVFTTQDVIYFPFKILT	SVGSNSPHCIYKKENKI	360
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Qy	361	VPSKEIYVWMLAEKI	POSQYDVVSDHVS	KVTFFNLNETKPRGFTYD	VAYCCNEHECHH 420
Db	361	VPSKEIYVWMLAEKI	POSQYDVVSDHVS	KVTFFNLNETKPRGFTYD	VAYCCNEHECHH 420
Qy	421	RYAELYVIDVNI	NSCETDGYLT	KMTCRWSTSTTQISLAEST	LQLRYHRSSLYCSDIPSIH 480
Db	421	RYAELYVIDVNI	NSCETDGYLT	KMTCRWSTSTTQISLAEST	LQLRYHRSSLYCSDIPSIH 480
Qy	481	PISPEKDCY	LOSDFGYECI	FOPIPELLSGYTMWIRINHS	LSGLSDSPCTCVLPDSVWPPLPP 540
Db	481	PISPEKDCY	LOSDFGYECI	FOPIPELLSGYTMWIRINHS	LSGLSDSPCTCVLPDSVWPPLPP 540
Qy	541	SSVRAEIT	INIGLLKISWEK	PVPFENNLIQFOIRYGLSGKEVQ	KMYEVDYDAKSYSVSLPV 600
Db	541	SSVRAEIT	INIGLLKISWEK	PVPFENNLIQFOIRYGLSGKEVQ	KMYEVDYDAKSYSVSLPV 600
Qy	601	PDLCAVAVQVQRKRLDGLG	YVWSNWPAYTVVMDIKVPMRG	PEFWRIINGDTMKKEKNV 660	
Db	601	PDLCAVAVQVQRKRLDGLG	YVWSNWPAYTVVMDIKVPMRG	PEFWRIINGDTMKKEKNV 660	
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Db	661	TLLMKPLMKND	SLCSVQRYVINHHTSCNGT	WSEVDVGNHKTFTFLWTQ	QAHTVTVVLAINSI 720
Qy	721	GASVANFNLT	TSWPMKVNIVQSLISAYPLNS	SCCVISWILSPSDYKLMYFI	IEWKNLNED 780
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Qy	781	GEIKWLRISSV	KYKYIYTHDRPIEPIEKYQ	FSLYPIFMEGVGPKPIINSFT	ODDIEKHQSDA 840
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Db	841	GLYIVPVIISS	ILLGLTLLSHQRMKKL	FWEDVPNPKNSWAOGLNF	OK-----PE 893
Qy	894	TFEHLFIKHT	-ASVTCGP-----	LLLEPETISEDISVDT	SKNKDE 933
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ID	Q92919	PRELIMINARY;	PRT;	896 AA.	
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DT	01-FEB-1997	(TREMBLrel. 02, Created)			
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE		LEPTIN RECEPTOR.			
GN	DB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	[1]				
RA	Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,				
RA	Matthews W.;				
RL	Curr. Biol. 6:0-0(0).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=97215244; PubMed=9061609;				
RA	Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,				
RA	Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;				
RT	"Cloning and characterization of a human leptin immunoadhesin.;"				
RT	J. Mol. Endocrinol. 18:77-85(1997).				
DR	EMBL; U66495; AAB07495.1; -.				

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DR EMBL; U50748; AAC23650.1; -.
DR HSSP; p16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SQ SEQUENCE 896 AA; 102489 MW; D37IC7A4186DEEF3 CRC64;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 NGHETAVEPKFNSSGTHFSPNLKATFHCCPRSEODRNCSCADNIEGKTFVSTVNSLVF 120
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DB 121 QQIDANWNTQCKLKGDLKLFICYVESLFPKLFNPNYNYKVHLLYVLPVLEDSPLVPQKGS 180
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DB 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIYSATSLLDVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLWSWDNSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 360
DB 301 GSSYEYQVRGKRLDGPGLWSWDNSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 360
QY 361 VPSKETVWMNLAETKIPQSOYDWSHDVSKVTFNINETKPRGKFTYDAVYCCNEHECHH 420
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AC Q13592;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT *Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.*;
RL Nat. Med. 2:585-589(1996).
DR EMBL; U52912; AAC50509.1; -.
DR HSSP; p16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.
SQ SEQUENCE 958 AA; 109419 MW; C7E0E8D18428677B CRC64;
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Query Match 77.1%; Score 4819.5; DB 4; Length 958;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 901; Conservative 7; Mismatches 25; Indels 25; Gaps 3;

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QY 61 NGHETAVEPKFNSSGTHFSPNLKATFHCCPRSEODRNCSCADNIEGKTFVSTVNSLVF 120
DB 61 NGHETAVEPKFNSSGTHFSPNLKATFHCCPRSEODRNCSCADNIEGKTFVSTVNSLVF 120
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DB 121 QQIDANWNTQCKLKGDLKLFICYVESLFPKLFNPNYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQWVHCNCSVHCCCLVPVPTAKLNDLLMCLKITSGGVIFQSPPLMSVQPINMYKPDPP 240
DB 181 FQWVHCNCSVHCCCLVPVPTAKLNDLLMCLKITSGGVIFQSPPLMSVQPINMYKPDPP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIYSATSLLDVDSILP 300
DB 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVYSENSTTVIREADKIYSATSLLDVDSILP 300
QY 301 GSSYEYQVRGKRLDGPGLWSWDNSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 360
DB 301 GSSYEYQVRGKRLDGPGLWSWDNSTPRVFTQDVIYFPPKILTSVGSNVSFHCIIYKKNKI 360
QY 361 VPSKETVWMNLAETKIPQSOYDWSHDVSKVTFNINETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKETVWMNLAETKIPQSOYDWSHDVSKVTFNINETKPRGKFTYDAVYCCNEHECHH 420
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: Patent NO. 6342220
: GENERAL INFORMATION:
: APPLICANT: Adams, Camellia
: APPLICANT: W.
: APPLICANT: Carter, Paul J.
: APPLICANT: Fendly, Brian M.
: APPLICANT: Gurney, Austin L.
: TITLE OF INVENTION: Agonist Antibodies
: FILE REFERENCE: P0979
: CURRENT APPLICATION NUMBER: US/08/918,148A
: CURRENT FILING DATE: 1997-08-25
: NUMBER OF SEQ ID NOS: 79
: SEQ ID NO 74
: LENGTH: 249
: TYPE: PRT
: ORGANISM: artificial
: US-08-918-148-74

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Query Match	68.6%	Score	892	DB	4	Length	249
Best Local Similarity	68.4%	Pred	No	1.8e-61			
Matches	171	Conservative	30	Mismatches	43	Indels	6
						Gaps	1

[illegible]

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1  RESULT 3
2  US-09-079-029-11
3  : Sequence 11, Application US/09079029
4  : Patent No. 6342369
5  : GENERAL INFORMATION:
6  : APPLICANT: Adams, Camilla W.
7  : APPLICANT: Ashkenazi, Avi J.
8  : APPLICANT: Chundharapal, Anan
9  : APPLICANT: Kim, Kyung J.
10 : TITLE OF INVENTION: Apo-2 Receptor
11 : NUMBER OF SEQUENCES: 14
12 : CORRESPONDENCE ADDRESS:
13 : ADDRESSEE: Genentech, Inc.
14 : STREET: 1 DNA Way
15 : CITY: South San Francisco
16 : STATE: California
17 : COUNTRY: USA
18 : ZIP: 94080
19 :
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: WinPatIn (Genentech)
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/09/079.029
27 : FILING DATE:
28 : CLASSIFICATION:
29 : ATTORNEY/AGENT INFORMATION:
30 : NAME: Marschang, Diane L.

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1 REGISTRATION NUMBER: 35,600
2 REFERENCE/DOCKET NUMBER: P110182
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: 650/225-5416
5 TELEFAX: 650/952-9881
6 INFORMATION FOR SEQ ID NO: 11:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 310 amino acids
9 TYPE: Amino acid
10 TOPOLOGY: Linear
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[illegible]

RESULT 4
 US-08-665-202-5
 Sequence No. 5, Application US/08665202
 Patent No. 5977322
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schlier, Robert
 TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498

Best Local Similarity 59.48; Pred. No. 1.7e-48;
Matches 149; Conservative 35; Mismatches 46; Indels 21; Gaps 6

[illegible]

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Query Match	55.5%	Score 722	DB 4	Length 288
Best Local Similarity	55.9%	Pred. No. 2.3e-48		
Matches 142	Conservative 47	Mismatches 95	Indels 12	Gaps 5

QY	1	EVLQVQAGAEVKKPEESLKISCSQSGCTFFSSYKKNMVRQAPDKRGLEMMGCIPIPETANY	60
		
	23	OVQLDQPAELVKKPPASVYSLSCASAGYFTGTGWIHWKKRPPDQGLMEITGVNPSRGRSY	82
Db		

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QY      61  AOKRGVRYTILADSTSTAAVYELSLSESDPAVYACARDVVPATSLRGMGMOCGTT 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      83  NEKRNRKNTTLVVDKSSSTTAYHQLSSLSSEDSAVIYCARER-----AICYDDAMRYMOGTT 138

QY      121  VTSSGGGGSGGGGGSGGGGSGSVLTQ--PASYSGSPGOSITISCTGTSSDVG--YNYVS 176
Db      139  VTSSGGGGSGGGGGSGGGGSGDSDIELSSGPSLSLAVSAGEKVMCKSSQSLNSRTFRKNYLA 198

QY      177  WYOOHPGKAPKPLMLIYEGSKRPSCYNSNPFSGSKSGSTASLITSLQLADPEDADYYC-SSYTT 225
Db      199  WYQORPGQSPRLILYMASTRTSGVPDRFTSGSCTDETLITSISSVQADLAIYCKOSYTL 258

QY      236  RSTRVFGGCTKTJV 249
Db      259  RT---FGGCTKLEI 269

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Qy 177 MYOQHPCAPLIMTDESKRPSGVSNNFSGSSASTALITISGLADEADAYC-SSYTT 235
Db 196 MYOQRPGQSPLLLIYNASTRTSGVPDKNFTGSSGSDPTLTIISSQAEDHLIYYCKGSYL 255
Qy 236 RSTRVGGGTRKLY 249
Db 256 RT---FGGGRKLEI 266 ,

RESULT 13
US-09-184-658-40
: Sequence 40, Application US/09184658
: Patent No. 6030792

Query Match	55.28;	Score 717;	DB 3;	Length 284;
Best Local Similarity	54.28;	Pred. No. 5.5e-48;		
Best 136; Conservative	46;	Mismatches 53;	Indels 16;	Gaps 4

Db 83 ADDEFGRAFALEHTSASATAYLQINNKNEDPATYFCARG-----GSLDYWGCGTT 132

QY 121 VTWSGGGGGGSGGGSGGGGSGSVLTQ--PASYSGSPGOSTITCTGTSVDGYNYVSWIQ 179

Db 133 LTWSGGGGSGGGSGGGSGGSGQIVLTQPVFEMASAPGKEXMTTSCASS----VSYMTWQ 188

QY 180 QHPGKAPKLMTYEBSKRPBGYSNNFSGSKSGSTASLTISGLQADEMDYTCSSYTRRSTR 239

Db 189 QKPGSPRLTLHAHSNLSAAGVPVAFSGGSGTSTSLTISRMEADEADATYYCCQWRMS--YTR 247

QY 240 VEGGSTRKLTVL 250

Db 248 TFGGCTKLEIT 258

RESULT 14
 US-09-260-527-1
 : Sequence 1, Application US/09260527A
 : Patent No. 6228599
 : GENERAL INFORMATION:
 : APPLICANT: Knox, J.P.
 : APPLICANT: Mikkelson, J.D.
 : APPLICANT: Willards, W. G.
 : TITLE OF INVENTION: ANTI BODY
 : FILE REFERENCE: DPOU19.001AUS
 : CURRENT APPLICATION NUMBER: US/09/260,527A
 : CURRENT FILING DATE: 1999-02-26
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 1
 : LENGTH: 280
 : TYPE: PRT
 : ORGANISM: UNKNOWN
 : FEATURE:
 : OTHER INFORMATION: Anti-homogalacturonan specific antibodies from a
 : OTHER INFORMATION: phage display library known as the Synthetic scFv
 : OTHER INFORMATION: Library (#1) from the Centre for Protein
 : OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
 US-09-260-527-1

Query Match 54.9%; Score 714; DB 4; Length 280;
Best Local Similarity 59.7%; Pred. No. 9.2e-48;
Matches 151; Conservative 34; Mismatches 52; Indels 16; Gaps 7.

RESULT 15
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCES
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF INVENTIONS: 30
TITLE OF INVENTION: ANTIBODIES
NUMBER OF INVENTIONS: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILDEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
ZIP: 22201
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 350
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 54.5%; Score 709; DB 2; Length 244;
Best Local Similarity 56.8%; Pred. No. 1.9e-47;
Matches 147; Conservative 37; Mismatches 49; Indels 26; Gaps 7;

QY 1 EVOLVSGAEVKKPGRSLKISCGSGFTSSYKAMVROAPGKGLMAGIPIRGTANY 60
DB 1 EVOLOQSGAEVKKPGRSLKISCGSGFTSSYKAMVROAPGKGLMAGIPIRGTANY 60
QY 61 AOKFOGRTVITADESTAYMELSLRSEDYAYYCA-RD-----RVVVPATSLRGMDV 114
DB 61 NEFKSKALITVDKSSSTAYMQLSLTSPDSAVYYCASRDYDGRY-----FDY 110
QY 115 WSGGTTVTVSSGGGGSGGGGGGSGQSVLTQ-PASVSGSGPGOSITISCTGTSSDVGYN 173
DB 115 WSGGTTVTVSSGGGGSGGGGGGSGQSVLTQ-PASVSGSGPGOSITISCTGTSSDVGYN 173
QY 174 YVSWYQHQPKAPKLMITGSKRPSCVSNRPSGSKSGSTASLTISGLQADEADYIC--- 230
DB 167 YMYWYQKPGSSRLIYDTSNLSAGVPYRFSGSGSGTYSYLTISRMEADATYICQOM 226
QY 231 SSTTSTSTRVFGGGLTV 249

DB 227 SSYPMPYT--FGGGLKLEI 243

Search completed: August 15, 2002, 16:22:15
Job time: 425 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:27:06 ; Search time 111.01 Seconds
(without alignments)
520.399 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKKPGESLKI.....SSYTRSTRVFGGKTLTVL 250

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 698052 seqs, 231078099 residues

Total number of hits satisfying chosen parameters: 698052

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1163	89.5	249	5	US-09-959-373A-2
2	1092.5	84.0	242	1	PCT-US02-16106-16
3	1092.5	84.0	242	6	US-10-151-882-16
4	1012	77.8	272	5	US-09-791-537-845
5	980	75.4	245	6	US-10-039-785-47
6	980	75.4	245	6	US-10-139-785-47
7	967	74.4	245	1	PCT-US02-16106-15
8	967	74.4	245	6	US-10-151-882-15
9	966	74.3	254	5	US-09-791-537-32035
10	965	74.2	245	6	US-10-039-785-51
11	965	74.2	245	6	US-10-139-785-51
12	948	72.9	245	6	US-10-039-785-43
13	948	72.9	245	6	US-10-139-785-43
14	943.5	72.6	248	1	PCT-US02-16106-19
15	943.5	72.6	248	6	US-10-151-882-19
16	939	72.2	245	6	US-10-039-785-42
17	939	72.2	245	6	US-10-139-785-46
18	939	72.2	245	6	US-10-139-785-42
19	939	72.2	245	6	US-10-139-785-46
20	937	72.1	245	6	US-10-039-785-52
21	937	72.1	245	6	US-10-139-785-52
22	934.5	71.9	248	1	PCT-US02-16106-17
23	934.5	71.9	248	6	US-10-151-882-17
24	928	71.4	245	6	US-10-039-785-45
25	928	71.4	245	6	US-10-039-785-48
26	928	71.4	245	6	US-10-139-785-45

27	928	71.4	245	6	US-10-139-785-48	Sequence 48, Appl
28	923	71.0	245	6	US-10-039-785-49	Sequence 49, Appl
29	923	71.0	245	6	US-10-139-785-49	Sequence 49, Appl
30	903	69.5	246	5	US-09-791-537-70804	Sequence 70804, A
31	896.5	69.0	252	1	PCT-US02-11474-73	Sequence 73, Appl
32	896.5	69.0	252	6	US-10-120-414-73	Sequence 73, Appl
33	894	68.8	249	1	PCT-US02-16106-18	Sequence 18, Appl
34	894	68.8	249	6	US-10-151-882-18	Sequence 18, Appl
35	856	65.8	241	1	PCT-US02-16106-21	Sequence 21, Appl
36	856	65.8	241	6	US-10-151-882-21	Sequence 21, Appl
37	848.5	65.3	252	1	PCT-US02-16106-14	Sequence 14, Appl
38	848.5	65.3	252	6	US-10-151-882-14	Sequence 14, Appl
39	836.5	64.3	254	1	PCT-US02-16106-24	Sequence 24, Appl
40	836.5	64.3	254	6	US-10-151-882-24	Sequence 24, Appl
41	836	64.3	253	1	PCT-US02-11474-76	Sequence 76, Appl
42	836	64.3	253	6	US-10-120-414-76	Sequence 76, Appl
43	833.5	64.1	252	1	PCT-US02-16106-13	Sequence 13, Appl
44	833.5	64.1	252	6	US-10-151-882-13	Sequence 13, Appl
45	826.5	63.6	240	1	PCT-US02-16106-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-959-373A-2
; Sequence 2, Application US/09959373A
; GENERAL INFORMATION:
; APPLICANT: Zardi, Luciano
; TITLE OF INVENTION: A tenascin-c isoform as a marker for neoplasias
; FILE REFERENCE: 1875PT
; CURRENT APPLICATION NUMBER: US/09/959,373A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: FI99A000094
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-959-373A-2

Query Match	89.5%	Score 1163;	DB 5;	Length 249;
Best Local Similarity	89.8%	Pred. No. 2.3e-62;		
Matches	225;	Conservative 11;	Mismatches 11;	Indels 4; Gaps 2;
QY	1	EVQLVQSGAEVKKPGESLKI	SCSGGFTFSYKMNWYRQAPGKLEWGGIPIFGTANY	60
Db	1	QVQLVQSGAEVKKPGSSVKVSKASGGTFSYATISWYRQAPGQGLEWGGIPIFGTANY	60	
QY	61	AQKFGQGVTTTADSTAYMELSSLRSEDTAVYVCARDRVVVPATSLRGG-MDVWGQGT	119	
Db	61	AQKFGQGVTTTADSTAYMELSSLRSEDTAVYVCARSRI---TIFGGGAFDIWGRGT	117	
QY	120	TVTVSSGGGSGGGSGGGSQSVLTQTPASVSGSPGQISITCTGTSDVGGYVYVSWYQ	179	
Db	118	MVTVSSGGGSGGGSGGGSQSVLTQTPASVSGSPGQISITCTGTSDVGGYVYVSWYQ	177	
QY	180	QHPCKAPKLMYEGSKPPSGVSNRFGSKSGTASLTISGLQADEADYYCSTYTRSTR	239	
Db	178	QHPCKAPKLMYEGSKPPSGVSNRFGSKSGTASLTISGLQADEADYYCSTYTRSTR	237	
QY	240	VFGGKTLTVL 250		
Db	238	VFGGKTLTVL 248		
RESULT 2				
PCT-US02-16106-16				
; Sequence 16, Application PC/TUS0216106				
; GENERAL INFORMATION:				

```

; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554pCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A027A11 scfV
; PCT-US02-16106-16

```

Query Match	84.0%	Score	1092.5	DB 1	Length	242			
Best Local Similarity	83.6%	Pred. No.	3.5e-59						
Matches	209	Conservative	15	Mismatches	17	Indels	9	Gaps	1
Qy	1	EVQLVQSGAEVKKPGESLKISQCGSGGTFSSYKKNWVRQAPGKGLWMGGIPIFGTANY	60						
Db	1	QVQLQSGAEVKKPGSSVKYSCAKSGGTFTYAITWVRQAPGQGLWMGDIIVPFGIPNY	60						
Qy	61	AQKFGQRTVITADSTAYMELSSLSRSDTAVYYCARDRVVVPATSLRGMDVWGQTT	120						
Db	61	AQMFDQRTVITADSTAYLELSLGAEDTAVYYCARG-----SQAFEIWGKGT	111						
Qy	121	VTSSGGGGGGGGGGGSGSVLTQTQPSVSGSPGQSITISCTGTSDDVGGYNTVSWYQQ	180						
Db	112	VTVSSGGGGGGGGGGGSGSVLTQTQPSVSGSPGQSITISCTGTSDDVGGYNVSWYQQ	171						
Qy	181	HPGKAPKLMIEYSGKPSGVSNRRSPGSKSGTASLTISGLQAEADAYCCSYTTRSTRV	240						
Db	172	HPGKAPKLMIEYSGKPSGVSNRRSPGSKSGTASLTISGLQAEADAYCCSYTTRSTRV	231						
Qy	241	FGGQTKLTVL	250						
Db	232	FGGQTKLTVL	241						

```

RESULT      3
US-10-151-882-16
; Sequence 16, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIORITY APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A027A11 scfv
US-10-151-882-16

```

Query Match	84.0%	Score 1092.5	DB 6	Length 242
Best Local Similarity	83.6%	Prctd. No. 3.5e-58		
Matches 209	Conservative 15	Mismatches 17	Indels 9	Gaps 1
QY	1	EVQLVQSGAEVKKPGESLKISQCSGGFTFSYKNNWVRQAPGKLEWNGGIPIFGTANY	60	
Db	1	QVQLVQSGAEVKKPGSSVKVSKASGGTFTSYATWVROAPGSGLEWNGDIPIVFGIPNY	60	

Qy	61	AQKQGRVVTITADESTSTAYMELSSLASDETAVYICARDRVVVYPATSLRGMDVMVGOGTT	120
Db	61	: :	
Qy	121	VTVSGGGGSGGGGSGGGGSGSVLTQPASVSGSPGOSITISCTGTSSDVGGINVSMWQQ	180
Db	112	VTVSGGGGSGGGGSGGGGSGSVLTQPASVSGSPGOSITISCTGTSSDVGGINVSMWQQ	171
Qy	181	HPGRAPKLMIYEGSKRPSGVSNRRPSSGKSQSGLTASLTSIGLQAEDAADYYCSSLTYSTRV	240
Db	172	HPGRAPKLMIYEGSKRPSGVSNRRPSSGKSQSGLTASLTSIGLQAEDAADYYCSSLTYSTRV	231
Qy	241	FGGKTUVTVL	250
Db	232	FGGKTUVTVL	241

```

RESULT 4
US-09-791-537-845
; Sequence 845, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dranzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 845
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-845

```

[illegible]

RESULT 5
US-10-039-785-47
; Sequence 47, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: .. Receptors
; FILE REFERENCE: PF50
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07


```

RESULT      6
US-10-139-785-47
; Sequence 47, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364

```

Query Match 74.4%; Score 967; DB 1; Length 245;
Best Local Similarity 75.8%; Pred. No. 1.1e-50;
Matches 191; Conservative 19; Mismatches 32; Indels 10; Gaps 4;

QY 1 EVQLVSGAEEVKPGESLKISCSQGSFTFSYKMNWVRQAPKGLEWMGGIPIFGTANY 60
:|||||:|||||:|||:|||||:|||||:|||||:|||||:|||||

```
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTSSYGIKRVWVQAPQGGLWMGGIIPFGTANY 60
QY 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYICARDRVVVPATSLRGGMDVWGQGT 120
Db 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYICARSNPOYDA-----FDINGQGT 114
QY 121 VIVSSGGGGGGGGGGGSGSVLTQTPASVSGSPGQSITISCTGSSDYGNYVSWYQQ 180
Db 115 VIVSSGGGGGGGGGGGSGSVLTQTPPSVSGTSGQRTVSCGGRSNIGS-NTVKWYQQ 173
QY 181 HPKAPKLMYEGSKRPVSVNRFSGSKSGSTASLTISGLQAEADYYCSTYTRSTR- 239
Db 174 LFGTAPKLLIYNDQRPVSGVPPDRFSGSKSGNTASLTISGLQAEADYYCQSYDS-SLRG 232
QY 240 -VFGGQTKLTVL 250
Db 233 SVFEGGQTKLTVL 244

RESULT 8
US-10-151-882-15
; Sequence 15, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A004G02 scFv
US-10-151-882-15

Query Match 74.4%; Score 967; DB 6; Length 245;
Best Local Similarity 75.8%; Pred. No. 1.1e-50;
Matches 191; Conservative 19; Mismatches 32; Indels 10; Gaps 4;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTSSYKMNWVQAPGKGLWGMGGIIPFGTANY 60
Db 1 QVQLVQSGAEVKKPGSSVKVSKASGGTSSYGIKRVWVQAPQGGLWMGGIIPFGTANY 60
QY 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYICARDRVVVPATSLRGGMDVWGQGT 120
Db 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYICARSNPOYDA-----FDINGQGT 114
QY 121 VIVSSGGGGGGGGGGGSGSVLTQTPASVSGSPGQSITISCTGSSDYGNYVSWYQQ 180
Db 115 VIVSSGGGGGGGGGGGSGSVLTQTPPSVSGTSGQRTVSCGGRSNIGS-NTVKWYQQ 173
QY 181 HPKAPKLMYEGSKRPVSVNRFSGSKSGSTASLTISGLQAEADYYCSTYTRSTR- 239
Db 174 LFGTAPKLLIYNDQRPVSGVPPDRFSGSKSGNTASLTISGLQAEADYYCQSYDS-SLRG 232
QY 240 -VFGGQTKLTVL 250
Db 233 SVFEGGQTKLTVL 244

RESULT 9
US-09-791-537-32035
; Sequence 32035, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomeix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
```

```
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32035
; LENGTH: 254
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-32035

Query Match 74.3%; Score 966; DB 5; Length 254;
Best Local Similarity 73.1%; Pred. No. 1.3e-50;
Matches 190; Conservative 19; Mismatches 33; Indels 18; Gaps 2;

QY 1 EVQLVQSGAEVKKPGESLKISCGSGFTSSYKMNWVQAPGKGLWGMGGIIPFGTANY 60
Db 2 QVQLVESGGGVVQPGSRSLRSCAASGFTFRNYGVHVRQAPGKGLWVAVISYDGSNKYY 61
QY 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYICARDRVVVPATSLRGG----- 111
Db 62 ADSVKGRTFISRDNSKNTLYLQMNLSLRVEDTAVYYCAR-----RWYGGSGYGHFYS 113
QY 112 -MDVMGQGTTVTVSSGGGGGGGGGSGSVLTQTPASVSGSPGQSITISCTGSSDVG 170
Db 114 YNDGNGKGTKVTVSSGGGGGGGGGSGSVLTQTPASVSGSPGQSITISCTGSSDVG 173
QY 171 GYNYVSWTQOHGPKAPKLMYEGSKRPVSVNRFSGSKSGSTASLTISGLQAEADYYC 230
Db 174 GYNYVSWTQOHGPKAPKLMYEGSKRPVSVNRFSGSKSGNTASLTISGLQAEADYYC 233
QY 231 SSYTRSTRVFGGQTKLTVL 250
Db 234 SSYTRSTRVFGGQTKLTVL 253

RESULT 10
US-10-039-785-51
; Sequence 51, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
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FEATURE:
OTHER INFORMATION: T1015A07 scFv
US-10-039-785-51

Query Match 74.2%; Score 965; DB 6; Length 245;

Best Local Similarity 75.3%; Pred. No. 1.4e-50;

Matches 189; Conservative 21; Mismatches 33; Indels 8; Gaps 2;

QY 1 EVOLVOSGAEVKKPGESLKIISCGSGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
|||||
Db 1 EVOLVOSGAEVKKPGASVKVSKISGDSFTAYFIHMLRQAPGEGLEWGFNPISGTADS 60
|||||
QY 61 AQKFGQGRVTTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMVWGQGIT 120
|||||
Db 61 PQKFGHVRVAMTRDTSISTAYMELTRLASDDTAIYYCARQH-----HSNTFDPWGQGITL 113
|||||
QY 121 VTVSSGGGGGGGGGGGGGGS-QSVLTQPASVSGSPQISITISCTGTSSDVGGINYYVSWYQ 179
|||||
Db 114 VTVSSGGGGGGGGGGGGGGSQAQALTPASMSGSPQISITISCTGTSSDVGGINYYVSWYQ 173
|||||
QY 180 QHPGKAPKLMYEGSRKPSGVNRFSGSGSTASLTISGLQAEDEADYYCSTYTRSTR 239
|||||
Db 174 QHPGKAPKLMYAVTNRPSCVSNRFSASKSGNTASLTISGLQAEDEADYYCSTYSSNTW 233
|||||
QY 240 VFGGGTKLTVL 250
|||||
Db 234 VFGGGTKVTVL 244

RESULT 11

US-10-139-785-51

Sequence 51, Application US/10139785

GENERAL INFORMATION:

APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/369,860

PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/327,364

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/323,807

PRIOR FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: 60/309,176

PRIOR FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 60/294,981

PRIOR FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: 60/293,473

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 51

LENGTH: 245

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: T1015A07 scFv

US-10-139-785-51

Query Match

Best Local Similarity 74.2%; Score 965; DB 6; Length 245;

Matches 189; Conservative 21; Mismatches 33; Indels 8; Gaps 2;

QY 1 EVOLVOSGAEVKKPGESLKIISCGSGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
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Db 1 EVOLVOSGAEVKKPGASVKVSKISGDSFTAYFIHMLRQAPGEGLEWGFNPISGTADS 60
|||||
QY 61 AQKFGQGRVTTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMVWGQGIT 120
|||||
Db 61 PQKFGHVRVAMTRDTSISTAYMELTRLASDDTAIYYCARQH-----HSNTFDPWGQGITL 113
|||||
QY 121 VTVSSGGGGGGGGGGGGGGS-QSVLTQPASVSGSPQISITISCTGTSSDVGGINYYVSWYQ 179
|||||
Db 114 VTVSSGGGGGGGGGGGGGGSQAQALTPASMSGSPQISITISCTGTSSDVGGINYYVSWYQ 173
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QY 180 QHPGKAPKLMYEGSRKPSGVNRFSGSGSTASLTISGLQAEDEADYYCSTYTRSTR 239
|||||
Db 174 QHPGKAPKLMYAVTNRPSCVSNRFSASKSGNTASLTISGLQAEDEADYYCSTYSSNTW 233
|||||
QY 240 VFGGGTKLTVL 250
|||||
Db 234 VFGGGTKVTVL 244

QY 1 EVOLVOSGAEVKKPGESLKIISCGSGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
|||||
Db 1 EVOLVOSGAEVKKPGASVKVSKISGDSFTAYFIHMLRQAPGEGLEWGFNPISGTADS 60
|||||
QY 61 AQKFGQGRVTTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMVWGQGIT 120
|||||
Db 61 PQKFGHVRVAMTRDTSISTAYMELTRLASDDTAIYYCARQH-----HSNTFDPWGQGITL 113
|||||
QY 121 VTVSSGGGGGGGGGGGGGGS-QSVLTQPASVSGSPQISITISCTGTSSDVGGINYYVSWYQ 179
|||||
Db 114 VTVSSGGGGGGGGGGGGGGSQAQALTPASMSGSPQISITISCTGTSSDVGGINYYVSWYQ 173
|||||
QY 180 QHPGKAPKLMYEGSRKPSGVNRFSGSGSTASLTISGLQAEDEADYYCSTYTRSTR 239
|||||
Db 174 QHPGKAPKLMYAVTNRPSCVSNRFSASKSGNTASLTISGLQAEDEADYYCSTYSSNTW 233
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QY 240 VFGGGTKLTVL 250
|||||
Db 234 VFGGGTKVTVL 244

RESULT 12
US-10-039-785-43
Sequence 43, Application US/10039785
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 245
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: T1014G03 scFv
US-10-039-785-43

Query Match 72.9%; Score 948; DB 6; Length 245;

Best Local Similarity 74.6%; Pred. No. 1.5e-49;

Matches 188; Conservative 20; Mismatches 34; Indels 10; Gaps 3;

QY 1 EVOLVOSGAEVKKPGESLKIISCGSGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
|||||
Db 1 EVOLVOSGAEVKKPGASVKLSKRSVSGDTFTAYFIHWRQAPGCGLEWGFNPISGTAGS 60
|||||
QY 61 AQKFGQGRVTTITADESTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMVWGQGIT 119
|||||
Db 61 AEFKRGHVRVAMTRDTSISTAYMELNRLTFDDTAVYYCARQH-----RGNTFDPWGQGIT 112
|||||
QY 120 TTVTVSSGGGGGGGGGGGGGGS-QSVLTQPASVSGSPQISITISCTGTSSDVGGINYYVSWY 178
|||||

Db 113 LVTVSSGGGGGGGGGSAQAALTPASVSGSPGQSIITISCTGTSSDITGAYKYVSWY 172
QY 179 QHPGKAPKLMYEGSRKPSGVSNRFSKSGTASLTISGLQAEADYYCSTYTRST 238
Db 173 QHPGKAPKLMYIEVSNRPSGVSNRFSKSGTASLTISGLQADDEADYYCNSYQYNT 232
QY 239 RVFGGGTKLTVL 250
Db 233 WVFEGGTKLTVL 244

RESULT 13-
US-10-139-785-43
; Sequence 43, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014G03 scFv
US-10-139-785-43

Query Match 72.9%; Score 948; DB 6; Length 245;
Best Local Similarity 74.8%; Pred. No. 1.5e-49;
Matches 186; Conservative 20; Mismatches 34; Indels 10; Gaps 3;
QY 1 EVLVQSSGAEVKPGESLKISCOGSGTFFSSYKMNWVRQAPGKGLWGGIPIFGTANY 60
Db 1 EVLVQSSGAEVKPGASVKLSRVSGDTFTAYFIHWYRQAPGQGLWGNFNPISGTAGS 60
QY 61 AOKFQGRVTTTADSTSTAYMELSSLRSEDTAVYICARDRVVVPATSLRGG-MDVWGQGT 119
Db 61 AEKFRGRVAMTRDTSISTAYMELNRLTFDDTAVYICARQH-----RGNTFDPWQGGT 112
QY 120 TTVTVSSGGGGGGGGGGGGS-QSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVYVSWY 178
Db 113 LVTVSSGGGGGGGGGSAQAALTPASVSGSPGQSIITISCTGTSSDITGAYKYVSWY 172
QY 179 QHPGKAPKLMYEGSRKPSGVSNRFSKSGTASLTISGLQAEADYYCSTYTRST 238
Db 173 QHPGKAPKLMYIEVSNRPSGVSNRFSKSGTASLTISGLQADDEADYYCNSYQYNT 232
QY 239 RVFGGGTKLTVL 250
Db 233 WVFEGGTKLTVL 244

Db 233 WVFEGGTKLTVL 244

RESULT 14
PCT-US02-16106-19
; Sequence 19, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A053H04 scFv
PCT-US02-16106-19

Query Match 72.6%; Score 943.5; DB 1; Length 248;
Best Local Similarity 73.9%; Pred. No. 2.8e-49;
Matches 187; Conservative 26; Mismatches 31; Indels 9; Gaps 4;
QY 1 EVLVQSSGAEVKPGESLKISCOGSGTFFSSYKMNWVRQAPGKGLWGGIPIFGTANY 60
Db 1 EVLVQSSGAEVKPGSSVKVSKASGGTFFSNYALSWYRQAPGQGLWGGIPLFDTPNY 60
QY 61 AOKFQGRVTTTADSTSTAYMELSSLRSEDTAVYICARDRVVVPATSLRGGMDVWGQGT 120
Db 61 AOKFQGRVTTTADSTSTAYMELSSLRSEDTAVYICARGN-----TQPR-PFDPWKGQTT 114
QY 121 VTVSSGGGGGGGGGGGGS-QSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVYVSWY 179
Db 115 VTVSSGGGGGGGGGSAQAALTPQSSVSGAPGQRTVTSCTGSSSNIGAGYEVNMYQ 174
QY 180 QHPGKAPKLMYEGSRKPSGVSNRFSKSGTASLTISGLQAEADYYCSTYTR--RS 237
Db 175 QLPGTAPKLLIYGDTRNPSPGVPDRFSGSKSGTSASLAITGLQAEADYYCQSYDSGPGG 234
QY 238 TRVFGGTKLTVL 250
Db 235 PVVFGGTKLTVL 247

RESULT 15
US-10-151-882-19
; Sequence 19, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A053H04 scFv
US-10-151-882-19

Query Match 72.6%; Score 943.5; DB 6; Length 248;

Best Local Similarity 73.9%; Pred. No. 2.8e-49;
Matches 187; Conservative 26; Mismatches 31; Indels 9; Gaps 4;

QY	1	EVQLVQSGAEVKKPGESLKISQCGSGFTFSSYKKNWVROAPGKGLEWMGGIIPFGTANY	60
Db	1	EVQLVQSGAEVKKPGSSVKYCKRASGTFNSYAIISWVROAPGQGLEWMGGIIPFDTPNY	60
QY	61	AQKFGQRTVITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMVWGQTT	120
Db	61	AQKFGQRTVITADESTSTAYMELSSLRSEDTAVYYCARGN-----TGPR-PFDPWGKGT	114
QY	121	VTVSSGGSGSGGGGGGS-QSVLTQPASVSGSPGQITISCTGTSSDYGYNYYSWYQ	179
Db	115	VTVSSGGSGSGGGGGGSAQAVLTQPSVSGAPGORVIVCTGSSSNIGAGYEYVNWYQ	174
QY	180	QHPGKAPKLMIEGSKRPSGVSNRFSKSGSTASLTISGLQAEDEADYYCSYTT--RS	237
Db	175	QLPGTAPKLLIYGDTNRPSGVDPDRFSKSGSGTSASLAITGLQAEDEANYCYQSYDSGPG	234
QY	238	TRVFGGSKLTVL	250
Db	235	PVVFGGSKLTVL	247

Search completed: August 15, 2002, 16:27:07
Job time: 372 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 15:34:04 ; Search time 410.32 Seconds
(without alignments)
214.455 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKPGESLKI.....SSYTRSTRVFGGKTTLVL 250

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA_Main:*

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26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1300	100.0	250	11	US-08-779-457-49
2	1152.5	88.7	254	1	PCT-US01-19110-1412
3	1152.5	88.7	254	22	US-09-880-748-1412
4	1149	88.4	253	1	PCT-US01-19110-1813
5	1149	88.4	253	22	US-09-880-748-1813
6	1147.5	88.3	252	1	PCT-US01-19110-1666
7	1147.5	88.3	252	22	US-09-880-748-1666

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8 1139 87.6 253 1 PCT-US01-19110-1880
9 1139 87.6 253 22 US-09-880-748-1880
10 1136 87.4 251 1 PCT-US01-19110-1756
11 1136 87.4 251 22 US-09-880-748-1756
12 1133.5 87.2 254 1 PCT-US01-19110-1699
13 1133.5 87.2 254 22 US-09-880-748-1699
14 1130 86.9 247 1 PCT-US01-19110-1770
15 1130 86.9 247 22 US-09-880-748-1770
16 1129.5 86.9 254 1 PCT-US01-19110-1450
17 1129.5 86.9 254 22 US-09-880-748-1450
18 1128 86.8 247 1 PCT-US01-19110-1434
19 1128 86.8 247 22 US-09-880-748-1434
20 1128 86.8 247 22 US-09-880-748-1434
21 1128 86.8 247 22 US-09-880-748-1434
22 1126 86.6 251 1 PCT-US01-19110-1397
23 1126 86.6 251 22 US-09-880-748-1397
24 1124 86.5 247 1 PCT-US01-19110-1661
25 1124 86.5 247 22 US-09-880-748-1661
26 1123.5 86.4 250 1 PCT-US01-19110-947
27 1123.5 86.4 250 22 US-09-880-748-947
28 1121 86.2 247 1 PCT-US01-19110-1744
29 1121 86.2 247 22 US-09-880-748-1744
30 1120.5 86.2 246 1 PCT-US01-19110-1589
31 1120.5 86.2 246 22 US-09-880-748-1589
32 1116 85.8 247 1 PCT-US01-19110-1704
33 1116 85.8 247 22 US-09-880-748-1704
34 1115 85.8 245 1 PCT-US01-19110-846
35 1115 85.8 245 22 US-09-880-748-846
36 1115 85.8 245 22 US-09-880-748-846
37 1115 85.8 245 22 US-09-880-748-1743
38 1115 85.8 249 1 PCT-US01-19110-1748
39 1115 85.8 249 22 US-09-880-748-1748
40 1114.5 85.7 250 1 PCT-US01-19110-1439
41 1114.5 85.7 250 22 US-09-880-748-1439
42 1114.5 85.7 250 22 US-09-880-748-1439
43 1114.5 85.7 250 22 US-09-880-748-1581
44 1113.5 85.7 252 1 PCT-US01-19110-1656
45 1113.5 85.7 252 22 US-09-880-748-1656

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ALIGNMENTS

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RESULT 1
US-08-779-457-49
; Sequence 49, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96

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Sequence 1880, Ap
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Sequence 1656, Ap
Sequence 1656, Ap

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585005
FILING DATE: 01/08/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0986P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-779-457-49

Query Match 100.0%; Score 1300; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.9e-99;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVSGAEVKKPGESLAKISCGSGFTFSSYKMNVRQAPGKLEWVGIIPIFGTANY 60
DB 1 EVOLVSGAEVKKPGESLAKISCGSGFTFSSYKMNVRQAPGKLEWVGIIPIFGTANY 60
QY 61 AOKFQGRVITADESTSTAYMELSLRSEDVAVYICARDRVVVPATSLRGMDVWGQTT 120
DB 61 AOKFQGRVITADESTSTAYMELSLRSEDVAVYICARDRVVVPATSLRGMDVWGQTT 120
QY 121 VTSSGGGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSWYQ 180
DB 121 VTSSGGGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSWYQ 180
QY 181 HPKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQADEADYICSSYTTSTRV 240
DB 181 HPKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQADEADYICSSYTTSTRV 240
QY 241 FGGGTKLTVL 250
DB 241 FGGGTKLTVL 250

RESULT 2
PCT-US01-19110-1412
Sequence 1412, Application PC/TUS0119110
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523PCT
CURRENT APPLICATION NUMBER: PCT/US01/19110
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1412
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-19110-1412

Query Match 88.7%; Score 1152.5; DB 1; Length 254;

Best Local Similarity 87.4%; Pred. No. 1.1e-86;
Matches 221; Conservative 14; Mismatches 15; Indels 3; Gaps 1;
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DB 1 QVOLQSGAEVKKPGSSVKSVKSCGGTFFSSVIAISVWRAPQGLEWVGIIPIFGTANY 60
QY 61 AOKFQGRVITADESTSTAYMELSLRSEDVAVYICARD---RVVVPATSLRGMDVWGQ 117
DB 61 AOKFQGRVITADESTSTAYMELSLRSDDTAVYICARDGIYDILTTLVSYNGMDVWGK 120
QY 118 GTTVTVSSGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSW 177
DB 121 GTMTVTVSSGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSW 180
QY 178 YQOHGKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQADEADYICSSYTTTRS 237
DB 181 YQOHGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQADEADYICSSYTTTRS 240
QY 238 TRVFGGTTKLTVL 250
DB 241 TRVFGGTTKLTVL 253

RESULT 3
US-09-880-748-1412
Sequence 1412, Application US/09880748
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1412
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1412

Query Match 88.7%; Score 1152.5; DB 22; Length 254;
Best Local Similarity 87.4%; Pred. No. 1.1e-86;
Matches 221; Conservative 14; Mismatches 15; Indels 3; Gaps 1;
QY 1 EVOLVSGAEVKKPGESLAKISCGSGFTFSSYKMNVRQAPGKLEWVGIIPIFGTANY 60
DB 1 QVOLQSGAEVKKPGSSVKSVKSCGGTFFSSVIAISVWRAPQGLEWVGIIPIFGTANY 60
QY 61 AOKFQGRVITADESTSTAYMELSLRSEDVAVYICARD---RVVVPATSLRGMDVWGQ 117
DB 61 AOKFQGRVITADESTSTAYMELSLRSDDTAVYICARDGIYDILTTLVSYNGMDVWGK 120
QY 118 GTTVTVSSGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSW 177
DB 121 GTMTVTVSSGGGGGGGGGSGQSQSVLTQPASVSGSPGQSIITISCTGTSSDVGYNVSW 180
QY 178 YQOHGKAPKLMIEGSKRPSGVNRFSGSKSGSTASLTISGLQADEADYICSSYTTTRS 237
DB 181 YQOHGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQADEADYICSSYTTTRS 240
QY 238 TRVFGGTTKLTVL 250


```

Qy 61 A QKFGQGVTTTADESTSTAYMELSSLRSEDYAVYYCAR--DRVVVYPATSLRGMDVWGOG 119
Db 61 A QKFGQGVTTTADESTSTAYMELSSLRSEDYAVYYCARGGVDILTGYVYLR-GMDVWGGRG 119

Qy 119 TTWTVSSGGGGGGGGGGGSGGGSOSVLTQPAVSVSGSPQGSITTSCTGTSDDVGGYNYVSWY 178
Db 120 TMTWTVSSGGGGGGGGGGGSGGGSOSVLTQPAVSVSGSPQGSITTSCTGTSDDVGGYNYVSWY 179

Qy 179 QQHPGKAPKLMWIEGSKRPSGVNRRFSGSKSGSTASLITISGLQAEADYDYCSSYTTTST 238
Db 180 QQHPGKAPKLMWIEGSKRPSGVNRRFSGSKSGTASLITISGLQAEADYDYCSSYTTTST 239

Qy 239 RVFGGGTKLTVL 250
Db 240 RVFGGGTKLTVL 251

RESULT 7
US-09-880-748-1666
; Sequence 1666, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1666

Query Match 88.3%; Score 1147.5; DB 22; Length 252;
Best Local Similarity 88.5%; Pred. No. 2.7e-86;
Matches 223; Conservative 13; Mismatches 13; Indels 3; Gaps

Qy 1 EVOLVQSGAEVKKPGESLKISCGSGFTTSSYKMNVRQAPKGLQEWGGIIPFGTANY 60
Db 1 QVOLLQSAAEVKKPGESVKVSKASGCTTSSYAIWSVRQAPQGLQEWGGIIPFGTANY 60

Qy 61 A QKFGQGVTTTADESTSTAYMELSSLRSEDYAVYYCAR--DRVVVYPATSLRGMDVWGOG 118
Db 61 A QKFGQGVTTTADESTSTAYMELSSLRSEDYAVYYCARGGVDILTGYVYLR-GMDVWGGRG 119

Qy 119 TTWTVSSGGGGGGGGGGGSGGGSOSVLTQPAVSVSGSPQGSITTSCTGTSDDVGGYNYVSWY 178
Db 120 TMTWTVSSGGGGGGGGGGGSGGGSOSVLTQPAVSVSGSPQGSITTSCTGTSDDVGGYNYVSWY 179

Qy 179 QQHPGKAPKLMWIEGSKRPSGVNRRFSGSKSGSTASLITISGLQAEADYDYCSSYTTTST 238
Db 180 QQHPGKAPKLMWIEGSKRPSGVNRRFSGSKSGTASLITISGLQAEADYDYCSSYTTTST 239

Qy 239 RVFGGGTKLTVL 250
Db 240 RVFGGGTKLTVL 251

RESULT 8
PCT-US01-19110-1880
; Sequence 1880, Application PC/TUS0119110

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; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 254
; TYPE: PRF
; ORGANISM: Homo sapiens
PCT-US01-19110-1699

Query Match      87.2%; Score 1133.5; DB 1; Length 254;
Best Local Similarity 87.0%; Pred. No. 3.9e-85;
Matches 220; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCOGSGFTFSSYKMNWVRQAPGKGLWMGIIPIFGTANY 60
DB 1 QVQLQSGAEVKKPGSSVKSCRASGCTFSSYAISWVRQAPGCGLEMMGRIIPILGIANY 60
QY 61 AQKFGQGRVTITADESTAYMELSSLSRSEDYAVYICARD---RVVVPATSLRGMQVWGQ 117
DB 61 AQKFGQGRVTITADKSTAYMELSSLSRSEDYAVYICARDYRNYDILTGHPYGYMDVWGR 120
QY 118 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSW 177
DB 121 GTTVTVSSGGGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSW 180
QY 178 YQHPGKAPKLMIEGSKRPSGVNRFSGSKGSTASLTISGLQAEDEADYYCSTYTR 237
DB 181 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSTYTR 240
QY 238 TRVFGGKTLTVL 250
DB 241 TRVFGGKTLTVL 253

RESULT 13
US-09-880-748-1699
; Sequence 1699, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 254
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-880-748-1699

Query Match      87.2%; Score 1133.5; DB 22; Length 254;
Best Local Similarity 87.0%; Pred. No. 3.9e-85;
Matches 220; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

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Matches 220; Conservative 12; Mismatches 18; Indels 3; Gaps 1;

QY 1 EVOLVQSGAEVKKPGESLKISCOGSGFTFSSYKMNWVRQAPGKGLWMGIIPIFGTANY 60
DB 1 QVQLQSGAEVKKPGSSVKSCRASGCTFSSYAISWVRQAPGCGLEMMGRIIPILGIANY 60
QY 61 AQKFGQGRVTITADESTAYMELSSLSRSEDYAVYICARD---RVVVPATSLRGMQVWGQ 117
DB 61 AQKFGQGRVTITADKSTAYMELSSLSRSEDYAVYICARDYRNYDILTGHPYGYMDVWGR 120
QY 118 GTTVTVSSGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSW 177
DB 121 GTTVTVSSGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSW 180
QY 178 YQHPGKAPKLMIEGSKRPSGVNRFSGSKGSTASLTISGLQAEDEADYYCSTYTR 237
DB 181 YQHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSTYTR 240
QY 238 TRVFGGKTLTVL 250
DB 241 TRVFGGKTLTVL 253

RESULT 14
PCT-US01-19110-1770
; Sequence 1770, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF533PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1770
; LENGTH: 247
; TYPE: PRF
; ORGANISM: Homo sapiens
PCT-US01-19110-1770

Query Match      86.9%; Score 1130; DB 1; Length 247;
Best Local Similarity 87.3%; Pred. No. 7.3e-85;
Matches 219; Conservative 12; Mismatches 14; Indels 6; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCOGSGFTFSSYKMNWVRQAPGKGLWMGIIPIFGTANY 60
DB 1 EVOLVQSGAEVKKPGSSVKSCRASGCTFSSYAISWVRQAPGCGLEMMGRIIPFGARY 60
QY 61 AQKFGQGRVTITADESTAYMELSSLSRSEDYAVYICARDRVVVPATSLRG-GMDVWGQ 119
DB 61 AQKFGQGRVTITADELTATYMLKTLRSDDYAVYICAR-----AGTSLMNGMDVWGRGT 115
QY 120 TTVTVSSGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSWY 179
DB 116 LVTVSSGGGGGGGSGGGSQSVLTQPAVSQSPGQITISCTGTSSDVGGYNYVSWY 175
QY 180 QHPGKAPKLMIEGSKRPSGVNRFSGSKGSTASLTISGLQAEDEADYYCSTYTRSTR 239
DB 176 QHPGKAPKLMIEGSKRPSGVNRFSGSKSGNTASLTISGLQAEDEADYYCSTYTRSTR 235
QY 240 VFGGGKTLTVL 250
DB 241 VFGGGKTLTVL 253

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Db 236 VFGGGTKLTVL 246

RESULT 15

US-09-880-748-1770
; Sequence 1770, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1770
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1770

Query Match 86.9%; Score 1130; DB 22; Length 247;
Best Local Similarity 87.3%; Pred. No. 7.3e-85;
Matches 219; Conservative 12; Mismatches 14; Indels 6; Gaps 2;

QY 1 EVLVVSGAEVKKPGESLKISCGSGGTFSSYKMNVRQAPKGLWMGGIIPFGTANY 60
Db 1 EVLVVSGAEVKKPGESLVKISCGSGGTFSSYKMNVRQAPKGLWMGGIIPFGPARY 60
QY 61 AQKFGQRTITADESTAYMELSLRSEDYVYICARDRVVVPATSLRG-GMDVVRGQT 119
Db 61 AEKFGQRTITADELRTAYMELKTLRSDDTAVYICAR----AGTSLMNYGMDVVRGRT 115
QY 120 TVTVSSGGGGGGGGGGGGGQSVLTPASVSGSPGQSITISCTGTSSDVGYNVYSWYQ 179
Db 116 LVTVSSGGGGGGGGGGGGGQSVLTQPASVSGSPGQSITISCTGTSSDVGYNVYSWYQ 175
QY 180 QHPGKAPKLMYEGSKRPQSVNRFSGSKSGTASLTISGLQAEDEADYVCSSYTTTRSTR 239
Db 176 QHPGKAPKLMYEGSKRPQSVNRFSGSKSGTASLTISGLQAEDEADYVCSSYTTTRSTR 235
QY 240 VFGGGTKLTVL 250
Db 236 VFGGGTKLTVL 246

Search completed: August 15, 2002, 16:34:05
Job time: 765 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: August 15, 2002, 16:24:03 ; Search time 101.13 Seconds
(without alignments)
274.582 Million cell updates/sec

Title: US-08-779-457-49
Perfect score: 1300
Sequence: 1 EVQLVQSGAEVKPGESLKI.....SSYTRTRVFGGTKLTVL 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1300	100.0	250	18 AAW24062	Human WSX receptor
2	1163	89.5	249	21 AAB36083	Recombinant human
3	926.5	71.3	244	20 AAY06718	Antibody 12E10 sin
4	926	71.2	245	22 AAB67618	Human leukocyte an
5	918	70.6	245	22 AAB67617	Human leukocyte an
6	907.5	69.8	239	22 AAB69603	Huntingtin intrabo
7	896.5	69.0	243	22 AAG65591	Anti-hEDRF antibod
8	892	68.6	249	20 AAY06713	Antibody 10F6 sing
9	879.5	67.7	304	22 AAG63634	Amino acid sequenc
10	879.5	67.7	304	22 AAG63639	Amino acid sequenc
11	865	66.5	245	22 AAB67619	Human leukocyte an

12	857	65.9	310	20 AAW83324	Single chain Apo-2
13	826.5	63.6	249	18 AAW24061	Human WSX receptor
14	826	63.5	245	22 AAB67621	Human leukocyte an
15	821	63.2	245	22 AAB67623	Human leukocyte an
16	818	62.9	245	22 AAB67622	Human leukocyte an
17	817	62.8	258	18 AAW08487	C6 human sFv antib
18	813.5	62.6	242	21 AAY15127	Anti-murine CTLA-4
19	810.5	62.3	240	21 AAY15124	Anti-murine CTLA-4
20	810.5	62.3	240	21 AAY15125	Internalising anti
21	809.5	62.3	246	21 AAY58235	Human SCFv2 agains
22	807	62.1	237	19 AAW49691	H6FXscFv(CEA6)trip
23	802.5	61.7	330	20 AAW94267	H6FXscFv(CEA6)trip
24	802.5	61.7	331	20 AAW94268	H6FXtripBscFv(CEA6
25	802.5	61.7	592	20 AAW94269	H6FXscFv(CEA6)trip
26	801.5	61.7	242	21 AAY95209	Anti-platelet glyc
27	798.5	61.4	236	19 AAW49690	Human SCFv1 agains
28	793.5	61.0	272	16 AAR80381	Anti-HIV-1 Mab 447
29	791.5	60.9	242	20 AAY21881	Amino acid sequenc
30	790.5	60.8	272	16 AAR80391	Anti-HIV-1 Mab 447
31	789.5	60.7	272	16 AAR80408	Anti-HIV-1 Mab 447
32	789.5	60.7	272	16 AAR80399	Anti-HIV-1 Mab 447
33	788.5	60.7	272	16 AAR80384	Anti-HIV-1 Mab 447
34	788.5	60.7	272	16 AAR80385	Anti-HIV-1 Mab 447
35	787.5	60.6	272	16 AAR80400	Anti-HIV-1 Mab 447
36	787.5	60.6	272	16 AAR80392	Anti-HIV-1 Mab 447
37	787.5	60.6	272	16 AAR80393	Anti-HIV-1 Mab 447
38	787.5	60.6	272	16 AAR80394	Anti-HIV-1 Mab 447
39	787.5	60.6	272	16 AAR80395	Anti-HIV-1 Mab 447
40	787.5	60.6	272	16 AAR80396	Anti-HIV-1 Mab 447
41	787.5	60.6	272	16 AAR80397	Anti-HIV-1 Mab 447
42	787.5	60.6	272	16 AAR80398	Anti-HIV-1 Mab 447
43	787.5	60.6	272	16 AAR80387	Anti-HIV-1 Mab 447
44	787.5	60.6	272	16 AAR80378	Anti-HIV-1 Mab 447
45	787.5	60.6	272	16 AAR80379	Anti-HIV-1 Mab 447

ALIGNMENTS

RESULT 1

AAW24062

ID AAW24062 standard; Protein; 250 AA.

XX AAW24062;

XX 17-MAR-1998 (first entry)

XX Human WSX receptor agonist antibody clone #4.

XX Human: WSX receptor; clone #4; identification: purification;
XX ligand; activator; antibody; agonist; proliferation; obesity;
XX differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
XX Type II diabetes; polycystic ovarian disease;
XX cardiovascular disease; osteoarthritis; dermatological disorder;
XX hypertension; insulin resistance; hypercholesterolaemia;
XX hypertriglyceridaemia; cancer; cholelithiasis.

OS Homo sapiens.

XX WO9725425-A1.

XX 17-JUL-1997.

XX 07-JAN-1997; 97WO-US00325.

XX 20-JUN-1996; 96US-0667197.

XX 08-JAN-1996; 96US-0585005.

XX (GETH) GENENTECH INC.

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

XX Rodrigues ML;

DR WPI; 1997-372864/34.
 XX WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Example 14; Pages 121-122; 219pp; English.
 XX
 PS The present sequence is an agonist antibody clone to the human WSX
 CC receptor, which can be used to identify and purify ligands and
 CC activators. An anti-WSX receptor antibody can be used as an agonist
 CC to activate the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX
 XX Sequence 250 AA;

Query Match 100.0%; Score 1300; DB 18; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1.3e-80;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGSAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWMGGLIPIFGTANY 60
 Db 1 evqlvsgsaevkkpgeslkiscgsgftssykmnvrqapgkglewmggilpifgtany 60
 QY 61 AQKFGQRTVITADESTAYMELSLRSEDVAVYICARDRVVVPATSLRGMDVMGQGT 120
 Db 61 aqkfgqrvtitadesstaymelslrsedtavvycardrvvvpatslrgmdvmgqgtt 120
 QY 121 VTVSSGGGGGGGGGGGGGQSVLTQPAVSQSPGQSITISCTGTSSDVGGINVYSWYQ 180
 Db 121 vtssgggggggggggggqsvltqpasvsgspgqsitiscgtssdvgginyvswyq 180
 QY 181 HPQKAPKLMYEGSKRPSGVSNRFGSKGSTASLTISGLQAEDEADYVCSSYTTSTRV 240
 Db 181 hpqkapklmlyegskrpsgvsnrfgskgstasltisglqadeadyyccsyttstrv 240
 QY 241 FGGGTGLTVL 250
 Db 241 fgggtgltvl 250

RESULT 2
 AAB36083
 ID AAB36083 standard; Protein; 249 AA.
 XX
 AC AAB36083;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Recombinant human antibody scFv TN11.
 XX
 KW Human; antibody scFv; TN11; Tenascin-C; domain C-containing TNC;
 KW CTN-C.
 XX
 OS Homo sapiens.
 XX WO2000063699-A1.
 XX
 XX 26-OCT-2000.

XX 19-APR-2000; 2000WO-EP03550.
 XX
 PR 20-APR-1999; 99IT-FI00094.
 XX
 PA (PHIL-) PHILOGEN SRL.
 XX
 XX Zardi L;
 PI
 XX
 DR WPI; 2000-687225/67.
 DR N-PSDB; AAC67868.
 XX
 PT Ligands used for diagnosis and treatment of human neoplasias, are
 PT capable of identifying the tenascin-C isoform containing domain C of
 PT tenascin-C -
 XX
 PS Disclosure; Page 5-6; 31pp; English.
 XX
 CC The present sequence is a recombinant human antibody scFv. Antibody
 CC TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
 CC recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
 CC only capable of recognising TN-C isoforms containing domain C (CTN-C).
 CC TN11 is useful for detecting the presence of TN-C isoforms in vitro or
 CC in vivo for diagnosing pathologies expressing the CTN-C isoforms of TN-C.
 CC It is useful for the preparation of formulations for the treatment of
 CC human neoplasias.
 XX
 XX Sequence 249 AA;

Query Match 89.5%; Score 1163; DB 21; Length 249;
 Best Local Similarity 89.6%; Pred. No. 2.3e-71;
 Matches 225; Conservative 11; Mismatches 11; Indels 4; Gaps 2;

QY 1 EVQLVSGSAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWMGGLIPIFGTANY 60
 Db 1 evqlvsgsaevkkpgeslkiscgsgftssykmnvrqapgkglewmggilpifgtany 60
 QY 61 AQKFGQRTVITADESTAYMELSLRSEDVAVYICARDRVVVPATSLRG-MDVMGQGT 119
 Db 61 aqkfgqrvtitadesstaymelslrsedtavvycardrvvvpatslrggmdvmgqgt 117
 QY 120 VTVSSGGGGGGGGGGGGGQSVLTQPAVSQSPGQSITISCTGTSSDVGGINVYSWYQ 179
 Db 118 mvtvssgggggggggggqsvltqpasvsgspgqsitiscgtssdvgginyvswyq 177
 QY 180 HPQKAPKLMYEGSKRPSGVSNRFGSKGSTASLTISGLQAEDEADYVCSSYTTSTR 239
 Db 178 hpqkapklmlyegskrpsgvsnrfgskgstasltisglqadeadyyccsytttrstr 237
 QY 240 VFGGTGLTVL 250
 Db 238 vfgggtgltvl 248

RESULT 3
 AAY06718
 ID AAY06718 standard; Protein; 244 AA.
 XX
 AC AAY06718;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Antibody 12E10 single chain Fv (scFv) fragment.
 XX
 KW Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
 KW megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
 KW bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
 KW myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
 KW neuromuscular; muscular dystrophy; complementarity determining region.
 XX
 OS Homo sapiens.

[illegible]

```

ID  AAB67618 standard; Protein; 245 AA.
XX
XX  AAB67618;
AC
XX  29-MAY-2001 (first entry)
DT
XX
XX  Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_2.
DE
XX
XX  Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;
KW  miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.
XX
XX  Homo sapiens.
OS
XX
XX  WQ200114558-A1.
PN
XX
XX  01-MAR-2001.
PD
XX
XX  28-AUG-2000; 2000MO-EP08388.
XX
XX  26-AUG-1999; 99EP-0116691.
XX
XX  (MORP-) MORPHOSYS AG.
PA
XX
XX  Kretschmar T, Tesar M, Marget M, Kroenke M;
PI
XX
XX  WPI; 2001-218451/22.
DR
XX
XX
XX
XX  Novel isolated human immunoglobulin or functional immunoglobulin
PT  fragment specific for human leukocyte antigen Cw6, useful for treatment
PT  of humans and for human leukocyte antigen phenotyping -
XX
XX
XX  Claim 3; Fig 1; 23pp; English.
XX
XX  AAB67617-23 represent single chain antibody (scFv) fragments which
CC  are specific for human leukocyte antigen (HLA)-Cw6. The fragments are
CC  derived from a synthetic human combinatorial antibody library based on
CC  molecular consensus frameworks and CDRs randomised with trinucleotides.
CC  The specification describes a human immunoglobulin fragments specific
CC  for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in
CC  studies of natural killer cell silencing as well as miscarriages.
CC  HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.
CC  Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin
CC  fragments are useful for the preparation of a pharmaceutical for the
CC  treatment of humans. They are also useful for HLA phenotyping.
XX
XX  Sequence 245 AA;
SQ

Query Match 71.2%; Score 926; DB 22; Length 245;
Best Local Similarity 72.5%; Pred. No. 2.3e-55;
Matches 185; Conservative 17; Mismatches 37; Indels 16; Gaps 3;

QY 1 EVQLVQSGAEVKPKGESLKISCGSGTFFSYKNNVYRQAPKGLEWGGIPIFGTANY 60
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 qvqlvsgaevkpkpssvkcscksggflfssyalswvqepggglewggilpifgany 60

QY 61 AQKQFGRVTITADESTTAYMELSLRSEDATVYTCARDRVVPATSLRGGMDYWGQGT 120
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 aqkfgrvtitadesttaymelsslrsedatvyyca-----gfdyfmdftwgggtl 112

QY 121 VTVS-----SGGGSGGGGGSGQSQSVLTOPASVSGSPGQSINISCTGTSDDVGGNYV 175
DB 1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 113 vtvsaggsgsgsgsgsgsgsgsdleltqppsvsvapgtariscsg---dalgdka 169

QY 176 SWYQHQPQKAPKLMIYEGSKRPSGVSNRFSGSKSGSVASLTISGLQADEADYYCSSVTT 235
DB 1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 170 swyqhqpqgqapvlvyddsdrrpsipferfsgnsngtaltisgtqadeadyvcqsydi 229

QY 236 RSTRVFGGGTKLTVL 250
DB 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 230 hdsyvfqgqtkltvl 244

```


Qy	181	HPGKAPKLMIVEGSKRPSGVSNFRFSKSGVSNASLTISGLQADEADYYC	SSYTRTRPRV	240
		: : : : : : : : :		
Db	171	ypgkaptllydvsnrpsglsnfrfskgsgdtsltisglqadeadyccsf	-ansgpl	229
Qy	241	FGGQTKLTVL	250	
Db	230	fggqtkvtvl	239	
RESULT	7			
AAAG65591				
ID	AAAG65591	standard; Protein; 243 AA.		
AC	XX			
AC	XX	AAG65591;		
XX	XX			
DT	DT	07-JAN-2002 (first entry)		
XX	XX			
DE	XX	Anti-hEDRF antibody ell amino acid sequence.		
XX	XX			
KW	KW	Human; erythroid differentiation related factor; hEDRF; antianemic;		
KW	KW	erythrocyte deficiency; antibody ell.		
XX	XX			
OS	OS	Homo sapiens.		
XX	XX			
FH	FH	Key Location/Qualifiers		
FT	FT	Misc-difference 208		
FT	FT	/note= "encoded by NCC"		
FT	FT	Misc-difference 216		
FT	FT	/note= "encoded by NAC"		
FT	FT	Misc-difference 221		
FT	FT	/note= "encoded by TNN"		
FT	FT	Misc-difference 230		
FT	FT	/note= "encoded by NCT"		
XX	XX			
PN	PN	EP1130030-AL.		
XX	XX			
PD	PD	05-SEP-2001.		
XX	XX			
PF	PF	27-FEB-2001; 2001EP-0104821.		
XX	XX			
PR	PR	02-MAR-2000; 2000US-0517225.		
XX	XX			
PA	PA	(HOFF) ROCHE DIAGNOSTICS CORP.		
XX	XX			
PI	PI	Xu H, Mahoney W, Schueler P, Harriman WD;		
XX	XX			
DR	DR	WPI: 2001-608195/70.		
DR	DR	N-PSDB; AAH47763.		
XX	XX			
PT	PT	Novel human erythroid differentiation related factor and		
PT	PT	polynucleotides encoding it useful for treating anemia and other		
PT	PT	erythrocyte deficiencies and for detecting expression of the factor in		
PT	PT	humans		
XX	XX			
PS	PS	Disclosure; Fig 5; 29pp; English.		
XX	XX			
CC	CC	The invention provides a human erythroid differentiation related factor		
CC	CC	(hEDRF). The hEDRF polypeptide and the encoding polynucleotide are used		
CC	CC	for treating anemias and other erythrocyte deficiencies. The hEDRF		
CC	CC	protein is useful for producing antibodies, useful in screening assays		
CC	CC	identify pharmaceutical compounds of interest and compounds which bind		
CC	CC	hEDRF. The polynucleotides are useful for producing hEDRF or its rela		
CC	CC	polypeptides. The antibodies are useful for separating or detecting th		
CC	CC	corresponding antigen e.g. for detection/quantitation of hEDRF in sampl		
CC	CC	taken from human subjects. Quantification of hEDRF at immunohistochem		
CC	CC	level finds value in evaluating the potential of the tissue site to		
CC	CC	contribute towards the production of new erythroid cells. The present		
CC	CC	sequence represents the amino acid sequence of an anti-hEDRF antibody		
CC	CC	ell.		
XX	XX			
SQ	SQ	Sequence 243 AA;		

	Query Match	69.0%; Score 896.5; DB 22; Length 243;
	Best Local Similarity	70.0%; Pred. No. 2.3e-53;
	Matches 175; Conservative	21; Mismatches 45; Indels 9; Gaps 2;
QY	1	EVLVLSGAEVKKGESLKI SCGGSGFTFSSYKMNVRQAPCKGLEWGGGIPIFGTANY 60
DB	2	qvlvlvsgggglvqpqgsirlscasgftfdyhmhwraqpgklwsvsglswnsgsigy 61
		: : : : : : :
QY	61	AQKPGQRVTITADESTPAYMELSLRSFDTAVYYCARDRVVVPATSLRGGMDVMWGQT 120
DB	62	adsvkgfrtisrdnakntlylqm-tlrvedlavycsrd-----lgaddswgqgtl 112
		: : : : : :
QY	121	VTVSGGGSGGGSGGGGSOSVLTQPASVSGSPQGSTISCTGTSSDVGYNVYWVQQ 180
DB	113	vtvsrgggsgggsgggsgqsaltqprsvsgspqsvtictgtssdvvgynvyswyqq 172
		: :
QY	181	HPGKAPKLMIYEGSKRPDSVNRFSKSGSGTASLTISGLQAEDEADYYCSYTTRSTRV 240
DB	173	hpgkapklimiyevsnrppgvpdrrfsgsksgntaslxisglqtexegdyxcssytssxyv 232
		: :
QY	241	FGGKTCLTVL 250
DB	233	fgtgtktltv 242
RESULT	8	
AAAY06713		
ID	AAV06713 standard; Protein; 249 AA.	
XX	AC	AAV06713;
XX	DT	17-JUN-1999 (first entry)
XX	DE	Antibody 10F6 single chain Fv (scFv) fragment.
KW	Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;	
KW	megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;	
KW	bone marrow hypoplasia; disseminated intravascular coagulation; anemia;	
KW	myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;	
KW	neuromuscular; muscular dystrophy; complementarity determining region.	
OS	Homo sapiens.	
XX	WO9910494-A2.	
XX	04-MAR-1999.	
XX	21-AUG-1998; 98WO-US17364.	
XX	25-AUG-1997; 97US-0918148.	
PA	(GETH) GENENTECH INC.	
XX	Adams CW, Carter PJ, Fendly BM, Gurney AL;	
XX	WPI; 1999-204666/17.	
XX	New thrombopoietin receptor agonist antibodies - useful for	
PT	treating immunological or hematological disorders	
XX	Disclosure; Fig 1; 86pp; English.	
CC	The invention relates to an agonist antibody (Ab) which binds to a	
CC	thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can	
CC	be used in the same way and for the same indications as thrombopoietin	
CC	(TPO). They can stimulate proliferation, differentiation or growth of	
CC	megakaryocytes. They may also be able to stimulate megakaryocytes to	
CC	increase platelet production. They can be used for treating	
CC	immunological or hematopoietic disorders, especially thrombocytopenia.	
CC	Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia	
CC	following chemotherapy or bone marrow transplant) may be effectively	
CC	treated with the antibody compounds as well as disorders such as	
CC	disseminated intravascular coagulation (DIC), immune thrombocytopenia	

```

Query Match          69.0%; Score 896.5; DB 22; Length 243;
Best Local Similarity 70.0%; Pred. No. 2.3e-53;
Matches 175; Conservative 21; Mismatches 45; Indels 9; Gaps 2;

QY      1 EVQLVDSGAEVKKPGESLKISCGSGFTFSSYKMNWVRQAPCKGLEWMGGIIPFGTANY 60
Db       :||||| :|| ||:|| ||||| | :||||| ||||| :| |:|
QY      2 QVQLVQSGGGLVPQGSLIRLSCAASGFITFDYAMHWVQAPKGLEWVGSIWNSSGISGY 61
Db       | :||| :| :| :||| :||| :||| :||| :||| :|||
QY     61 AOKPQGRVTITADESTPAYMELSSLRSSEDTAVYYCARDRVVVVPATSLRGGMDVMWGQT 120
Db       | :||| :| :| :||| :||| :||| :||| :||| :|||
QY     62 adsvkgftridnakntlylqm-tlrvedlavycsrd-----lggaddswggqtl 112
Db       | :||| :| :| :||| :||| :||| :||| :||| :|||
QY    121 VTVSGSGSGSGSGSGGGGSQSVLTQPASVSGSPQSITICTGTSSDVGGINVYWVQQ 180
Db       :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    113 vtvssggsgsgsgsgsggsqsaltprrsvsgspqsvtictgttssdvvgynvyswvqq 172
Db       | :||| :| :| :||| :||| :||| :||| :||| :|||
QY    181 HPGRAPKLMIYEGRKRPSSGVNRRFSKSGSSTASLTISGLQAEDEADYCSYTTTRSTRV 240
Db       :||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY    173 hpgrapklimyevsnrppgvprdfsgsksgntaslxisglqtexegdyxcssytssxyv 232
Db       | :||| :| :| :||| :||| :||| :||| :||| :|||
QY    241 FGGTGKTLTVL 250
Db       || |||||
QY    233 fgtgkltvl 242
Db       || |||||

RESULT      8
AAV06713
ID   AAY06713 standard; Protein; 249 AA.
XX
AC   AAY06713;
XX
DT   17-JUN-1999 (first entry)
XX
DE   Antibody 10F6 single chain Fv (scFv) fragment.
XX
KW   Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;
KW   megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;
KW   bone marrow hypoplasia; disseminated intravascular coagulation; anemia;
KW   myelodysplasia; myelotoxic chemotherapy; leukaemia; tumour; MuSK; CDR;
KW   neuromuscular; muscular dystrophy; complementarity determining region.
XX
OS   Homo sapiens.
XX
PN   WO9910494-A2.
XX
PD   04-MAR-1999.
XX
PF   21-AUG-1998; 98WO-US17364.
XX
PR   25-AUG-1997; 97US-0918148.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Adams CW, Carter PJ, Fendly BM, Gurney AL;
XX
WI   WPI; 1999-204666/17.
XX
PT   New thrombopoietin receptor agonist antibodies - useful for
PT   treating immunological or hematological disorders
XX
PS   Disclosure; Fig 1; 86pp; English.
XX
CC   The invention relates to an agonist antibody (Ab) which binds to a
CC   thrombopoietin receptor (TPO-R). The antibodies which bind the TPO-R can
CC   be used in the same way and for the same indications as thrombopoietin
CC   (TPO). They can stimulate proliferation, differentiation or growth of
CC   megakaryocytes. They may also be able to stimulate megakaryocytes to
CC   increase platelet production. They can be used for treating
CC   immunological or hematopoietic disorders, especially thrombocytopenia.
CC   Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia
CC   following chemotherapy or bone marrow transplant) may be effectively
CC   treated with the antibody compounds as well as disorders such as
CC   disseminated intravascular coagulation (DIC), immune thrombocytopenia

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PR 09-FEB-1998; 98US-0020746.
PR 15-MAY-1997; 97US-0857216.
PA (GETH ) GENENTECH INC.
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 1999-045228/04.
XX N-PSDB; AAV72534.
XX Human Apo-2 polypeptide inducing apoptosis - useful to treat
XX conditions linked with decreased apoptosis e.g. cancer, and produce
XX antibodies to increase or decrease apoptosis
XX Example 14; Fig 16; 134pp; English.
XX The present invention describes human Apo-2. Apo-2 can be used
XX therapeutically to induce apoptosis in mammalian cells, and so is useful
XX to treat conditions associated with decreased apoptosis e.g. cancer.
XX Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
XX (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
XX binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
XX can be used to identify agents activating Apo-2, useful to treat
XX mammalian cancer cells, and to produce Apo-2 chimeras useful
XX therapeutically (e.g. those containing immunoglobulin sequences can be
XX inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
XX tag polypeptide allow Apo-2 detection and purification using anti-tag
XX antibodies). It can be used to produce antibodies which can be combined
XX with a (particularly pharmaceutically acceptable) carrier in compositions
XX or used to produce dimeric molecules (especially homodimeric molecules
XX comprising first and second Apo-2 antibodies). Agonistic (especially
XX single-chain) antibodies can be administered to induce apoptosis in
XX mammalian cancer cells, and antagonistic antibodies used to block
XX excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
XX antibodies may also be used diagnostically e.g. to detect Apo-2
XX expression in cells/tissues and in Apo-2 purification. The present
XX sequence represents a single chain Apo-2 antibody, designated 24C4.
XX Sequence 310 AA;
XX
XX Query Match 65.9%; Score 857; DB 20; Length 310;
XX Best Local Similarity 66.7%; Pred. No. 1.4e-50;
XX Matches 170; Conservative 29; Mismatches 40; Indels 16; Gaps 4;
QY 1 EVOLVSGAEVKKPGESLKITSQSGGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
DB 40 qvqlvsgggvpgprsrifscasagfifssygmhvrqpgkglewagifdydgmkyy 99
QY 61 AOKFQGRVITADESTAYMELSSRLSEDTAVYYICARDRVVVPATSLRGG---MDVWGQ 117
DB 100 adsvkgftlsrdnsnkntlylqmnsiraedtavyycardr-----gyyymdvwgk 149
QY 118 GTTVTVSSGGGGGGGGGGGSGQSVLTQPASVSGSPGQGITISCTGTSDDVGYNVSW 177
DB 150 gttvtvssgggggggggggggggggggggggggggggggggggggggggggggggg 209
QY 178 YQHPGKAPKLMIVEGSKRPSGVSNRFGSGKSGTASLTISGLQADEADAYCYSSYTTRS 237
DB 210 yqlqlptgkpllyddnrspgvdpfrfsgsrsgcsaslaigtqadeadeaycqsyds- 268
QY 238 TR--VFQGGPKLTVL 250
DB 269 lrgsvfggggkvtvl 283
RESULT 13
ID AAW24061
XX AAW24061 standard; Protein; 249 AA.
XX AAW24061;
XX 17-MAR-1998 (first entry)
DT
```

```
XX Human WSX receptor agonist antibody clone #3.
XX
XX Human: WSX receptor; clone #3; identification: purification;
XX ligand; activator; antibody; agonist; proliferation; obesity;
XX differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
XX Type II diabetes; polycystic ovarian disease;
XX cardiovascular disease; osteoarthritis; dermatological disorder;
XX hypertension; insulin resistance; hypercholesterolaemia;
XX hypertriglyceridaemia; cancer; cholelithiasis.
XX
XX Homo sapiens.
XX
XX WO9725425-A1.
XX
XX 17-JUL-1997.
XX
XX 07-JAN-1997; 97WO-US00325.
XX
XX 20-JUN-1996; 96US-0667197.
XX
XX 08-JAN-1996; 96US-0585005.
XX
XX (GETH ) GENENTECH INC.
XX
XX Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
XX Rodrigues ML;
XX WPI; 1997-372864/34.
XX
XX WSX receptor and related antibodies and ligands - used to develop
XX products for diagnosis and therapy, e.g. for improving
XX haematopoiesis or for treating tumours
XX
XX Example 14; Pages 120-121; 219pp; English.
XX
XX The present sequence is an agonist antibody clone to the human WSX
XX receptor, which can be used to identify and purify ligands and
XX activators. An anti-WSX receptor antibody can be used as an agonist
XX to activate the WSX receptor, leading to enhanced proliferation or
XX differentiation of a cell expressing the WSX receptor. It can also
XX be used to decrease body weight and/or fat-depot weight and/or food
XX intake in an obese mammal. WSX receptor ligands can be used to
XX enhance proliferation or differentiation of lymphoid, myeloid or
XX erythroid blood cell lineages. This is useful when a mammal,
XX i.e. anaemia, is suffering from decreased blood cell levels,
XX especially a human, is suffering from chemotherapy, radiation therapy or bone
XX marrow transplantation therapy. It can also be used to repopulate
XX blood cells in a mammal. The products can also be used to treat,
XX e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
XX polycystic ovarian disease, cardiovascular diseases,
XX osteoarthritis, dermatological disorders, hypertension, insulin
XX resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
XX and cholelithiasis.
XX
XX Sequence 249 AA;
XX
XX Query Match 63.6%; Score 826.5; DB 18; Length 249;
XX Best Local Similarity 66.8%; Pred. No. 1.3e-48;
XX Matches 169; Conservative 26; Mismatches 51; Indels 7; Gaps 5;
QY 1 EVOLVSGAEVKKPGESLKITSQSGGFTSSYKMNVRQAPGKLEWGGIIPFGTANY 60
DB 1 evqlvsgaeavkpgasvksckasgytftgyymvvrqpggglewgmwgnpsgntny 60
QY 61 AOKFQGRVITADESTAYMELSSRLSEDTAVYYICARDRVVVPATSLRGG--MDVWGQ 118
DB 61 aqkfqgrvtmtrdtsigtaymelsrissddtavyycardryygsayhrsgyyymdvwgrg 120
QY 119 TTVTVSSGGGGGGGGGGGSGQSVLTQPASVSGSPGQGITISCTGTSDDVGYNVSW 178
DB 121 tlvtvssggggggtggggsgggggs-seltqpavsvaigtvtvricqgds--lrsy-yaswy 176
```

D	b	113	vtsassagggsgggsgggsgggsgggsdieltqppsvsvapggatiscsg---dalgdka	169
Q	y	176	SWYQHFGKAPKLMIYEKGSRPSGVSNRFGSGKSGSTASLTISGLQAEDAEADYYCCSSYTT	235
			: : : : : : : : : : :	
D	b	170	swyqqkpgapvlvyddsd:psgiiperfsgnsngntatlisgtqaedeaddyccsydd	229
Q	y	236	RSTRVFGGGTKLTVL	250
D	b	230	hdriavgggtklvtl	244
			AC AC	
XX			AAB67623;	
XX			29-MAY-2001 (first entry)	
XX			Human leukocyte antigen-Cw6 specific scFv fragment from clone Cw6_7.	
DE				
XX			Human leukocyte antigen; HLA; HLA-Cw6; natural killer cell silencing;	
KW			miscarriage; abortion; psoriasis; antibody; HLA phenotyping; ss.	
KW				
OS			Homo sapiens.	
XX			WO200114558-A1.	
PN				
XX			01-MAR-2001.	
XX			28-AUG-2000; 2000WO-EP08388.	
P	F			
PF			26-AUG-1999; 99EP-0116691.	
PR			(MORP-) MORPHOSYS AG.	
XX				
PA			Kretzschmar T, Tesar M, Marget M, Kroenke M;	
XX			WPI; 2001-219451/22.	
DR				
XX			Novel isolated human immunoglobulin or functional immunoglobulin	
PT			fragment specific for human leukocyte antigen Cw6, useful for treatment	
PT			of humans and for human leukocyte antigen phenotyping -	
PT				
XX			Claim 3; Fig 1; 23pp; English.	
PS				
CC			AAB67617-23 represent single chain antibody (scFv) fragments which	
CC			are specific for human leukocyte antigen (HLA)-Cw6. The fragments are	
CC			derived from a synthetic human combinatorial antibody library based on	
CC			molecular consensus frameworks and CDRs randomised with trinucleotides.	
CC			The specification describes a human immunoglobulin fragments specific	
CC			for HLA-Cw6. The HLA-Cw6 serotype is considered highly relevant in	
CC			studies of natural killer cell silencing as well as miscarriages.	
CC			HLA-Cw6 demonstrates a disequilibrium in some recurrent abortions.	
CC			Psoriasis may also be linked to HLA-Cw6. The anti-HLA-Cw6 immunoglobulin	
CC			fragments are useful for the preparation of a pharmaceutical for the	
CC			treatment of humans. They are also useful for HLA phenotyping.	
XX				
SQ			Sequence 245 AA;	
			Query Match 63.2%; Score 821; DB 22; Length 245;	
			Best Local Similarity 65.9%; Pred. No. 2.9e-48;	
			Matches 168; Conservative 23; Mismatches 48; Indels 16; Gaps 4;	
Q	y	1	EVQLVQSGAEVKPKGSIKSCQSGFTFSYKMNWVROAFCKGLEWMGGIIPFGTANY	60
D	b	1	evqlvqsgaevkpkgeslkiskcgsgysftsygwivmqbpkglewmgilypgdsdtry	60
Q	y	61	AOKFQGRVTITADESTSTAYNELSLRSREDTAHYVCARDRVVPATSLRGMDVWGQT	120
			: : : : : : : : :	
D	b	61	spsfgqgvtsiadksistaylqwsalskasdtamyrcar---fvpy-----mdnwgggtl	112

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	506	38.9	111	1	LV2B_HUMAN	P01705 homo sapien
2	494.5	38.0	112	1	LV2K_HUMAN	P04209 homo sapien
3	469	36.1	111	1	LV2H_HUMAN	P01711 homo sapien
4	482	35.5	111	1	LV2D_HUMAN	P01707 homo sapien
5	457	35.2	111	1	LV2F_HUMAN	P01709 homo sapien
6	454	34.9	111	1	LV2G_HUMAN	P01706 homo sapien
7	452	34.8	111	1	LV2C_HUMAN	P01710 homo sapien
8	451	34.7	111	1	LV2A_HUMAN	P01704 homo sapien
9	435	33.5	109	1	LV2E_HUMAN	P01708 homo sapien
10	430	33.1	111	1	LV2I_HUMAN	P01712 homo sapien
11	420	32.3	117	1	HV1A_HUMAN	P01742 homo sapien
12	411.5	31.7	110	1	LV2J_HUMAN	P01713 homo sapien
13	401	30.8	117	1	HV1B_HUMAN	P01743 homo sapien
14	385	29.6	130	1	LV1G_HUMAN	P06316 homo sapien
15	384	29.5	117	1	HV1J_HUMAN	P23083 homo sapien
16	380.5	29.3	112	1	LV1B_HUMAN	P01700 homo sapien
17	380	29.2	117	1	HV1C_MOUSE	P01757 mus musculus
18	378.5	29.1	147	1	HV1C_HUMAN	P01744 homo sapien
19	375	28.8	111	1	LV1D_HUMAN	P01702 homo sapien
20	374	28.8	109	1	LV1F_HUMAN	P04208 homo sapien
21	372.5	28.7	114	1	HV0O_MOUSE	P01741 mus musculus
22	372.5	28.7	118	1	HV5I_MOUSE	P06330 mus musculus
23	372	28.6	117	1	HV12_MOUSE	P01756 mus musculus
24	371	28.5	103	1	LV1E_HUMAN	P01703 homo sapien
25	367	28.2	140	1	HV02_MOUSE	P01746 mus musculus
26	365.5	28.1	120	1	HV5O_MOUSE	P06329 mus musculus
27	365	28.1	111	1	LV2L_HUMAN	P80422 homo sapien
28	362.5	27.9	139	1	HV07_MOUSE	P01751 mus musculus
29	361.5	27.8	137	1	HV1I_MOUSE	P01755 mus musculus
30	361	27.8	120	1	HV03_MOUSE	P01747 mus musculus
31	353	27.2	111	1	LV1A_HUMAN	P01699 homo sapien
32	353	27.2	111	1	LV1C_HUMAN	P01701 homo sapien
33	351	27.0	109	1	LV1I_HUMAN	P06888 homo sapien

DE
OS

ty ransoda chaiti v-ii reytom nig-04.
Homo sapiens (Human)

P06887 homo sapien
P06317 homo sapien
P01745 mus musculus
P06889 homo sapien
P01771 homo sapien
P01768 homo sapien
P06318 homo sapien
P01808 mus musculus
P01769 homo sapien
P01721 homo sapien
P06319 homo sapien
P06326 homo sapien

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1] NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=85204383; PubMed=3922791;
RA Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT myeloma-associated systemic amyloidosis."
RL FEBS Lett. 185:139-141(1985).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
DR PIR; A01971; L2HUNG.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;

Query Match 38.0%; Score 494.5; DB 1; Length 112;
Best Local Similarity 84.7%; Pred. No. 6.6e-28;
Matches 94; Conservative 12; Mismatches 4; Indels 1; Gaps 1;

QY 141 QSVLTQPASVSGSPGQSIITISCTGTSDDVGGYNYVSWYQQHKGAPKAPKLMYEGSKRPSGV 200
DB 1 QSALTQPRSVSGSPGQSVTISCTGTSDDVGGYNYVSWYQQHKGAPKAPKLMYDVSRRPSGI 60

QY 201 SNRFGSKSGSTASLTISGLQAEDEADYYCSTYTRSTR-VFEGGKTLTVL 250
DB 61 SNRFGSKSGSTASLTISGLQAEDEADYYCSTFTTNSRAVFGGKTLTVL 111

RESULT 3
LV2F_HUMAN
ID LV2F_HUMAN STANDARD; PRT; 111 AA.
AC P01711.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig lambda chain V-II region VII.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1] NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=71215142; PubMed=5087637;
RA Pontingl H., Hilschmann N.;
RT "Structural rule of antibodies. Complete primary structure of a
RT monoclonal immunoglobulin L chain of the lambda type, subgroup II
RT (Bence Jones protein VII).";
RL Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01977; L2HUVL.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11445 MW; 3913736B3EF367E0 CRC64;

Query Match 36.1%; Score 469; DB 1; Length 111;
Best Local Similarity 84.4%; Pred. No. 3.7e-26;
Matches 92; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
```

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QY 142 SVLTQPASVSGSPGQSIITISCTGTSDDVGGYNYVSWYQQHKGAPKAPKLMYEGSKRPSGV 201
DB 2 SALTQPASVSGSLGQSIITISCTGTSDDVGGYNYVSWYQQHKGAPKAPKLMYSEVNRPSGV 61

QY 202 NFRFSKSGSTASLTISGLQAEDEADYYCSTYTRSTRVFEGGKTLTVL 250
DB 62 DFRFSKSGSTASLTISGLQAEDEADYYCSTYSSNSVYVFGGKTLTVL 110

RESULT 4
LV2D_HUMAN
ID LV2D_HUMAN STANDARD; PRT; 111 AA.
AC P01707.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region TRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1] NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=80114123; PubMed=118915;
RA Scholz R., Yang C., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal
RT IgA1-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of
RT the L-chain, lambda-type, subgroup II.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1918(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01973; L2HUTR.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 90 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12E8F6E1 CRC64;

Query Match 35.5%; Score 462; DB 1; Length 111;
Best Local Similarity 80.0%; Pred. No. 1.1e-25;
Matches 88; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPGQSIITISCTGTSDDVGGYNYVSWYQQHKGAPKAPKLMYEGSKRPSGV 200
DB 1 QSALTQPRSVSGSPGQSVTISCTGTSDDVGGYNSVSWYQQHKGAPKAPKLMIFDVKRPSGV 60

QY 201 SNRFGSKSGSTASLTISGLQAEDEADYYCSTYTRSTRVFEGGKTLTVL 250
DB 61 PDRLSKSGSDTASLTISGLRADDEADYYCSTYAGRYSVIFGGGKTLTVL 110

RESULT 5
LV2F_HUMAN
ID LV2F_HUMAN STANDARD; PRT; 111 AA.
AC P01709.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region MGC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1] NCBI_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=75013804; PubMed=4415202;
RA Fett J.W., Deutsch H.F.;
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FT NON_TER 111
SQ SEQUENCE 111 AA; 11785 MW; 92F5A1BF72421BAC CRC64;

Query Match 34.8%; Score 452; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 5.4e-25;
Matches 86; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPQGSITISCTGTSDDVGGYVSWYQOHPGKAPKLMYEGSKRPSGV 200
Db 1 QSVLTQPASVSGSPQGSITISCTGTSDDVGGYVSWYQOHPGKAPKLMYEGSKRPSGV 60

QY 201 SNRFGSKSGTASLTISGLQAEADYVCSYTRSTRVFGGGTKLTVL 250
Db 61 PDRFSGSKSGTASLTISGLQAEADYVCSYVDDNNFVFGGGTKLTVL 110

RESULT 8
LV2E_HUMAN
ID LV2A_HUMAN STANDARD; PRT; 111 AA.
AC P01704;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig lambda chain V-II region TOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80048495; PubMed=500108;
RA Nabeshima Y., Ikenaka T.;
RT "Primary structure of cryo Bence-Jones protein (TOG) from the urine
of a patient with IgD myeloma.";
RL Mol. Immunol. 16:439-444(1979).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
QY PIR; A01969; L2HUTG.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region;
FT MOD_RES 1
FT DISULFID 22 90
FT SITE 91
FT BY SIMILARITY.
FT APPEARS TO BE A FREE BUT UNREACTIVE
FT SULFHYDRYL GROUP.
SQ SEQUENCE 111 AA; 11713 MW; FD20AEF4CE5364E2 CRC64;

Query Match 34.7%; Score 451; DB 1; Length 111;
Best Local Similarity 76.4%; Pred. No. 6.3e-25;
Matches 84; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPQGSITISCTGTSDDVGGYVSWYQOHPGKAPKLMYEGSKRPSGV 200
Db 1 QSVLTQPASVSGSPQGSITISCTGTSDDVGGYVSWYQOHPGKAPKLMYEGSKRPSGV 60

QY 201 SNRFGSKSGTASLTISGLQAEADYVCSYTRSTRVFGGGTKLTVL 250
Db 61 SHRFSGSKSGTASLTISGLQAEADYVCSYRTSGTIIFGGGYIVVL 110

RESULT 9
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA immunoglobulin. V. Amino acid
sequence of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
MARKERS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
QY PIR; A01974; L2HUBR.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1
FT DISULFID 22 90
FT SITE 91
FT BY SIMILARITY.
FT APPEARS TO BE A FREE BUT UNREACTIVE
FT SULFHYDRYL GROUP.
SQ SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;

Query Match 33.5%; Score 435; DB 1; Length 109;
Best Local Similarity 78.2%; Pred. No. 7.8e-24;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

QY 141 QSVLTQPASVSGSPQGSITISCTGTSDDVGGYVSWYQOHPGKAPKLMYEGSKRPSGV 200
Db 1 QSVLTQPASVSGSPGSHVTSICIGTSSNVGDYKYVSWYQOHPGKAPKLIYEVSSRPSGV 60

QY 201 SNRFGSKSGTASLTISGLQAEADYVCSYTRSTRVFGGGTKLTVL 250
Db 61 PDRFSGSKSGTASLTISGLQAEADYVCSYI--GSYVFGTGTKVIVL 108

RESULT 10
LV2I_HUMAN
ID LV2I_HUMAN STANDARD; PRT; 111 AA.
AC P01712;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig lambda chain V-II region WIN.
DE Ig lambda chain V-II region WIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79062503; PubMed=102365;
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT "Amino acid sequence of the human myeloma lambda chain Win.";
RL Biochim. Biophys. Acta 537:9-21(1978).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
QY PIR; A01978; L2HUNW.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT MOD_RES 1
FT DISULFID 22 90
FT NON_TER 111
FT BY SIMILARITY.
SQ SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

Query Match 33.1%; Score 430; DB 1; Length 111;
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Best Local Similarity 75.5%; Pred. No. 1,8e-23;
Matches 83; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 141 QSVLTQPSVSGSGQSTISCTGTSDDVGGYVSWYQHPGKAPKLMYEGSKRPSGV 200
    ||||| |||||:|||||:|:||||:||||| |||||:|||||
Db 1 QSALTQPPRVSGSPQSVTISCTGTSYVNTGYNVSWYQDDPGKVPKLMYVDVKRPSGV 60
    :|||||:|||||:|||||:|||||:|||||:|||||
QY 201 SNRFGSGSGTASLTISGLQADEADYYCCSYTTRSTRVFGGKTLTVL 250
    :|||||:|||||:|||||:|||||:|||||:|||||
Db 61 PLRFGSGSGTASLTISGLQANNEADYYCCSYTSLIFGGGKTLTVL 110
    :|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR; A02023; GIHUEU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 96
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 32.3%; Score 420; DB 1; Length 117;
Best Local Similarity 65.9%; Pred. No. 9.1e-23;
Matches 85; Conservative 12; Mismatches 16; Indels 16; Gaps 2;

QY 1 EVQLVQSGAEVKKPESLKISKQSGFTFSYKMNVRQAPQKGLWGMGIIPFTANY 60
    :|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVQSGAEVKKPESLVKVKSCASGFTFSRGAIIWVQAPQGLWGMGIIPFTANY 60
    :|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AOKFGQRTVITADESTAYMELSLRSDTAVYCARDVRVVPATSLRGGMVWG---- 116
    :|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFGQRTVITADESTNTAYMELSLRSDTAFYFCA-----GGYGIYSPEY 108
    :|||||:|||||:|||||:|||||:|||||:|||||

QY 117 QGTTVTSS 125
    :|||||
Db 109 NGGLVTSS 117
    :|||||

RESULT 12
LV2J_HUMAN
ID LV2J_HUMAN STANDARD; PRT; 110 AA.
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AC P01713;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region NIG-58.
Db 1 QSALTQPPRVSGSPQSVTISCTGTSYVNTGYNVSWYQDDPGKVPKLMYVDVKRPSGV 60
    :|||||:|||||:|||||:|||||:|||||:|||||
QY 201 SNRFGSGSGTASLTISGLQADEADYYCCSYTTRSTRVFGGKTLTVL 250
    :|||||:|||||:|||||:|||||:|||||:|||||
Db 61 PLRFGSGSGTASLTISGLQADEADYYCCSYTTRSTRVFGGKTLTVL 109
    :|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
HV1B_HUMAN
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region H33 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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DR EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 30.8%; Score 401; DB 1; Length 117;
Best Local Similarity 77.6%; Pred. No. 1.8e-21;
Matches 76; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPKESLKISCGSGFTFSSYKMNWVRQAPCKGLEWMGGIPIFGTANY 60
Db 20 QQLVQSGAEVKKPKGKSVKSCSGYTFNSYHMWVRQAPCKGLEWMGGIIPNSGGSTSY 79

Qy 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYYCAR 98
Db 80 AOKFOGRVTMTDRDTSYVHMLSLRSEDYAVYYCAR 117

RESULT 14
LVIG_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence";
RL Nucleic Acids Res. 12:8407-8414(1984).
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CC -----
DR EMBL: X01147; CAA25598.1; -.
DR PIR: A01966; L1HUBL.
DR HSP: P01703; 7FAB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 130 IG LAMBDA CHAIN V-I REGION BL2.
FT DOMAIN 20 115 V SEGMENT.
FT DOMAIN 116 130 J SEGMENT.
FT DISULFID 41 108 BY SIMILARITY.
FT NON_TER 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;

Query Match 29.6%; Score 385; DB 1; Length 130;
Best Local Similarity 65.2%; Pred. No. 2.6e-20;
Matches 75; Conservative 20; Mismatches 18; Indels 2; Gaps 2;

Qy 137 GGSQSVLTPASVSGSPGQGITITCTSDVGGYNTVSWYQQHPGKAPKLMIEYEGSKR 196
Db 16 GSWAQSVLTQPPSVSAAPQKVTISCSGSSNIGN-DYVSWYQQVPQTAPKLLIYDNKR 74

Qy 197 PSQVSNRESGSGKSGSTASLTITSLGLOADEADYYCSSY-TTRSTRVFGGSKLTIVL 250
Db 75 PSQIPDRFSGSGKSGTSATLGTGLQTGDEADYYCGTWNNSLGSWVFGGSKLTIVL 129

RESULT 15
HVIG_HUMAN STANDARD; PRT; 117 AA.
AC HVIG_HUMAN 23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region V35 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukuhara S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus";
RL EMBO J. 7:1047-1051(1988).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X07448; -; NOT_ANNOTATED_CDS.
DR PIR: S00476; HVH035.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
FT NON_TER 117
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 29.5%; Score 384; DB 1; Length 117;
Best Local Similarity 74.5%; Pred. No. 2.7e-20;
Matches 73; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEVKKPKESLKISCGSGFTFSSYKMNWVRQAPCKGLEWMGGIPIFGTANY 60
Db 20 QQLVQSGAEVKKPKGKSVKSCSGYTFNSYHMWVRQAPCKGLEWMGGIIPNSGGTNY 79

Qy 61 AOKFOGRVTITADESTAYMELSLRSEDYAVYYCAR 98
Db 80 AOKFOGRVTSTRDTSISTAYMELSLRSEDYAVYYCAR 117

Search completed: August 15, 2002, 16:36:09
Job time: 719 sec

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Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 100 TPLSKDKFIISRNAKNTLYLQMSKVRSEDATLYFCAR-----ASYGHSAVWGQGT 152
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 179
Db 153 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 180 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 210 QKQKSPQLLYNNAKTLADGVPSRFSKSGSTOYSLKINSLOPEDFSGYCOHFWT-TPY 268
Qy 240 VFGGCKTLTV 249
Db 269 TFGGCKLEI 278

RESULT 2
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 43.7%; Score 567.5; DB 11; Length 218;
Best Local Similarity 52.1%; Pred. No. 7.1e-36;
Matches 114; Conservative 38; Mismatches 58; Indels 9; Gaps 3;

Qy 1 EVOLVSGAEVKKPGESLKISQSGFTFSYKMMNVRQAPGKGLWMGGIPIFGTANY 60
Db 3 QVKLQSGPELKKPGETVIRISKASGYTFTTAGMQWQKMPGKGLKWIGWINTHSGVPKY 62
Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 63 ABEFKGREFAFSLETSASTAYLQISNLKNEATATYFCMR-----WDYDGGFAYWGQGT 115
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 178
Db 116 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 179 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 176 QKQKSPQLLYNNAKTLADGVPSRFSKSGSTOYSLKINSLOPEDFSGYCOHFWT-TPY 268

RESULT 4
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clio. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
HSP; P01772; 2FB4.

Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 1 QVKLQSGPELKKPGETVIRISKASGYTFTTAGMQWQKMPGKGLKWIGWINTHSGVPKY 60
Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 61 ADDFKRFAFSLETSASTAYLQISNLKNEATATYFCAR-----KDLLRYFDYWGQGT 113
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 179
Db 114 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 180 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 171 HKPGKGRSAHTLHIV-----IQGIPSRFSKSGSRDYSFISNLEPEDATYYCLHYDN 226
Qy 236 RSTRVFGGCKTL 247
Db 227 LHT--FGGCKTL 236

RESULT 3
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
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DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MRP5 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 43.7%; Score 567.5; DB 11; Length 218;
Best Local Similarity 52.1%; Pred. No. 7.1e-36;
Matches 114; Conservative 38; Mismatches 58; Indels 9; Gaps 3;

Qy 1 EVOLVSGAEVKKPGESLKISQSGFTFSYKMMNVRQAPGKGLWMGGIPIFGTANY 60
Db 3 QVKLQSGPELKKPGETVIRISKASGYTFTTAGMQWQKMPGKGLKWIGWINTHSGVPKY 62
Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 63 ABEFKGREFAFSLETSASTAYLQISNLKNEATATYFCMR-----WDYDGGFAYWGQGT 115
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 178
Db 116 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 179 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 176 QKQKSPQLLYNNAKTLADGVPSRFSKSGSTOYSLKINSLOPEDFSGYCOHFWT-TPY 268

RESULT 4
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clio. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
HSP; P01772; 2FB4.

Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 100 TPLSKDKFIISRNAKNTLYLQMSKVRSEDATLYFCAR-----ASYGHSAVWGQGT 152
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 179
Db 153 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 180 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 210 QKQKSPQLLYNNAKTLADGVPSRFSKSGSTOYSLKINSLOPEDFSGYCOHFWT-TPY 268
Qy 240 VFGGCKTLTV 249
Db 269 TFGGCKLEI 278

RESULT 2
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 43.7%; Score 567.5; DB 11; Length 218;
Best Local Similarity 52.1%; Pred. No. 7.1e-36;
Matches 114; Conservative 38; Mismatches 58; Indels 9; Gaps 3;

Qy 1 EVOLVSGAEVKKPGESLKISQSGFTFSYKMMNVRQAPGKGLWMGGIPIFGTANY 60
Db 3 QVKLQSGPELKKPGETVIRISKASGYTFTTAGMQWQKMPGKGLKWIGWINTHSGVPKY 62
Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 63 ABEFKGREFAFSLETSASTAYLQISNLKNEATATYFCMR-----WDYDGGFAYWGQGT 115
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 178
Db 116 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 179 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 176 QKQKSPQLLYNNAKTLADGVPSRFSKSGSTOYSLKINSLOPEDFSGYCOHFWT-TPY 268

RESULT 4
Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clio. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
HSP; P01772; 2FB4.

Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 1 QVKLQSGPELKKPGETVIRISKASGYTFTTAGMQWQKMPGKGLKWIGWINTHSGVPKY 60
Qy 61 AOKFOGRVTITADESTSTAYMELSLRSEDATVYYCARNDRVVVPATSLRGMDVWGQGT 120
Db 61 ADDFKRFAFSLETSASTAYLQISNLKNEATATYFCAR-----KDLLRYFDYWGQGT 113
Qy 121 VTVSSGGSGGGGGGSGSVLTQ-PASVSGSPQSTITISCTGSSDVGYNVVSQY 179
Db 114 VTVSSGGSGGGGGGSGGGGDIETQSPASUSASVGEFTVITCRASGNI---HNTLAWYQ 209
Qy 180 QHPGKAPKLMIEYSGSRPSVNSRFSKSGSTASLTISGLQAEADYVYCSSYTRSTR 239
Db 171 HKPGKGRSAHTLHIV-----IQGIPSRFSKSGSRDYSFISNLEPEDATYYCLHYDN 226
Qy 236 RSTRVFGGCKTL 247
Db 227 LHT--FGGCKTL 236

RESULT 3
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
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Query Match      33.0%; Score 429; DB 4; Length 125;
Best Local Similarity 66.4%; Pred. No. 1.3e-25;
Matches 83; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

QY 1 EVOLVQSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKGLWMGWIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVOLVESGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWIPNSGGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFOGRVTTTADSTSTAYMELSLRSDDTAVYYCARDVVVPATSLRGGMVWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKVQGRVTWTRDTTISTAYMELSLRSDDTAVYYCARDVVVPATSLRGGMVWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 VTVSS 125
   |||||
Db 121 VTVSS 125
   |||||

RESULT 8
ID Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match      33.0%; Score 428.5; DB 11; Length 170;
Best Local Similarity 53.8%; Pred. No. 2.1e-25;
Matches 85; Conservative 23; Mismatches 31; Indels 19; Gaps 3;

QY 1 EVOLVQSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKGLWMGWIPIFGTANY 60
   :||:| ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QVQLQQSGEVVVRPGVSKVSKASGYTFTDYSMLHKLNNHQAQSLGWIITSDYDNTNY 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFOGRVTTTADSTSTAYMELSLRSDDTAVYYCARDVVVPATSLRGGMVWGQ 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 NQKFKGKATMTVDKSSITAYMELRLTSDSAIYYCARG-----AYYGSFYFDYWGQ 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 118 GTTVTVSSGGGGGGGGGGGQSQVLTQPASVSSPG 155
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 116 GTTVTVSSGGGGGGGGGGGSE-----SSSPG 144
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
Q9UL94 PRELIMINARY; PRT; 119 AA.
ID Q9UL94;
AC Q9UL94;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match      32.9%; Score 428; DB 4; Length 119;
Best Local Similarity 66.7%; Pred. No. 1.5e-25;
Matches 86; Conservative 11; Mismatches 18; Indels 14; Gaps 2;

QY 1 EVOLVQSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKGLWMGWIPIFGTANY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVOLVESGAEVKKPGASVKVSKASGYTFTGYMHVVRQAPGQGLEWMGWIPNSWTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFOGRVTTTADSTSTAYMELSLRSDDTAVYYCARDVVVPATSLRGGMVWG 116
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AOKFOGKVTMTKDTISITAYMELSLRSDDTAVYYCARG-----GGRLHFDPMG 110
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 117 QGTTVTVSS 125
   |||||
Db 111 QGTLTVSS 119
   |||||

RESULT 10
Q96GA6 PRELIMINARY; PRT; 614 AA.
ID Q96GA6;
AC Q96GA6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Straussberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAO9851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match      32.9%; Score 428; DB 4; Length 614;
Best Local Similarity 32.0%; Pred. No. 1e-24;
Matches 122; Conservative 31; Mismatches 82; Indels 146; Gaps 12;

QY 1 EVOLVQSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKGLWMGWIPIFGTANY 60
   ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 QMOLVQSGAEVKKPGSSVKVSKASGYTFTYRLHVRQAPGQALEWMGWITPFGNTNY 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 AOKFOGRVTTTADSTSTAYMELSLRSDDTAVYYCARDVVVPATSLRGGMVWGQGT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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```
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 37.0%; Score 491.5; DB 4; Length 124;
Best Local Similarity 75.8%; Pred. No. 6.1e-33;
Matches 97; Conservative 9; Mismatches 17; Indels 5; Gaps 2;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 60
D 1 EVOLVESGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 60
QY 61 AOKFGQRTVMTDTSIGTAYMELSLRSDDTAVYICARDRY-YGSSAYHRGSYYMDVWGR 119
D 61 AOKFGQRTVMTDTSIGTAYMELSLRSDDTAVYICARDRY-YGSSAYHRGSYYMDVWGR 119
QY 120 GTLVTVSS 127
D 117 GTLVTVSS 124

RESULT 8
Q96QSO PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE PUTATIVE MATRIX CELL ADHESION MOLECULE-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tilson M.D.;
RT "Homo sapiens putative microfibrillar protein with Ig-like domain 3
mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 36.1%; Score 479.5; DB 4; Length 159;
Best Local Similarity 72.5%; Pred. No. 7.8e-32;
Matches 95; Conservative 11; Mismatches 20; Indels 5; Gaps 3;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 60
D 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 79
QY 61 AOKFGQRTVMTDTSIGTAYMELSLRSDDTAVYICARDR--YGGSSAYHRGSYY--MDV 116
D 80 SOKFGRLTMTDTSITVYMDLSRLSDDTAVYFCAREMEITFG-GAVSKGFYYIGMDV 138
QY 117 WGRGTLTVSS 127
D 139 WQGGTTLTVSS 149

RESULT 9
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CG6C10F38 CRC64;

Query Match 36.0%; Score 479; DB 11; Length 170;
Best Local Similarity 63.4%; Pred. No. 9.3e-32;
Matches 90; Conservative 17; Mismatches 29; Indels 6; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 60
D 3 QVQLQSGPEVVRPGVSVKISCKSGYFTFTDYSMHLKMNHAQSLEWIGIITTYDNTNY 62
QY 61 AOKFGQRTVMTDTSIGTAYMELSLRSDDTAVYICARDRYGSSAYHRGSYYMDVWGRG 120
D 63 NQKFKGKATMTVDKSSITAYMELARLTSDSAIIYCARGAYYGS-----FYFEDWGGG 116
QY 121 TLTVSSGGGTGGGGSGGGGS 142
D 117 TTVTVSSGGGTGGGGSGGGGS 138

RESULT 10
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 35.0%; Score 465.5; DB 4; Length 614;
Best Local Similarity 44.6%; Pred. No. 5.5e-30;
Matches 112; Conservative 23; Mismatches 67; Indels 49; Gaps 9;

QY 1 EVOLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 60
D 20 QMQLVQSGAEVKKPGASVKVSCKASGYTFTGYMYWVRQAPQGQLEWGMWNPNSGGTNY 79
QY 61 AOKFGQRTVMTDTSIGTAYMELSLRSDDTAVYICARDRYGSS---AYHRGSYYMDVW 117
D 80 AOKFQDQRTVITDRSMNTAYMELSLRSDTAMYYCARG--YSSWDAAF-----DIW 130
QY 118 GRGTLTVSSGGGTGGGGSGGGSGGSELQDPFAVSVALG----QTVITCQDGL--RSY 171
D 131 GOGTMVTVSS-----GSASAPTLFLPLVSCENSPSDTSSVAVGCLADFLPDSI 178
QY 172 YASWYQOKPGQAPVLVLYCKNN----RPSGIPDRFSSSSSGNTASLTITCAQAEADYY 227
```

```
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

Query Match 41.1%; Score 546; DB 4; Length 107;
Best Local Similarity 98.1%; Pred. No. 1.8e-37;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 144 ELTQDPVAVSVALGQVTRITCOGDSLSRSYASWYQKPGQAPVLVYGNKRRPSGIPDRFS 203
DB 1 ELTQDPVSVVALGQVTRITCOGDSLSRSYASWYQKPGQAPVLVYGNKRRPSGIPDRFS 60

QY 204 GSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVL 249
DB 61 GSSSGNTASLTITGAQAEADYYCNSRDSGNHVVFGGTTKLTVL 106

RESULT 5
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;

Query Match 41.1%; Score 546; DB 4; Length 125;
Best Local Similarity 81.9%; Pred. No. 2.2e-37;
Matches 104; Conservative 9; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVOLVQSAGAEVKKPGASVKVSKASGYFTGYIMHWVRQAPQGLEWMGWINPNSSGNTY 60
DB 1 EVOLVQSAGAEVKKPGASVKVSKASGYFTGYIMHWVRQAPQGLEWMGWINPNSSGNTY 60

QY 61 AOKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYICARDRYGSSAYHRGSYIMDVWGRG 120
DB 61 AOKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYICARDRYGSSAYHRGSYIMDVWGRG 118

QY 121 TLVTVSS 127
DB 119 TMVTVSS 125

RESULT 6
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (Tremblrel. 13, Created)
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DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 39.8%; Score 529; DB 4; Length 119;
Best Local Similarity 81.9%; Pred. No. 5e-36;
Matches 104; Conservative 7; Mismatches 8; Indels 8; Gaps 3;

QY 1 EVOLVQSAGAEVKKPGASVKVSKASGYFTGYIMHWVRQAPQGLEWMGWINPNSSGNTY 60
DB 1 EVOLVQSAGAEVKKPGASVKVSKASGYFTGYIMHWVRQAPQGLEWMGWINPNSSGNTY 60

QY 61 AOKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYICARDRYGSSAYHRGSYIMDVWGRG 120
DB 61 AOKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYICARDRYGSSAYHRGSYIMDVWGRG 112

QY 121 TLVTVSS 127
DB 113 TLVTVSS 119

RESULT 7
ID Q9UL92 PRELIMINARY; PRT; 124 AA.
AC Q9UL92;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035022; AAD56258.1; -.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 124
```

```
QY 61 AOKFOGRTVMTDRDTSIGTAYMELSLRLSDDDTAVYVCARDRYGSSAYHRGSIYMDVWGRG 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 TPSLKDRFIISDRNAKNTLYLQMSKVRSEDALYICARSIYGHSA-----WGQG 150

QY 121 TLVTVSSGGGTGGGGGGSS-ELTDPA-VSVALGOTVITCOGDSLSRYASWQO 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 151 TTVTVSSGGGTGGGGGGSDIELTQSPASLSASVGETVITCRASGNTHNYLAWFOQ 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 KPGQAPVLVIYKNNRPSGIDPRFSGSSSGNTASITITGAQAEADYICNRSRDSNGH- 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 211 KQKSPQLLVYNAKTLADGVPSRSGSGGTQYSLKINSLOPEDFGSYC-----QHF 263

QY 238 ----VFFGGGKLV 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 WTPVTFGGGTKEI 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL MOL. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
FT NON_TER 1 241
FT NON_TER 241 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 48.4%; Score 643; DB 11; Length 241;
Best Local Similarity 52.2%; Pred. No. 5.6e-45;
Matches 133; Conservative 33; Mismatches 61; Indels 28; Gaps 7;

QY 1 EVOLVOSGAEVKPKGASVKVSKASGYTFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 QVKLQSGPELKKPGETVKISKASGYTFTDYGNNWVRQAPGKGLKMWGINTYTGEPT 60

QY 61 AOKFOGRTVMTDRDTSIGTAYMELSLRLSDDDTAVYVCARD--RYYGSSAYHRGSIYMDVW 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCARDLLRYF-----DYW 108

QY 118 GRGTLTVSSGGGTGGGGGGSS-ELTDPA-AVSVALGOTVITCOGDSLSRYASW 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 GOGTIVTVSSGGGGGGGGSDIELTQSPSSLSASLGKGVITCKASODINKYIAW 168

QY 176 YQKPGQAP-----VLVIYKNNRPSGIDPRFSGSSSGNTASITITGAQAEADYICNSR 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 169 YQHKPKGKPRSAHTLHIYIQ-----PCIPSRFSGSGGRDYFSISNLEPDITATYCLHY 224

QY 232 DSSGNHVFGGKTL 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 D----NLRTFGGKTL 236

RESULT 3
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
```

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DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MRP5 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RA "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 527E4FA8F7982817 CRC64;

Query Match 42.6%; Score 566.5; DB 11; Length 218;
Best Local Similarity 50.2%; Pred. No. 8.9e-39;
Matches 111; Conservative 39; Mismatches 56; Indels 15; Gaps 4;

QY 1 EVOLVOSGAEVKPKGASVKVSKASGYTFTGYMYWVRQAPQGGLWGMWNPNSGGTNY 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 QVKLQSGPELKKPGETVKISKASGYTFTAGMQWQKMPGKGLKIGWINTHSGVPKY 62

QY 61 AOKFOGRTVMTDRDTSIGTAYMELSLRLSDDDTAVYVCARDRYGSSAYHRGSIYMDVWGRG 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 ABEFKGRFAFSLETSASTAYLQISLNKEDTATYFCMRWDYDGGPAY-----WGQG 113

QY 121 TLVTVSSGGGTGGGGGGSS-ELTDPA-VSVALGOTVITCOG--DSLRSIYAS 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 TTVTVSSGGGGGGGGSGSDIVITQSPASLSVSLGORATISCRASEVDNIGISFMN 173

QY 175 WYQKPGQAPVLVIYKNNRPSGIDPRFSGSSSGNTASLT 215
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 WFQKPGQPPKLLIYAASKQSGVPAGLLASGSGTDFSLNI 214

RESULT 4
Q9NSD6
ID Q9NSD6 PRELIMINARY; PRT; 107 AA.
AC Q9NSD6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOCYTE;
RA Hohmann A.;
RT "Autolymnity.";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; L43092; AAA69746.2; -.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:35:36 ; Search time 91.6 Seconds
(without alignments)
470.259 Million cell up

Title: US-08-779-457-48
 Perfect score: 1329
 Sequence: 1 EVQLVSGAEVKPPGASVKY.....SRDSSGNHVFGGTFKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 5622222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

[illegible]

Post-processing:	Minimum Match	0%
100%	100%	100%

Maximum Match 100%
Plotting first 45 summer loc

Database :

```

Database :
SP_RKMBL19:
1:  sp_archaea.*
2:  sp_bacteria.*
3:  sp_fungi.*
4:  sp_human.*
5:  sp_invertebrate.*
6:  sp_mammal.*
7:  sp_mhc.*
8:  sp_organelle.*
9:  sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_invertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	647.5	48.7	298	11	Q9QYF0		Q9qyf0 mus musculus
2	643	48.4	241	11	Q921A6		Q921a6 mus musculus
3	566.5	42.6	218	11	Q925S1		Q925s1 mus musculus
4	546	41.1	*	107	Q9NSD6		Q9nsd6 homo sapien
5	546	41.1	125	4	Q9UL95		Q9ul95 homo sapien
6	529	39.8	119	4	Q9UL94		Q9ul94 homo sapien
7	491.5	37.0	124	4	Q9UL92		Q9ul92 homo sapien
8	479.5	36.1	159	4	Q96Q50		Q96q50 homo sapien
9	479	36.0	170	11	Q925S2		Q925s2 mus musculus
10	465.5	35.0	614	4	Q96GA6		Q96ga6 homo sapien
11	450.5	33.9	500	4	Q9BRV0		Q9brv0 homo sapien
12	450	33.9	119	5	Q9GY22		Q9gy22 schistosoma
13	433	32.6	117	11	Q9QXE9		Q9qxe9 mus musculus
14	431	32.4	146	11	Q924R8		Q924r8 mus musculus
15	429.5	32.3	145	11	Q924Q7		Q924q7 mus musculus
16	425	32.0	146	11	Q924Q3		Q924q3 mus musculus

Query Match 48.7%; Score 647.5; DB 11; Length 298;
Best Local Similarity 50.2%; Pred. NO. 3.1e-45;
Matches 128; Conservative 36; Mismatches 68; Indels 23; Gaps 5;

[illegible]

17	423.5	31.9	116	4	Q9UL89	Q9ul89 homo sapien
18	423.5	31.9	145	11	Q924R3	Q924r3 mus musculus
19	423	31.8	117	11	Q9QXF0	Q9qxf0 mus musculus
20	421.5	31.7	278	11	Q921K1	Q921k1 mus musculus
21	420.5	31.6	488	11	Q91WR1	Q91wr1 mus musculus
22	417.5	31.4	145	11	Q924R1	Q924r1 mus musculus
23	417	31.4	144	11	Q924P5	Q924p5 mus musculus
24	417	31.4	173	11	Q9D8L4	Q9d8l4 mus musculus
25	416	31.3	142	11	Q924Q1	Q924q1 mus musculus
26	414.5	31.2	143	11	Q924P9	Q924p9 mus musculus
27	412.5	31.0	145	11	Q924R4	Q924r4 mus musculus
28	412	31.0	481	11	Q91WT1	Q91wt1 mus musculus
29	410.5	30.9	143	11	Q924R7	Q924r7 mus musculus
30	409.5	30.8	145	11	Q924Q6	Q924q6 mus musculus
31	409	30.8	147	11	Q925S3	Q925s3 mus musculus
32	408.5	30.7	143	11	Q924Q5	Q924q5 mus musculus
33	407	30.6	463	11	Q991C4	Q991c4 mus musculus
34	406.5	30.6	145	11	Q924Q9	Q924q9 mus musculus
35	406	30.5	157	4	Q95978	Q95978 homo sapien
36	405.5	30.5	143	11	Q924R0	Q924r0 mus musculus
37	405.5	30.5	143	11	Q91VA2	Q91va2 mus musculus
38	404.5	30.4	145	11	Q924P7	Q924p7 mus musculus
39	401.5	30.2	468	11	Q991J31	Q991j31 mus musculus
40	401.5	30.2	496	4	Q96DK0	Q96dk0 homo sapien
41	400.5	30.1	143	11	Q91V67	Q91v67 mus musculus
42	399.5	30.1	141	11	Q924Q4	Q924q4 mus musculus
43	399	30.0	140	11	Q924R2	Q924r2 mus musculus
44	398	29.9	142	11	Q924Q2	Q924q2 mus musculus
45	398	29.9	150	4	Q9Y298	Q9y298 homo sapien

ALIGNMENTS

RESULT	1
Q9QYF0	
ID	PRELIMINARY; PRT; 298 AA.
AC	Q9QYF0;
DC	Q9QYF0;
DT	01-WAY-2000 (TREMBLrel. 13, Created)
DD	01-WAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	CN 8 SCFV.
CN	CN 8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	NCBI_TaxId=10090;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=BALB/C; TISSUE=SPLEEN;
RX	MEDLINE=20183931; PubMed=10706631;
RA	Shinochara N., Demura T., Fukuda H.;
RT	"Isolation of a vascular cell wall-specific monoclonal antibody
RT	recognizing a cell polarity by using a phage display subtraction
RT	method.";
RL	Proc. Natl. Acad Sci. U.S.A. 97:2585-2590(2000).

Query Match 48.7%; Score 647.5; DB 11; Length 298;

Best Local Similarity 50.28; Pred. No. 3.1e-45;

Matches 128; **Conservative** 36; **Mismatches** 68; **Indels** 23;

	QY	EVQLVQSGLAEVKKPKGAASVKVSCKASKGYTFTGYYMYWVRQAQQGLENGMWINPNSGGTN	60
		: : : : : : : : : :	:
D _B	40	QVKLOOSGGGLVPKGSLKLSCAASGSDFSRYYMSWVRQAPSGKEWTGEINPDOSTNY	99

Search completed: August 15, 2002, 16:24:03
Job time: 313 sec

PS Disclosure; Fig 5; 89pp; English.

XX The present sequence is that of human single chain antibody (scFv)
 CC H1b-1, which is directed against platelet glycoprotein Ib (GPIb).
 CC H1b-1 is composed of a heavy chain variable region (see AAY95189).
 CC and light chain variable region (see AAY95194) joined via a peptide
 CC linker. The H1b series of scFv was isolated from a human synthetic
 CC VH and VL scFv library by 3 rounds of phagemid selection against
 CC transfected CHO cells expressing the GPIb alpha component of the
 CC GPIb/IX/V complex on their surface, followed by a 4th round of
 CC selection against washed human platelets, and 2 final rounds in
 CC which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AAY95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by Escherichia coli, the H1b scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences
 CC and are therefore attractive potential reagents for therapeutic
 CC purposes. They provide a new class of antithrombotic agents,
 CC useful for the prevention of platelet-dependent thrombi in
 CC diseased arteries, bypass grafts, dialysis etc., and can also be
 CC used as diagnostic reagents. Methods of inhibiting aggregation
 CC of platelets, of binding human platelet GPIb alpha and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.

XX Sequence 238 AA;

Query Match 69.5%; Score 924; DB 21; Length 238;
 Best Local Similarity 72.4%; Pred. No. 5e-55;
 Matches 181; Conservative 22; Mismatches 33; Indels 14; Gaps 3;

Qy 1 EVQLVQSGAEVKPKGASVKVSKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60
 Db 1 EVQLVESGGGVVPRGSGSLRLSCAASGFFDDYGMVSRQAPGKGLWVSGINWNGSGTGY 60
 Qy 61 AQKFGQRTVMTDTSIGTAYMELSKLSDDTAVYYCARYDRYGSAYHRGSYMDVWGRG 120
 Db 61 ADSVKGRFTISRDHAKNSLYIQMNSLRaedtavyycaarlk-----mphawgqg 108
 Qy 121 TLVTVSSGGGTGGGGGGG-SSELTQDPAVSVVALGQTVRTTCGDSLSRYASWYQOK 179
 Db 109 LTVTVSSGGGGGGGGGGGSLSSLTQDPAVSVVALGQTVRTTCGDSLSRYASWYQOK 168
 Qy 180 PQGAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDADYICNSRDSGHNHV 239
 Db 169 PQGAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDADYICNSRDSGHNH-v 227

Qy 240 FGGGKLTVL 249
 Db 228 fgggkltvl 237

RESULT 15
 AAB46055
 ID AAB46055 standard; Peptide: 236 AA.

XX AAB46055;

XX 23-MAR-2001 (first entry)

XX Human TF anti-idiotypic antibody fragment K9+.

XX MUC1: human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW anti-idiotypic antibody; cytosolic; virucidal; antibacterial; TF antigen;
 KW antiparasitic; infectious disease.

OS Homo sapiens.

XX WO200073430-A2.

PN 07-DS-2000.

PD

XX

PF 29-MAY-2000; 2000WO-DE01809.

PR 27-MAY-1999; 99DE-1024405.

PR 09-SEP-1999; 99DE-1043016.

XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

PI Goletz S, Karsten U;

XX WPI; 2001-049937/06.

XX Vaccines against conformation-dependent or non-peptide antigens, based
 PT on DNA encoding peptide which mimics the antigen, useful e.g. as
 PT antitumor vaccines -
 PS Disclosure; Page 13; 36pp; German.

XX

CC This invention describes a novel vaccine (V1) against
 CC conformation-dependent antigens (CDA) comprising DNA (I) and/or an
 CC antibody, or peptide which immunologically imitates CDA, is new. (1)
 CC encodes a region of an anti-idiotypic antibody (Ab2) or another peptide
 CC which: (a) specifically binds to the binding site of an antibody (Ab1)
 CC or an antigen binding molecule; and (b) immunologically mimics the
 CC initial antigen. The epitope is partially or completely
 CC conformation-dependent, and has an immunogenic structure defined by a
 CC specific spatial conformation of amino acids. (1) is used in the form
 CC of linear or circular naked DNA and/or with a viral vector and/or
 CC adjuvants. The products of the invention have cytostatic, virucidal,
 CC antibacterial and antiparasitic. The invention also describes (1) a
 CC corresponding vaccine (V2) against antigens which are not proteins or
 CC peptides, as defined above but which have epitopes which show an
 CC immunogenic structure; (2) preparing (V1) and (V2); (3) human
 CC anti-idiotypic antibody fragments against the MUC1-conformation epitope
 CC having one of 31 approximately 60 residue amino acid sequences, all
 CC fully defined in the specification; (4) MUC1-conformation epitope mimics
 CC having one of 16 9-17 residue amino acid sequences, all fully in the
 CC specification; (5) anti-idiotypic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3), (4), (5), or (6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible.

XX Sequence 236 AA;

Query Match 68.2%; Score 907; DB 22; Length 236;
 Best Local Similarity 70.0%; Pred. No. 7e-54;
 Matches 175; Conservative 28; Mismatches 31; Indels 16; Gaps 3;

Qy 1 EVQLVQSGAEVKPKGASVKVSKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY 60

Db 1 EVQLVESGGGVVPRGSGSLRLSCAASGFFDDYGMVSRQAPGKGLWVSGINWNGSGTGY 60

Qy 61 AQKFGQRTVMTDTSIGTAYMELSKLSDDTAVYYCARYDRYGSAYHRGSYMDVWGRG 120

Db 61 ADSVKGRFTISRDHAKNSLYIQMNSLRaedtavyycaardpfh-----pwgqg 107

Qy 121 TLVTVSSGGGTGGGGGGG-SSELTQDPAVSVVALGQTVRTTCGDSLSRYASWYQOK 179

Db 108 LTVTVSSGGGGGGGGGGGSLSSLTQDPAVSVVALGQTVRTTCGDSLSRYASWYQOK 167

Qy 180 PQGAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDADYICNSRDSGHNHV 239

Db 168 PQGAPVLVIYGNKNNRPSGIPDRFSGSSGNTASLTITGAQAEDADYICNSRDSG--tv 225

Qy 240 FGGGKLTVL 249

Db 226 fgggkltvl 235

FT Region 227..237
 XX /note= "framework region 4"
 PN WO200026667-A1.
 XX 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US25495.
 PF 30-OCT-1998; 98US-0106275.
 PR (MILL/) MILLER J L.
 XX PA Miller JL;
 XX WPI; 2000-365744/31.
 XX Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX
 PS Disclosure; Fig 7; 89pp; English.
 CC The present sequence is that of human single chain antibody (scFv)
 CC HIB-3, which is directed against platelet glycoprotein Ib (GPiB).
 CC HIB-3 is composed of a heavy chain variable region (see AAY95210)
 CC and light chain variable region (see AAY95215) joined via a peptide
 CC linker. The HIB series of scFv was isolated from a human synthetic
 CC VH and VL scFv library by 3 rounds of phagemid selection against
 CC transfected CHO cells expressing the GPiB alpha component of the
 CC GPiB/IX/V complex on their surface, followed by a 4th round of
 CC selection against washed human platelets, and 2 final rounds in
 CC which attempts were made to displace scFv from washed platelets by
 CC flooding with murine monoclonal antibody or mimotope peptide (see
 CC AAY95229). Whether displayed as surface proteins on a phagemid or
 CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
 CC capable of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences
 CC and are therefore attractive potential reagents for therapeutic
 CC purposes. They provide a new class of antithrombotic agents,
 CC useful for the prevention of platelet-dependent thrombi in
 CC diseased arteries, bypass grafts, dialysis etc., and can also be
 CC used as diagnostic reagents. Methods of inhibiting aggregation
 CC of platelets, of binding human platelet GPiB alpha and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.
 XX
 SQ Sequence 237 AA;
 Query Match 69.7%; Score 926; DB 21; Length 237;
 Best Local Similarity 72.0%; Pred. No. 3.7e-55;
 Matches 180; Conservative 25; Mismatches 31; Indels 14; Gaps 3;
 Qy 1 EVQLVQSGAEVKKPKASVKYCKASGYFTGYMYWVRQAPGQGLEWMGWINPNSSGGTNY 60
 Db |||||::: : |||::: |||||::: |||::: |||||::: |||::: |||
 Qy 1 evqlvesgggvlvqp9gsrlscasgftfssyamsvwrqap9kglewysalsgsgsty 60
 Db |||||::: |||::: |||||::: |||::: |||||::: |||::: |||
 Qy 61 AOKFQGRVTMTSDTSGTAYMELSLRLSSDDTAVYVCARDRYGSSAYHRGSYIMDVWGRG 120
 Db |||||::: |||::: |||||::: |||::: |||||::: |||::: |||
 Qy 61 adsvkgrftisrdnsknltlylqmslraedtavyyca-----wksllmlwggg 108
 Db |||||::: |||::: |||||::: |||::: |||||::: |||::: |||
 Qy 121 TLVTVSSGGGTGGGGGGGGG-SSELTQDPAVSVVALGQTVRTTCQGDLSRYASWYQOK 179
 Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||
 Qy 109 tlvtvssggggsgggsggsalsseeltqdpavsalvgqtvrvtcggdlsrlyaswyqqk 168
 Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||
 Qy 180 PGQAPVLVIYGNKNNRPSGIPDRFSSSSGNTASLTITCAQAFDEADYYCNSRDSGSHVV 239
 Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||
 Qy 169 p9qapvlviygnknrpsgipdrfsgssgntaslcttgaqaeadyycnsrdsgnh-v 227
 Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||
 Qy 240 FGGGTKLTVL 249
 Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||
 Qy 228 fgggkltvl 237

RESULT 14

AAY95198
 ID AAY95198 standard; Protein; 238 AA.
 XX
 AC AAY95198;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Anti-platelet glycoprotein Ib human scFv HIB-1.
 XX
 KW Single chain antibody; scFv; human; HIB-1; glycoprotein Ib alpha;
 KW platelet; aggregation; antiaggregant; antithrombotic; thrombus;
 KW therapy; diagnostic.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..113
 FT /note= "heavy chain variable region"
 FT Region 1..30
 FT /note= "framework region 1"
 FT Region 31..34
 FT /note= "complementarity determining region 1"
 FT Region 35..49
 FT /note= "framework region 2"
 FT Region 50..66
 FT /note= "complementarity determining region 2"
 FT Region 67..98
 FT /note= "framework region 3"
 FT Region 99..104
 FT /note= "complementarity determining region 3"
 FT Region 105..113
 FT /note= "framework region 4"
 FT Peptide 114..130
 FT /note= "vector-derived linker"
 FT Region 131..238
 FT /note= "light chain variable region"
 FT Region 131..152
 FT /note= "framework region 1"
 FT Region 153..163
 FT /note= "complementarity determining region 1"
 FT Region 164..178
 FT /note= "framework region 2"
 FT Region 179..185
 FT /note= "complementarity determining region 2"
 FT Region 186..217
 FT /note= "framework region 3"
 FT Region 218..226
 FT /note= "complementarity determining region 3"
 FT Region 227..238
 FT /note= "framework region 4"
 XX WO200026667-A1.
 PN 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US25495.
 PF 30-OCT-1998; 98US-0106275.
 XX (MILL/) MILLER J L.
 XX Miller JL;
 XX WPI; 2000-365744/31.
 XX Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX

RESULT	12	
AAB46052		
ID	AAB46052 standard; Peptide; 240 AA.	
XX		
XX	AAB46052;	
XX		
DT	23-MAR-2001 (first entry)	
XX		
DE	Human TF anti-idiotypic antibody fragment K2+.	
XX		
KW	MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;	
KW	antidiotypic antibody; cytostatic; virucidal; antibacterial; TF antigen;	
KW	antiparasitic; infectious disease.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200073430-A2.	
XX		
PD	07-DEC-2000.	
XX		
PF	29-MAY-2000; 2000WO-DE01809.	
XX		
PR	27-MAY-1999; 99DE-1024405.	
PR	09-SEP-1999; 99DE-1043016.	
XX		
PA	{DELB-} DELBRUECK CENT MOLEKULARE MEDIZIN MAX.	
XX		
GO	Goletz S, Karsten U;	
PI		
XX	WPI; 2001-049937/06.	
DR		
XX		
PT	Vaccines against conformation-dependent or non-peptide antigens, based	
PT	on DNA encoding peptide which mimics the antigen, useful e.g. as	
PT	antitumor vaccines	
XX		
PS	Disclosure; Page 12-13; 36pp; German.	
XX		
CC	This invention describes a novel vaccine (V1) against	
CC	conformation-dependent antigens (CDA) comprising DNA (I) and/or an	
CC	antibody, or peptide which immunologically imitates CDA, is new. (I)	
CC	encodes a region of an antidiotypic antibody (Ab2) or another peptide	
CC	which: (a) specifically binds to the binding site of an antibody (Ab1)	
CC	or an antigen binding molecule; and (b) immunologically mimics the	
CC	initial antigen. The epitope is partially or completely	
CC	conformation-dependent, and has an immunogenic structure defined by a	
CC	specific spatial conformation of amino acids. (I) is used in the form	
CC	of linear or circular naked DNA and/or with a viral vector and/or	
CC	adjuvants. The products of the invention have cytostatic, virucidal,	
CC	antibacterial and antiparasitic. The invention also describes (1) a	
CC	corresponding vaccine (V2) against antigens which are not proteins or	
CC	peptides, as defined above but which have epitopes which show an	
CC	immunogenic structure: (2) preparing (V1) and (V2); (3) human	
CC	antidiotypic antibody fragments against the MUC1-conformation epitope	
CC	having one of 31 approximately 60 residue amino acids sequences, all	
CC	fully defined in the specification; (4) MUC1-conformation epitope mimics	
CC	having one of 16.9-17 residue amino acid sequences, all fully in the	
CC	specification; (5) antidiotypic antibody fragments against the TF	
CC	antigen having one of 24 approximately 200 residue amino acid sequences,	
CC	fully defined in the specification; (6) TF carbohydrate epitope mimetics	
CC	having one of 25 7-13 residue amino acid sequences, all fully defined in	
CC	the specification; and (7) DNA sequences encoding the fragments and	
CC	derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat	
CC	cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria	
CC	and parasites. The vaccines are effective in cases where vaccination has	
CC	previously not been possible.	
XX		
SQ	Sequence 240 AA;	

Query Match 70.4%; Score 936; DB 22; Length 240;
 Best Local Similarity 72.4%; Pred NO. 7.9e-56;


```

Db 230 gggtkltvl 238
RESULT 5
AAV15127
ID AAV15127 standard; Protein; 242 AA.
XX
XX
AC AAV15127;
XX
XX
DT 07-FEB-2000 (first entry)
XX
DE Anti-murine CTLA-4 M19 sfv.
XX
KW Anti-murine CTLA-4 sfv; M19 sfv; single chain antibody; murine CTLA4;
KW membrane-associated protein; chimeric construct; extracellular domain;
KW human CD8; ligand; activated T-cell; co-stimulatory signal; donor B7;
KW recipient CD28; T-cell proliferation;
KW xenograft-specific immunosuppression.
XX
XX
OS Mus sp.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 208
FT /note= "Corresponds to atc codon"
XX
XX
PN WO957266-A2.
XX
XX
PD 11-NOV-1999.
XX
XX
PF 30-APR-1999; 99WO-CB01350.
XX
XX
PR 30-APR-1998; 98GB-0009280.
XX
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX
PI Lechler IR, Dorling A;
XX
XX
DR WPI; 2000-038815/03.
DR N-PSDB; AAZ28999.
XX
XX
PT Inhibiting T-cell mediated rejection of xenotransplanted organs
XX
XX
PS Claim 9; Fig 11; 43pp; English.
XX
XX
CC The present sequence is the anti-murine CTLA-4 sfv (M19 sfv). This is a
CC membrane-associated protein which binds to CTLA-4. Chimeric constructs
CC comprising DNA sequences encoding the extracellular domain of murine
CC CTLA4 and human CD8 were used for the study of anti-CTLA4-sfv protein.
CC The anti-CTLA4 sfv functions as a ligand binding to CTLA-4 on activated
CC T-cells and antagonises the co-stimulatory signal provided by the
CC interaction between donor B7 and recipient CD28. Cells expressing the
CC anti-CTLA4 sfv failed to stimulate T-cell proliferation. This is used in
CC xenograft-specific immunosuppression.
XX
XX
SQ Sequence 242 AA;

Query Match 80.1%; Score 1064; DB 21; Length 242;
Best Local Similarity 83.6%; Pred. No. 1.9e-64;
Matches 209; Conservative 11; Mismatches 20; Indels 10; Gaps 3;

QY 1 EVOLVSGAEVKRPGASVKVSKASGYTFTGYYMYWRQAPGGGLEWMGWINPNSGGTNY 60
Db 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 qvqlvgsgeavkrpgasvkvsckasgytftsyymhwrqapggglewmglinpsggstsy 60
QY 61 AAKPQGRVMTDRTSICGTAYMELSLSSDDTAVYVCARDRYGSAVHRSYMDVWGGR 120
Db 1 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 aqkfqgrvmttrdtstctvymelslrsdsdtavycarvpynt-----lvfwgqg 112
QY 121 TLVTVSSGGGTGGGGGGGG-SSELTQDPAPVSVALGQTVRITCGQDSLSRYASWYQQK 179
Db 113 tlvtvssggggsgggsggsalsselltdqpavsalgqtvrictcqdslrsryaswyqqk 172

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QY 180 PGQAPVLVIYCKNNRPSGIPDRFSGSSSGNTASLTITGCAOAEDEADYYCNSRDSGNHVV 239
Db 173 pgqapvlviygnknrpsgipdrfsgsssgntasltitgcaadeadyycnsrdsg-ftv 231
QY 240 FGGGTKLTVL 249
Db 232 fgggtkltvl 241

RESULT 6
AAW49694
ID AAW49694 standard; Protein; 229 AA.
XX
AC AAW49694;
XX
DT 10-NOV-1998 (first entry)
XX
DE Human ScFv5 against alpha-1,3-galactosyl transferase.
XX
KW Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
KW sugar; N-acetyllactosamine; glycoprotein; glycolipid; antibody; pig;
KW graft tissue rejection; organ transplantation; xenotransplant; human;
KW single chain antibody.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
PN FR2751346-A1.
XX
XX
PD 23-JAN-1998.
XX
XX
PF 19-JUL-1996; 96FR-0009077.
XX
XX
PR 19-JUL-1996; 96FR-0009077.
XX
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX
PI Pourcel C, Soullou JP, Vanhove B;
XX
XX
DR WPI; 1998-112876/11.
DR N-PSDB; AAV49461.
XX
XX
PT Transgenic non-human donors of organs for human recipients -
XX containing DNA encoding antibodies that inhibit graft rejection
XX
XX
PS Claim 6; Page 56-57; 71pp; French.
XX
XX
CC This sequence represents a single chain antibody (ScFv5) constructed from
CC the sequence encoding a human antibody raised against the porcine enzyme
CC alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses
CC the attachment of a galactose sugar molecule on the N-acetyllactosamine
CC moiety found on surface glycoproteins and glycolipids. These sugar
CC molecules are partly responsible for raising anti-graft antibodies, which
CC lead to graft tissue rejection. The invention relates to a method of
CC inhibiting the graft rejection mechanism by introducing the sequence
CC encoding an antibody targeted to alpha-1,3-GT into the cells of animal,
CC especially a pig, from whom organs may be used for xenotransplants.
CC Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking
CC the galactose on the glycoproteins and glycolipids, thus preventing
CC induction of the rejection response.
XX
XX
SQ Sequence 229 AA;

Query Match 79.1%; Score 1051; DB 19; Length 229;
Best Local Similarity 84.7%; Pred. No. 1.3e-63;
Matches 200; Conservative 7; Mismatches 15; Indels 14; Gaps 1;

QY 14 PGASVKVSKASGYTFTGYYMYWRQAPGGGLEWMGWINPNSGNTYAKRFGQRTVTRD 73
Db 1 pgasvkvsckasgytftsyamhwrqapggglewmgwinagngntkysqkfgrvtrtd 60

```


DR WPI; 1997-372864/34.
 XX
 PT WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Example 14; Pages 120-121; 219pp; English.
 XX
 CC The present sequence is an agonist antibody clone to the human WSX
 CC receptor, which can be used to identify and purify ligands and
 CC activators. An anti-WSX receptor antibody can be used as an agonist
 CC to activate the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX
 SQ Sequence 249 AA;

Query Match 100.0%; Score 1329; DB 18; Length 249;
 Best Local Similarity 100.0%; Pred. No. 2.7e-82;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVQSGAEVKPKGASVKVCKASGYTFYCYMYWVRQAPGGGLEWMGWINPNSGCTNY 60
 DB 1 evqlvsgaevkpkgasvkvsckasgyftfgyymwvrqapggglewmgwinpnsqgtny 60
 QY 61 AQKFGQGVTRTDRISIGTAYMELSRSSDDTAVYICARDRYGSSAYHRGSYYMDVMGRG 120
 DB 61 aqkfgrgvtrtdrtsigtaymelsrlssddtavycardryygssayhrsgyymdvmvgrg 120
 QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGOTVTRITCGDSLRSYASWYQOKP 180
 DB 121 tlvtvssgggtggggggssseeltqdpavsvvalgqvtvritcggdslrsyyaswyqqkp 180
 QY 181 GQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240
 DB 181 gqapvlviygnknrrpsgipdrfsgsssgntasltitgaqaedeaddyycnsrdssghvfv 240
 QY 241 GGGTKLTVL 249
 DB 241 gggtkltvl 249

RESULT 2
 AAW49690
 ID AAW49690 standard; Protein; 236 AA.
 AC AAW49690;
 XX
 XX 10-NOV-1998 (first entry)
 XX Human ScFv1 against alpha-1,3-galactosyl transferase.
 XX Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;
 KW sugar; N-acetylglucosamine; glycoprotein; glycolipid; antibody; pig;
 KW graft tissue rejection; organ transplantation; xenotransplant; human;
 KW single chain antibody.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX

PN FR2751346-A1.
 XX
 PD 23-JAN-1998.
 XX
 PF 19-JUL-1996; 96PR-0009077.
 XX
 PR 19-JUL-1996; 96PR-0009077.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX Pourcel C, Soullou JP, Vanhove B;
 XX WPI; 1998-112876/11.
 DR N-PSDB; AAV49457.
 XX
 CC Transgenic non-human donors of organs for human recipients -
 CC containing DNA encoding antibodies that inhibit graft rejection
 PT
 PS Claim 6; Page 46-47; 71pp; French.
 XX
 CC This sequence represents a single chain antibody (ScFv1) constructed from
 CC the sequence encoding a human antibody raised against the porcine enzyme
 CC alpha-1,3-galactosyl transferase (alpha-1,3-GT). The enzyme catalyses
 CC the attachment of a galactose sugar molecule on the N-acetylglucosamine
 CC moiety found on surface glycoproteins and glycolipids. These sugar
 CC molecules are partly responsible for raising anti-graft antibodies, which
 CC lead to graft tissue rejection. The invention relates to a method of
 CC inhibiting the graft rejection mechanism by introducing the sequence
 CC encoding an antibody targeted to alpha-1,3-GT into the cells of animal,
 CC especially a pig, from whom organs may be used for xenotransplants.
 CC Neutralisation of the alpha-1,3-GT leads to tissues or organs lacking
 CC the galactose on the glycoproteins and glycolipids, thus preventing
 CC induction of the rejection response.
 XX
 SQ Sequence 236 AA;
 Query Match 83.1%; Score 1104; DB 19; Length 236;
 Best Local Similarity 84.7%; Pred. No. 3.7e-67;
 Matches 211; Conservative 9; Mismatches 15; Indels 14; Gaps 1;
 QY 1 EVQLVQSGAEVKPKGASVKVCKASGYTFYCYMYWVRQAPGGGLEWMGWINPNSGCTNY 60
 DB 1 evqlvsgaevkpkgasvkvsckasgyftfgyymwvrqapggglewmgwinagntky 60
 QY 61 AQKFGQGVTRTDRISIGTAYMELSRSSDDTAVYICARDRYGSSAYHRGSYYMDVMGRG 120
 DB 61 aqkfgrgvtrtdrtsigtaymelsrlssddtavycardryygssayhrsgyyaswyqqkp 120
 QY 121 TLVTVSSGGGTGGGGGGSSSELTQDPAVSVALGOTVTRITCGDSLRSYASWYQOKP 180
 DB 121 tlvtvssgggtggggggssseeltqdpavsvvalgqvtvritcggdslrsyyaswyqqkp 180
 QY 181 GQAPVLVIYGNKNNRPSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV 240
 DB 167 gqapvlviygnknrrpsgipdrfsgsssgntasltitgaqaedeaddyycnsrdssghvfv 226
 QY 241 GGGTKLTVL 249
 DB 227 gggtkltvl 235
 RESULT 3
 AAW49691
 ID AAW49691 standard; Protein; 237 AA.
 XX
 AC AAW49691;
 XX
 XX 10-NOV-1998 (first entry)
 XX Human ScFv2 against alpha-1,3-galactosyl transferase.
 XX Isoform; porcine; enzyme; alpha-1,3-galactosyl transferase; galactose;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:24:03 ; Search time 101.13 Seconds
(without alignments)
273.483 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
Sequence: 1 EVQIVQSGAEVKKPGASVKV.....SRDSSGNHVFEGGKTGLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1329	100.0	249	AAW24061	Human WSX receptor
2	1104	83.1	236	AAW49690	Human ScFv1 against
3	1073.5	80.8	237	AAW49691	Human ScFv2 against
4	1064.5	80.1	239	AAW49692	Human ScFv3 against
5	1064	80.1	242	AAW15127	Anti-murine CTLA-4
6	1051	79.1	229	AAW49694	Human ScFv5 against
7	1011.5	76.1	245	AAW67619	Human leukocyte an
8	997	75.0	309	AAW83322	Single chain Apo-2
9	963.5	72.5	312	AAW83323	Single chain Apo-2
10	951.5	71.6	282	AAE02185	PAM1 single chain
11	947.5	71.3	254	AAW49693	Human ScFv4 against

12	936	70.4	240	22	AAW46052	Human TF anti-idio
13	926	69.7	237	21	AAW95219	Anti-platelet glyc
14	924	69.5	238	21	AAW95198	Human TF anti-idio
15	907	68.2	236	22	AAW46055	Human leukocyte an
16	906.5	68.2	245	22	AAW67618	Human leukocyte an
17	904.5	68.1	245	22	AAW67617	Human leukocyte an
18	904	68.0	242	22	AAW46053	Human TF anti-idio
19	894.5	67.3	239	22	AAW46054	Human TF anti-idio
20	884.5	66.6	280	22	AAE02186	PAM2 single chain
21	865.5	65.1	245	22	AAW67621	Human leukocyte an
22	865.5	65.1	245	22	AAW67622	Human leukocyte an
23	865.5	65.1	245	22	AAW67623	Human leukocyte an
24	831.5	62.6	249	21	AAW36083	Recombinant human
25	826.5	62.2	250	18	AAW24062	Human WSX receptor
26	809.5	60.9	245	22	AAW67620	Human leukocyte an
27	792	59.6	304	22	AAG63634	Amino acid sequenc
28	792	59.6	304	22	AAG63639	Amino acid sequenc
29	773.5	58.2	258	18	AAW08487	C6 human sfv antib
30	767.5	57.8	310	20	AAW83324	Single chain Apo-2
31	763.5	57.4	256	13	AAW22583	ScFvB18 construct
32	763.5	57.4	428	18	AAW24027	Single chain anti
33	763.5	57.4	443	18	AAW24025	Single chain anti
34	760.5	57.2	402	15	AAW56485	ScFv PRAS110 and p
35	758.5	57.1	269	15	AAW54756	PRAS111 between H1
36	757.5	57.0	256	13	AAW22584	ScFvB18 construct
37	757.5	57.0	435	15	AAW56483	ScFv PRAS108 and p
38	756.5	56.9	241	20	AAW21882	Amino acid sequenc
39	755.5	56.8	269	15	AAW56482	ScFv PRAS107 and p
40	754.5	56.8	256	13	AAW22568	ScFvB18 construct
41	754	56.7	250	21	AAW44346	3B3 antibody Hom
42	750.5	56.5	256	13	AAW22582	ScFvB18 construct
43	749.5	56.4	415	15	AAW56484	ScFv PRAS109 and p
44	748.5	56.3	256	13	AAW22585	ScFvB18 construct
45	748.5	56.3	256	13	AAW22587	ScFvB18 construct

ALIGNMENTS

RESULT	1
AAW24061	
ID	AAW24061 standard; Protein; 249 AA.
XX	
XX	AAW24061:
XX	
DT	17-MAR-1998 (first entry)
XX	
DE	Human WSX receptor agonist antibody clone #3.
XX	
XX	Human; WSX receptor; clone #3; identification; purification;
KW	ligand; activator; antibody; agonist; proliferation; obesity;
KW	differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW	Type II diabetes; polycystic ovarian disease;
KW	cardiovascular disease; osteoarthritis; dermatological disorder;
KW	hypertension; insulin resistance; hypercholesterolaemia;
KW	hypertriglyceridaemia; cancer; cholelithiasis.
XX	
OS	Homo sapiens.
XX	
PN	WO9725425-A1.
XX	
PD	17-JUL-1997.
XX	
XX	07-JAN-1997; 97WO-US00325.
XX	
XX	20-JUN-1996; 96US-0667197.
PR	08-JAN-1996; 96US-0585005.
XX	
XX	(GETH) GENENTECH INC.
PA	
XX	Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
PI	Rodrigues ML;
XX	


```

QY 1 EVOLVSGAEVKKPGESLKISCKGSGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
Db 1 QVOLVSGAEVKKPGSSVKSCASGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
QY 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCARDVRV--VVPATSLRGMDVMGOG 118
Db 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCARDVRV--VVPATSLRGMDVMGOG 120
QY 119 TTVTVSS 125
Db 121 TTVTVSS 127

RESULT 13
L2HUNI
Ig lambda chain V-II region (Nei) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999
C:Accession: A01970
R:Carver, F.A.; Hilschmann, N.
Eur. J. Biochem. 26, 10-32, 1972
A:Title: The primary structure of a monoclonal human lambda-type immunoglobulin L-chain
A:Reference number: A01970; MUID:72233223
A:Accession: A01970
A:Molecule type: protein
A:Residues: 1-111 <GAK>
C:Comment: The sequence of the variable region only is shown.
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV4
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; glycoprotein; heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F:22-90/Disulfide bonds: #status predicted
F:96/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 38.9%; Score 506; DB 1; Length 111;
Best Local Similarity 87.3%; Pred. No. 1.1e-26;
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 141 QSVLTQPASVSGSPGSIISCTGTSDDYGVNYSWYQHPGKAPKLMYEGSKRPSGV 200
Db 1 QSALTQPASVSGSPGSIISCTGTSDDYGVNYSWYQHPGKAPKLMYEGSKRPSGV 60
QY 201 SNRFGSKSGTASLTISGLQAEDEADYCYSSYTRSTRVFGGGTKLTVL 250
Db 61 SNRFGSKSGTASLTISGLQAEDEADYCYSSYAGNSTRVFGGGTRTVTL 110

RESULT 14
B33548
Ig heavy chain V-1 region (AND) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: B33548
R:Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A:Reference number: A33548; MUID:89345575
A:Accession: B33548
A>Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-126 <KIP>
A:Experimental source: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

```

Query Match 38.8%; Score 504.5; DB 2; Length 126;
Best Local Similarity 76.7%; Pred. No. 1.5e-26;
Matches 102; Conservative 8; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVOLVSGAEVKKPGESLKISCKGSGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
Db 1 QVOLVSGAEVKKPGSSVKSCASGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
QY 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCARDVRVVPATSLRG-----GM 112
Db 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCAR-----VSIFGVQHYHYFM 113
QY 113 DVMGQGTTVTVSS 125
Db 114 DVMGLGTTTVTVSS 126

```

```

RESULT 15
PH0962
Ig heavy chain V region (G6+ T-L42) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0962
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0962
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-120 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-108/Region: complementarity-determining 3

```

```

Query Match 38.7%; Score 503.5; DB 2; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.7e-26;
Matches 100; Conservative 8; Mismatches 12; Indels 5; Gaps 1;

QY 1 EVOLVSGAEVKKPGESLKISCKGSGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
Db 1 QVOLVSGAEVKKPGSSVKSCASGFTSSYKMNVRQAPGKLEWGMGIIPIFGTANY 60
QY 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCARDVRVVPATSLRGMDVMGQGT 120
Db 61 AQKFGQGRVITADESTAYMELSSLSRSEDYAVYCARGV-----AGRPHFDYMGQGT 115
QY 121 VTVSS 125
Db 116 VTVSS 120

```

Search completed: August 15, 2002, 16:25:02
Job time: 302 sec

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RESULT 9
PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0961
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0961
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-119 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-107/Region: complementarity-determining 3

Query Match 39.8%; Score 517; DB 2; Length 119;
Best Local Similarity 81.6%; Pred. No. 2.2e-27;
Matches 102; Conservative 7; Mismatches 10; Indels 6; Gaps 1;

QY 1 EVLVSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWVGIIPIFGTANY 60
Db 1 QVLVSGAEVKKPGESVSKASGFTSSYAISSWRQAPGCGLEWVGIIPIFGTANY 60
QY 61 AQFQGRVITADESTAYMELSLRSEDYAVYICARDRVVVPATSLRGMDVWGQGT 120
Db 61 AQFQGRVITADESTAYMELSLRSEDYAVYICARGVYIY-----YGMVDVWGQGT 114
QY 121 VTVSS 125
Db 115 VTVSS 119

RESULT 10
S44105
Ig lambda chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44105
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A:Reference number: S44105
A:Accession: S44105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-112 <HAW>
A:Cross-references: EMBL:231388; NID:g472959; PIDN:CAA83263.1; PID:g940517
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 513.5; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 3.5e-27;
Matches 101; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 141 QSVLTAPASVSGSPGQSITISCTGTSSDVGYNVSWYQHPGKAPKLMYEGSKRPSGV 200
Db 1 QSALTQPASVSGSPGQSITISCTGTSSDVGYNVSWYQHPGKAPKLMYDVSNRPSGV 60
QY 201 SNRFSKSGSTASLTISGLQAEDEADYCYSSVYTRSTR-VFGGKTLTVL 250
Db 61 SNRFSKSGNTASLTISGLQAEDEADYCYSSYTSSTRYVFTGTKTVL 111
```

RESULT 11

```
PH0957
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0957
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0957
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-125 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-113/Region: complementarity-determining 3
```

```
Query Match 39.5%; Score 513; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 4.3e-27;
Matches 100; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVLVSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWVGIIPIFGTANY 60
Db 1 QVLVSGAEVKKPGESVSKASGFTSSYAISSWRQAPGCGLEWVGIIPIFGTANY 60
QY 61 AQFQGRVITADESTAYMELSLRSEDYAVYICARDRVVVPATSLRGMDVWGQGT 120
Db 61 AQFQGRVITADESTAYMELSLRSEDYAVYICARDGCGSGCYFWGDFWVGQGT 120
QY 121 VTVSS 125
Db 121 VTVSS 125
```

RESULT 12

```
PH0955
Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0955
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0955
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-127 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-115/Region: complementarity-determining 3
```

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Query Match 39.2%; Score 509; DB 2; Length 127;
Best Local Similarity 80.3%; Pred. No. 7.9e-27;
Matches 102; Conservative 9; Mismatches 14; Indels 2; Gaps 1;
```


A:Reference number: S41374
A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match 48.3%; Score 628; DB 2; Length 249;
Best Local Similarity 52.4%; Pred. No. 2.7e-34;
Matches 131; Conservative 36; Mismatches 73; Indels 10; Gaps 4;
QY 1 EVOLVSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWMGGIPIFGTANY 60
DB 1 QVQLQSGAEVLRPGASVKLSCTASGFNFKDDYIHVKVKORPEKLEWIAIPASGNKY 60
QY 61 AOKFQGRVTITADESTAYMELSLRSEDVAVYCARVVRVPATSLRGMDVMVGQGT 120
DB 61 VPRQKATITADTSNTAYLLSLTSEDVAVYCAR-----RDLYTSLGYWGQGT 114
QY 121 VVSSGGGGGGGGGGGQSGLVLTQ-PASVSGSPGQSITISCTGTSSD--GQYNYVSW 177
DB 115 VVSSRGGGGGGGGGGGDIETQSPSVVPIPGESVSISSCRSKSLLYSDGDSYLFW 174
QY 178 YQHPGKAPKLMYEGSKRPSGVNRFSGSKGSTASLTISGLQADEADYICSSYTRTS 237
DB 175 FLQPGQSPQLLYRMNLASGVDPDRFSGSGSTFTLRISRYAEADVGVYICMQH-REY 233
QY 238 TRYFEGGGTKL 247
DB 234 PLTFGAGTKL 243

RESULT 3
JC5322
p53 specific single-chain antibody Fab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydricioma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 45.5%; Score 591; DB 2; Length 233;
Best Local Similarity 51.2%; Pred. No. 6.5e-32;
Matches 127; Conservative 32; Mismatches 69; Indels 20; Gaps 5;
QY 6 QSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWMGGIPIFGTANYAQKFQ 65
DB 2 ESGAEVLRSGASVKLSCTTSQFNINDYIMHWKRPQGLEWIGRIDPENGADADTRSSG 61
QY 66 GRVTITADESTAYMELSLRSEDVAVYCARVVRVPATSLRGMDVMVGQGTITVSS 125
DB 62 VKATWTADTSNTAYLQLSLTSEDVAVYCAR-----NAGMDYWGQGTITVSS 109
QY 126 GGGSGGGGGGGGGQSGLVLTQ-PASVSGSPGQSITISCTGTSS-DVGGYNYVSWYQHPG 183
DB 110 GGGSGGRASGGGGDIETQSPASLAVSLGQRATISCRASKSVTSYGYMHWNQKPG 169
QY 184 KAPKLMYEGSKRPSGVNRFSGSKGSTASLTISGLQADEADYICSSY--TTRTRVF 241
DB 170 QPRLIYLYSNLESVGPAPRFGSGSGTDTLNIHPVEEEDAAITYCQHIRELTRSD--- 226
QY 242 GGTGKLTV 249
DB 227 -GGTKLEI 233

RESULT 4

S14683
Ig mu chain precursor, membrane-bound (cloné 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
A:Reference number: S14683; MUID:90332450
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:15/Domain: signal sequence #status predicted <SIG>
F:16-627/product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 41.3%; Score 537.5; DB 2; Length 627;
Best Local Similarity 36.9%; Pred. No. 5.7e-28;
Matches 144; Conservative 27; Mismatches 68; Indels 151; Gaps 12;
QY 1 EVOLVSGAEVKKPGESLKISCGSGFTSSYKMNVRQAPGKLEWMGGIPIFGTANY 60
DB 20 QVQLVSGAEVKKPGSSVKVSKASGDTFSSYALSWVRQAPGQGLEWMGGIPIFGTANY 79
QY 61 AOKFQGRVTITADESTAYMELSLRSEDVAVYCARVVRVPATSLRGMDVMVGQGT 112
DB 80 AOKFQGRVTITADESTAYMELSLRSEDVAVYCARVVRVPATSLRGMDVMVGQGT 139
QY 113 DVWGQGTITVSSGGGGGGGGGQSGLVLTQ-PASVSGSPG--QSITISCTG----- 164
DB 140 DVWGQGTITVSS-----GSASAPTFLPLVSCENSPSTSSVAVAGCLAQDPLPD 188
QY 165 -----TSSDVG-----GYNVYSWTQ-----QHPG-- 183
DB 189 SITFSNKKYKNSDITSSRGPSPVLRGGKYAATQVLLPSKDVMOGTDEHVCKVQHPNGN 248
QY 184 -----KAPKLMY-----EGSKR 196
DB 249 KEKNVPLPVIAPLPPKVSFVPRDGFNPRSKSLICQATGFSRQIQVSWLRGKQV 308
QY 197 PSGVSN---RFGSKSGS---TASLTIS-----GLQADEADYICS 231
DB 309 GSGVTTDQVQAEAKESGPTTYKVTITLIKESDWLSOSMFTCRVDHRLTFTQQNASSMCV 368
QY 232 SYTTRSTRVFG-----GKTKLTVL 250
DB 369 PDQDTAIRVFAIPSPFASIFLTKSTKLTLCL 398

RESULT 5

PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0960
R:Martin, T.; Duffy, S.P.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0960
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-136 <MAR>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1

Query Match 54.4%; Score 723.5; DB 4; Length 288;
Best Local Similarity 55.1%; Pred. No. 1.6e-52;
Matches 141; Conservative 44; Mismatches 54; Indels 17; Gaps 5;
1 EVOLVOSGAEVKKPGASVKSCKASGYTFGTGYMYVVRQAPCGGLEWGWGNTNPSGGTNY 60

23	QV	QVUQUPGAGLVPAGASVQUSCARSGITFTGTHWVKURPQUGDSEW1GEVNPSTGSRDI 82
61	QY	AQKQGRVTRMTRDSICTAYMELSRLSDDTAVVYCARDRYTGSSAYHRGSSYMMDMWGRG 120
83	Db	NEFKNKATLTVDKSSTAYMQLSSLLTSEDSAVVYCARERAYGYDD-----AMDYWGOG 136
121	QY	TLVTVSSGGGTGGGGGGGGSS-ELTQDP-AVSVALGOTVTRITCGDS-----LRSY 172
137	Db	TTVTVSSGGGGGGGGGGGGDIELSQSPSLAVSAGEKVTMCSKSSQSLLSNRKNY 196
173	QY	ASWYQKQPGQAPVLVIYGNKNNRPSGIPDRFSSSSSGNTASLTITGAQAEDEADYCYNSRD 232
197	Db	LAWYQRPQGGSPKLLIYWASTRTSGVYDPDRFTSGSGCTDFTLTISSVQAEDLAIYYCK--- 253
233	QY	SSGNHVVEGGGTKLTV 248
254	Db	QSYTLRTFFGGGTGLEI 269

```

/ BLAKEY, DAVID CHARLES
/
/ TITLE OF INVENTION: CHEMICAL COMPOUNDS
/
/ NUMBER OF SEQUENCES: 60
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: Pillsbury Winthrop, L.L.P.
/
/ STREET: 1100 New York Ave., N.W.
/
/ CITY: Washington
/
/ STATE: D.C.
/
/ COUNTRY: U.S.A.
/
/ ZIP: 20005
/
/ COMPUTER READABLE FORM:
/
/ MEDIUM TYPE: Floppy disk
/
/ COMPUTER: IBM PC compatible
/
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/
/ SOFTWARE: MS word
/
/ CURRENT APPLICATION DATA:
/
/ APPLICATION NUMBER: US/09/423,439
/
/ FILING DATE: 09-NO. 6339070-1999
/
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/
/ APPLICATION NUMBER: PCT/GB98/01294
/
/ FILING DATE: 05-MAY-1998
/
/ APPLICATION NUMBER: GB 9709421.3
/
/ FILING DATE: 10-MAY-1997
/
/ INFORMATION FOR SEQ ID NO: 32:

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US-08-491-988-5
; Sequence 5, Application US/08491988
; Patent No. 5973116
; GENERAL INFORMATION:
; APPLICANT: EPENETOS, AGAMEMNON A.
; APPLICANT: SPOONER, ROBERT A.
; APPLICANT: DEONARAIN, MAHENDRA
; TITLE OF INVENTION: Compounds for targeting
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491.988
; FILING DATE: 18-DEC-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-491-988-5

Query Match 57.1%; Score 758.5; DB 2; Length 435;
Best Local Similarity 60.1%; Pred. No. 3.4e-55;
Matches 152; Conservative 35; Mismatches 53; Indels 13; Gaps 4;

QY 1 EVQLVQSGAEVKKPKASVKVCKASGYFTFTGYMYWVRQAPCGQGLEWMGWINPNSGGTNY 60
DB 23 QVQLQPGAEVKKPKASVKVCKASGYFTFTSYMMHWKQRPGRGLEWIGRIDPNSGGTKY 82
QY 61 AOKFQGRVMTDRDTSIGTAYMELSLRSLSDDTAVYYCARDRYYGSSAYHRGSYIMDVWGRG 120
DB 83 NEKFKSKATLTVDKPSSTAYMQLSLTSEDSAVYYCARYDYVGSS-----YFDYWGQ 135
QY 121 TLVTVSSGGGGTGGGGGGGS-SELTQDPVAVSVALGQTVRTICQ---GDSLSRYIASWY 176
DB 136 TMTVTSSGGGGGGGGGGGGGSAVVTQESALTTSPGETVTLTCSRSTGAVTTSNVAWV 195
QY 177 QOKPGQAPVLVIYGNKRPSPGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSN 236
DB 196 QKPKPHLFTGLIGGNRNAPGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALMYS--N 253
QY 237 HVVFGGKTLTVL 249
DB 254 HNVFGGKTLTVL 266

RESULT 12
US-08-918-148-74
; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.

; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918.148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
; LENGTH: 249
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-74

Query Match 55.4%; Score 736.5; DB 4; Length 249;
Best Local Similarity 57.3%; Pred. No. 1.2e-53;
Matches 145; Conservative 40; Mismatches 55; Indels 13; Gaps 5;

QY 1 EVQLVQSGAEVKKPKASVKVCKASGYFTFTGYMYWVRQAPCGQGLEWMGWINPNSGGTNY 60
DB 3 QVQLQESGEMKPKGESLKISKCYGYSFATSWIGVWQMPGRGLEWMAIMYTPGNSDTRH 62
QY 61 AOKFQGRVMTDRDTSIGTAYMELSLRSLSDDTAVYYCARDRYYGSSAYHRGSYIMDVWGRG 120
DB 63 NPSFEDQVMTSADTSINTAYLQWSSLKASDTAMYYCARAGVAGG-----FDLWKGK 114
QY 121 TLVTVSSGGGGTGGGGGGGS-SELTQDPVAVSVALGQTVRTICQDS--LRSY-YASWY 176
DB 115 TMTVTSSGGGGGGGGGGGGGSQLTQFASVSGSPGSGITISCTGTSVGVGYNVSWY 174
QY 177 QOKPGQAPVLVIYGNKRPSPGIPDRFSGSSGNTASLTITGAQAEDEADYYCNSRDSN 236
DB 175 QOHGPKAPKLLIYGNRNRPSPGVDRFSKSGNTASLTISLQAEDEADYFCSTYAPPG- 233
QY 237 HVVFGGKTLTVL 249
DB 234 IIMFGGKTLTVL 246

RESULT 13
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MULLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 16:22:13 ; Search time 39.61 Seconds
(without alignments)
153.546 Million cell updates/sec

Title: us-08-779-457-48

Perfect score: 1329

Sequence: 1 EVQLVQSGAEVKKPGASVKV.....SRDSSGNHNVFGGKTLTVL 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	997	75.0	309	4	US-09-079-029-9
2	963.5	72.5	312	4	US-09-079-029-10
3	931.5	71.6	280	4	US-09-260-527-1
4	884.5	66.6	278	4	US-09-260-527-3
5	776.5	58.4	258	2	US-08-555-202-5
6	767.5	57.8	310	4	US-09-079-029-11
7	758.5	57.1	269	2	US-08-428-257A-72
8	758.5	57.1	269	2	US-08-491-988-3
9	758.5	57.1	402	2	US-08-491-988-9
10	758.5	57.1	415	2	US-08-491-988-7
11	758.5	57.1	435	2	US-08-491-988-5
12	736.5	55.4	249	4	US-08-918-148-74
13	727.5	54.7	244	2	US-08-553-497A-20
14	723.5	54.4	288	4	US-09-423-439-38
15	723.5	54.4	673	4	US-09-423-439-32
16	722.5	54.4	246	2	US-08-553-497A-24
17	711.5	53.5	267	4	US-09-485-737B-2
18	711.5	53.5	511	4	US-09-485-737B-85
19	711.5	53.5	711	4	US-09-485-737B-90
20	710	53.4	239	3	US-08-279-772A-8
21	710	53.4	239	4	US-08-902-486-11
22	710	53.4	599	1	US-08-463-163-3
23	709.5	53.4	244	2	US-08-553-497A-22
24	698.5	52.6	240	1	US-08-488-113B-148
25	698.5	52.6	240	1	US-08-477-484B-148
26	698.5	52.6	240	2	US-08-646-360-148
27	698.5	52.6	240	4	US-08-839-765-148

28	698.5	52.6	240	4	US-09-136-389-148	Sequence 148, Appl
29	696	52.4	270	2	US-08-652-507-2	Sequence 2, Appl
30	695	52.3	269	4	US-08-646-265A-109	Sequence 109, Appl
31	695	52.3	553	2	US-08-661-052-16	Sequence 16, Appl
32	695	52.3	553	4	US-09-188-082-16	Sequence 16, Appl
33	694	52.2	244	4	US-08-918-148-79	Sequence 79, Appl
34	693.5	52.2	242	2	US-08-553-497A-26	Sequence 26, Appl
35	693.5	52.2	249	2	US-08-797-689-18	Sequence 18, Appl
36	680	51.2	240	4	US-09-485-737B-91	Sequence 91, Appl
37	676.5	50.9	242	2	US-08-553-497A-28	Sequence 28, Appl
38	676.5	50.9	284	3	US-09-184-658-40	Sequence 40, Appl
39	670	50.4	281	4	US-09-423-439-44	Sequence 44, Appl
40	670	50.4	666	4	US-09-423-439-51	Sequence 51, Appl
41	667	50.2	240	2	US-08-800-198-8	Sequence 8, Appl
42	667	50.2	240	3	US-09-296-595-8	Sequence 8, Appl
43	664	50.0	241	1	US-08-235-838-11	Sequence 11, Appl
44	664	50.0	241	2	US-08-465-473B-11	Sequence 11, Appl
45	664	50.0	637	1	US-08-235-838-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-079-029-9
; Sequence 9, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chantharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-9

Query Match 75.0%; Score 997; DB 4; Length 309;

Best Local Similarity 76.3%; Pred. No. 4.6e-75;
Matches 190; Conservative 24; Mismatches 29; Indels 6; Gaps 2;

Oy 1 EVQLVQSGAEVKKPGASVKASGVTFTGYVWVRQAPGQGLWMTNPNSGGTNY 60
| | | | | : : : | : : : | | | | | : : : | | | | |
Db 40 EVQLVQSGGGVVERPGSLRLSCAASGFTDDYGHASWVRQAPGKGLWVSGINWNGSGTGY 99


```

; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 121575
; LENGTH: 262
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-791-537-121575

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	Query Match	82.7%	Score	1098.5;	DB	5; Length	262;		
	Best local similarity	85.5%;	Pred.	No. 2e-60;	Mismatches	213; Conservative	9; Indels	7; Gaps	2;
Qy	1	EVLVQSAGAEVKKPGASVKSCAKSGYFTGYVMWVRAPQGQLGWMGWINPNSGGTNY	60 :						
Dd	3	QVLVQSAGAEVKKPGASVKSKASYFTSYAMHWVRAPQRLEMGWINAGNNTKY	62 :						
Qy	61	AOKFQGRVTTRDTISGTATYWELSLRSSDTPAVYYCARDRYGSSAYHYGMVDWGRR	120 :						
Dd	63	SQKFQGRVTITRDTASTATYWELSSLRSSEDPVVYCA--RLTPNKFSRGH----	WGQQ 115 :						
Qy	121	TLVTVSSGGTGCGGGGGGSSELTDPAVSVALGQTVRTTCGDLSLRYSYAWSYOQKP	180 :						
Dd	116	TLTVSVRGGGGGGGGGGGSSELTDPAVSVALGQTVRTTCGDLSLRYSYAWSYOQKP	175 :						
Qy	181	GQAPLVIYGNRPSPGIPOBFSSSNGNTASLTITGAQEADADYCNSRDSSGHNVVF	240 :						
Dd	176	GQAPLVIYGNRPSPGIPDRFGSSSNGNTASLTITGAQEADADYCNSRDDSGNHVVF	235 :						
Qy	241	GGGTKLTVL	249 :						
Dd	236	GGGTKLTVL	244 :						

```

RESULT      3
PCT-US02-16106-20
; Sequence 20, Application PC/TUS0216106
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554PCT
; CURRENT APPLICATION NUMBER: PCT/US02/16106
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A030D09 scFv
PCT-US02-16106-20

```

```

Query Match      81.0%; Score 1076; DB 1; Length 250;
Best Local Similarity 83.5%; Pred. No. 4.6e-59;
Matches 208; Conservative 11; Mismatches 30; Indels 0; Gaps 0;

Qy 1 EVQLVQSGAEYKKPGASVKVSCKASQGYTFTCYGYMYWRQAPQGQGLEWMGWINPSSGTTY 60
    :||| ||||| ||||| ||||| ||| :||| ||||| ||||| ||||| ||||| ||||| |||||
Db #1 QVQLVQSGAEYKKPGSSVKYCKSTSGAFAHYAIAHWYRLAPAPQGQLEWMGDIIPIYVGSTTY 60
    :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

	Qy	61	AQKQGVRVWTRDTSIGTAYMELSRLSDDTA VYCCARDRYHCSSAYHRGSSYYMDVMGRG	120
	Dd	61	: : :	120
	Qy	121	TLVTVSSGGGTGGGGSGGSSELTODPAVSALGVTVRITCGDSLRSYYASWTQQKP	180
	Dd	121	: : :	180
	Qy	181	GQAPVLVIYGKNRPSGIPIORFSGSSSNGNTASLITCAQAEDADYYCNSRDSSGNHVVF	240
	Dd	181	: : :	240
	Qy	241	GGGTKLTVL	249
	Dd	241	: : :	249

```

RESULT      4
US-10-151-882-20
; Sequence 20, Application US/10151882
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A030D09 scFv
US-10-151-882-20

```

Query Match	81.0%;	Score 1076;	DB 6;	Length 250;
Best Local Similarity	83.5%;	Pred. No. 4.6e-59;		
Matches 208; Conservative	11;	Mismatches 30;	Indels 0;	Gaps 0;

```

RESULT      5
US-09-791-537-1444
; Sequence 1444, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF

```

FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1444
LENGTH: 262
TYPE: PRT
ORGANISM: synthetic construct
US-09-791-537-1444

Query Match 72.8%; Score 967.5; DB 5; Length 262;
Best Local Similarity 73.5%; Pred. No. 2.2e-52;
Matches 183; Conservative 26; Mismatches 33; Indels 7; Gaps 2;
QY 1 EVOLVSGAEVKKPGASVKVSCKASGCTTGTGYMYWVRQAPGQGLGWMGWINPNSGGTNY 60
Db 3 EVOLVESGGGLYKPGGSLRLSCAASGFTSDYMSWIRQAPGKGLWVSYISSSGSTIYY 62
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYSSAYHRSYMDVWGRG 120
Db 63 ADSVKGRFTISRDNKNSLYLQNMNSLAEDTAVYYCARHR---PGRMFRSPY----WGQG 115
QY 121 TLVTSSGGGGTGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 180
Db 116 TLVTSSGGGGGGGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 175
QY 181 GOAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHHVVF 240
Db 176 GOAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHHVVF 235
QY 241 GGGTKLTVL 249
Db 236 GGGTKLTVL 244

RESULT 6
US-09-791-537-118537
Query Match 69.9%; Score 928.5; DB 5; Length 253;
Best Local Similarity 72.3%; Pred. No. 5.3e-50;
Matches 180; Conservative 23; Mismatches 31; Indels 15; Gaps 2;
QY 1 EVOLVSGAEVKKPGASVKVSCKASGCTTGTGYMYWVRQAPGQGLGWMGWINPNSGGTNY 60
Db 2 EVOLVESGGGLIQQGSLRLSCAASGFTVSSNMYMSWVRQAPGKGLWVSYIY-SGGSTIY 60
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYSSAYHRSYMDVWGRG 120
Db 61 ADSVKGRFTISRDNKNSLYLQNMNSLAEDTAVLLCKRD-----LCDWGQG 106
QY 121 TLVTSSGGGGTGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 180
Db 107 TLVTSSGGGGGGGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 166

QY 181 GOAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHHVVF 240
Db 167 GOAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHHVVF 226
QY 241 GGGTKLTVL 249
Db 227 GGGTKLTVL 235
RESULT 7
US-09-949-039-2
Query Match 68.2%; Score 906; DB 5; Length 290;
Best Local Similarity 68.3%; Pred. No. 1.4e-48;
Matches 170; Conservative 37; Mismatches 32; Indels 10; Gaps 2;
QY 1 EVOLVSGAEVKKPGASVKVSCKASGCTTGTGYMYWVRQAPGQGLGWMGWINPNSGGTNY 60
Db 28 QVOLVSGGGVQVQGRSLRLSCAASGFTTSSYAMHWVRQAPGKGLWVSAISGGSTIY 87
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYSSAYHRSYMDVWGRG 120
Db 88 ADSVKGRFTISRDNKNSLYLQNMNSLAEDTAVYYCARDT-----RG--YFDLWGRG 137
QY 121 TLVTSSGGGGTGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 180
Db 138 TLVTSSGGGGGGGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 197
QY 181 GOAPVLVIYKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSNGHHVVF 240
Db 198 ROAPRLVIYKNNRPSGIPDRFSGSGTSGDTASLTISGLQAEDEADYYCHSRDSNADLVWF 257
QY 241 GGGTKLTVL 249
Db 258 GGGTKLTVL 266

RESULT 8
US-09-949-039-75
Query Match 75.9%; Score 928.5; DB 5; Length 253;
Best Local Similarity 72.3%; Pred. No. 5.3e-50;
Matches 180; Conservative 23; Mismatches 31; Indels 15; Gaps 2;
QY 1 EVOLVSGAEVKKPGASVKVSCKASGCTTGTGYMYWVRQAPGQGLGWMGWINPNSGGTNY 60
Db 2 EVOLVESGGGLIQQGSLRLSCAASGFTVSSNMYMSWVRQAPGKGLWVSYIY-SGGSTIY 60
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRSSDDTAVYYCARDRIYSSAYHRSYMDVWGRG 120
Db 61 ADSVKGRFTISRDNKNSLYLQNMNSLAEDTAVLLCKRD-----LCDWGQG 106
QY 121 TLVTSSGGGGTGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 180
Db 107 TLVTSSGGGGGGGGGGGGGSGGSELTDPAVSVALGQTVRITCGDLSRYSYASWYQOKP 166

Qy 237 HVFVGCTKLTVL 249
 |||||:||||
 Db 241 --VFVGCTQLTVL 251

US-10-120-414-73
; Sequence 73, Application US/10120414
; GENERAL INFORMATION:

```

; AFFILIATION: ROSEN, CLARY, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112p9
; CURRENT APPLICATION NUMBER: US/10/120,414

```

; COMMENT FILING DATE: 2002-04-12
 ; PRIOR APPLICATION NUMBER: 60/283,385
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/350,366

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; EASON FILES END. 2002 01 24
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73

```

```

; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
DS-10-120-414-73

```

Query Match	67.7%;	Score 900;	DB 6;	Length 252;
Best Local Similarity	70.4%;	Pred. No. 2.9e-48;		

Qy

1 EVOLVQSAGAEVKKPGASVKYSCCKASGYTFGGYYMYWVRQA PGGLEWMGWINPNSGGTNY 60
: : ::::: ::::: : : ::::: ::::: | | | |
Dd

1 QMQLVQSAGAEVKKPGSSVKYSCCKSGIFSSVAISWTQRAPG GLEWMGGIIPFGTANY 60

Qy	61	AQFQGRVTMTDRTNSIGTAYMELSSDDTAVYCCARDRYYGSSAY-HRGSYMDVWGK	119
		: : : : : : :	
Db	61	AQKEGRTITADESTSTAYNELSSLRSED TAVYCCARDQVRASGSPYYNYMDVGQ	120

Qy	120	GT	LT	V	S	G	G	G	G	G	G	S	---	E	L	T	Q	D	P	A	V	S	V	A	L	G	Q	T	V	R	I	T	C	O	G	S	L	R	S	Y	A	S	W	Y	176
Db	121	GT	LT	V	S	G	G	G	G	G	G	S	---	E	L	T	Q	D	P	A	V	S	V	A	L	G	Q	T	V	R	I	T	C	O	G	S	L	R	S	Y	A	S	W	Y	180

```
QY      177 QQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSNTASLTITGAQAEDADYCYCNRDSSGN 236  
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db      181 QQKPGQSPVLVIYQDSERPISGPFRFGNSNGTATITIRGTQPLDEADYCYQTWDSTG 240
```

Qy	237	HVVEGGGTKLTVL	249
		:	
Dh	241	--VEGGGTOITVL	251

RESULTS 11
US-10-039-785-42
; Sequence 42, Application US/10039785
; GENERAL INFORMATION:

7
;
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550

```

; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05

```

; PRIOR APPLICATION NUMBER: 60/341,237
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: 60/331,310
 ; PRIOR FILING DATE: 2001-11-14

; PRIOR FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,044
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: 60/327,364

; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: 60/323,807

```
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
US-10-039-785-42
```

```
Query Match 66.1%; Score 878.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. No. 6e-47;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVOLVSGAEVKKPGASVKVSCKASGTTFTGYMYVVRQAPGQGLEWMGWINPNSGGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVSGADVKRPGASVKVSCKISGDSFNAYFIHWVRQAPGQGLEWMGFNPDSTADS 60

QY 61 AQKFGQRTVMTDRTSITGAYMELSRLLSDDTAVYYCARDRYVGSSAYHRGSIYMDVWGRG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGHRTVMTDRTSSSTAFLESLRLSRDDTAVYYCVRQ-----HRGNTFAP-WGRG 111

QY 121 TLVTSSGGGTGGGGGGGSE--LTQDPVSVVALGOTVTRITCOG--DSLRSY-YASW 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 112 TWVTSSGGGGGGGGGSAQSVLTQPPSASGSPGQSVTISCTGTTSDVGGYNYVSW 171

QY 176 YQKQPCQAPVLYIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSG 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 172 YQHPGKAPKLMYIGNRPSGVPDRFSGSKGNTASLTITVSGLQAEADYYCNSYAGS- 230

QY 236 NHVFGGGTKLTVL 249
   |:|||||:|||||
Db 231 NMVFGGGTKLTVL 244
```

```
RESULT 12
US-10-139-785-42
; Sequence 42, Application US/10139785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 42
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014A04 scFv
US-10-139-785-42

Query Match 66.1%; Score 878.5; DB 6; Length 245;
Best Local Similarity 68.1%; Pred. No. 6e-47;
Matches 173; Conservative 28; Mismatches 38; Indels 15; Gaps 6;

QY 1 EVOLVSGAEVKKPGASVKVSCKASGTTFTGYMYVVRQAPGQGLEWMGWINPNSGGTNY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVOLVSGADVKRPGASVKVSCKISGDSFNAYFIHWVRQAPGQGLEWMGFNPDSTADS 60

QY 61 AQKFGQRTVMTDRTSITGAYMELSRLLSDDTAVYYCARDRYVGSSAYHRGSIYMDVWGRG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 AQKFGHRTVMTDRTSSSTAFLESLRLSRDDTAVYYCVRQ-----HRGNTFAP-WGRG 111

QY 121 TLVTSSGGGTGGGGGGGSE--LTQDPVSVVALGOTVTRITCOG--DSLRSY-YASW 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 112 TWVTSSGGGGGGGSAQSVLTQPPSASGSPGQSVTISCTGTTSDVGGYNYVSW 171

QY 176 YQKQPCQAPVLYIYGNRPSPGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSG 235
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 172 YQHPGKAPKLMYIGNRPSGVPDRFSGSKGNTASLTITVSGLQAEADYYCNSYAGS- 230

QY 236 NHVFGGGTKLTVL 249
   |:|||||:|||||
Db 231 NMVFGGGTKLTVL 244
```

```
RESULT 13
US-10-039-785-46
; Sequence 46, Application US/10039785
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: T1014B01 scFv
US-10-039-785-46
```

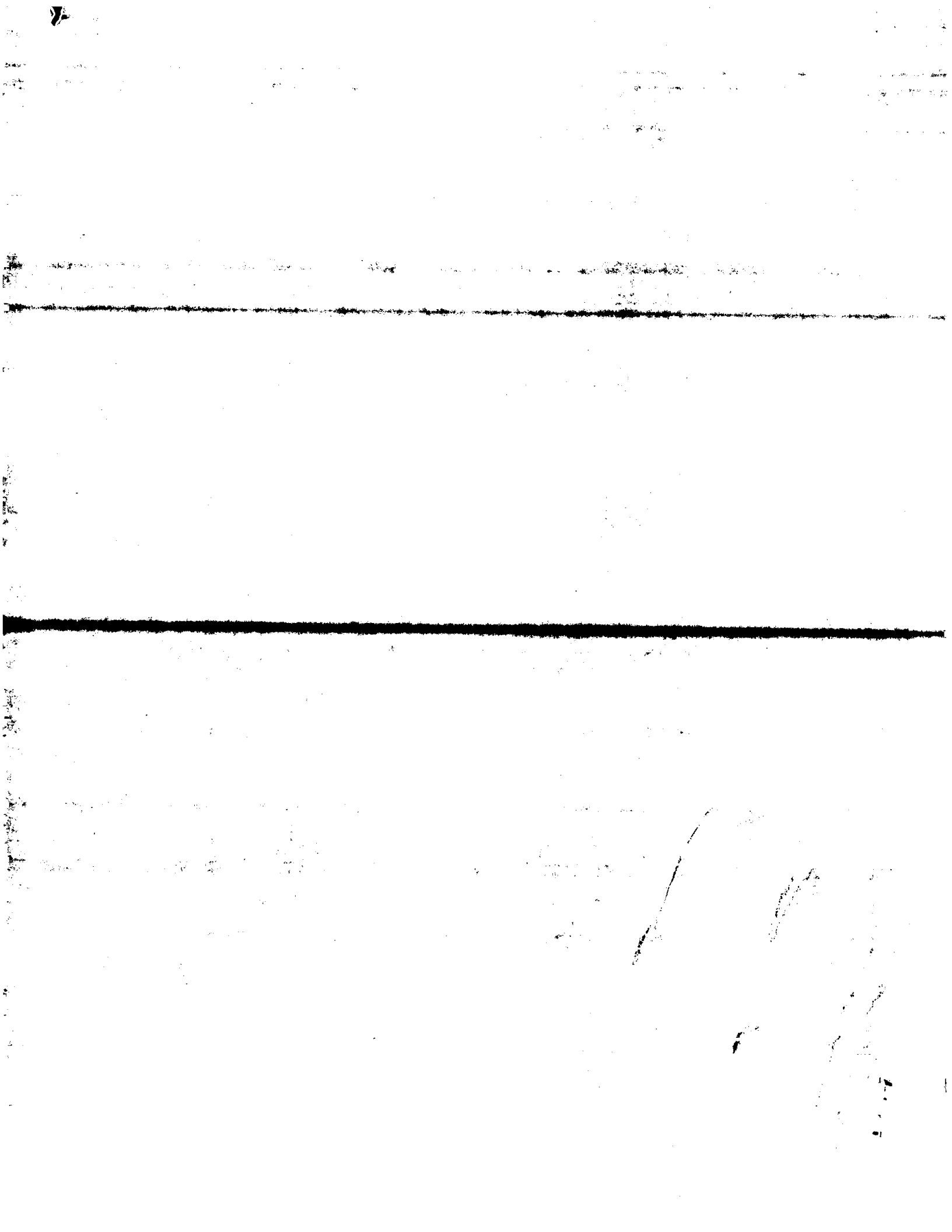

Db 172 YQHPGKAPELMISEVKNRPSGYPNRFSGSKSGNTASLTVSGLQADDEADYCSSYAGS - 230

QY 236 NHVFFGGGTKLTVL 249

! : ! ! ! ! ! ! ! ! ! !

Db 231 NNWFFGGGTKVTVL 244

Search completed: August 15, 2002, 16:27:06
Job time: 371 sec





Job time: 764 sec

; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2014
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2014

Query Match 88.9%; Score 1181.5; DB 1; Length 243;
Best Local Similarity 90.0%; Pred. No. 3.5e-98;
Matches 224; Conservative 8; Mismatches 10; Indels 7; Gaps 1;

QY 1 EVOLVQSGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
Db 1 QVNRESGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
Db 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
QY 121 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 180
Db 114 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 173
QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 240
Db 174 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 233
QY 241 GGGTKLTVL 249
Db 234 GGGTKLTVL 242

RESULT 13

US-09-880-748-2014
; Sequence 2014, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2014
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2014

Query Match 88.9%; Score 1181.5; DB 22; Length 243;
Best Local Similarity 90.0%; Pred. No. 3.5e-98;

Matches 224; Conservative 8; Mismatches 10; Indels 7; Gaps 1;
QY 1 EVOLVQSGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
Db 1 QVNRESGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
Db 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
QY 121 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 180
Db 114 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 173
QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 240
Db 174 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 233
QY 241 GGGTKLTVL 249
Db 234 GGGTKLTVL 242

RESULT 14

PCT-US01-19110-2021
; Sequence 2021, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2021
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2021

Query Match 88.6%; Score 1177; DB 1; Length 242;
Best Local Similarity 89.6%; Pred. No. 8.8e-98;
Matches 223; Conservative 8; Mismatches 10; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
Db 1 QVNRESGAEVKKPCASVKVCKASGYTFTGYIMYVWVRQAPCGGLEWGWINPNSGGTNY 60
QY 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
Db 61 AQKFGQVMTTRDTSIGTAYMELSLRLSSDDTAVYYCARDRYGSSAYHRGSYMDVWGRG 120
QY 121 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 180
Db 113 TLVTYSSGGGGTGGGGSGGSSSELTQDPAVSVALGQTVRITCGDLSRYSYASWYQKP 172
QY 181 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 240
Db 173 GOAPVLVIYGNKNNRPSGIPDRFSGSSSGNTASLTITGAQAEADYCYNRSRDSGNHVV 232
QY 241 GGGTKLTVL 249
Db 234 GGGTKLTVL 242

QY	62	KQFGQVWTMRDTSIGTAYMELSRSSDDTAVYYCARRDRYGGSSAYHRGSYTMDVWGRGT	121
Db	62	KQFGQVWTMRDTSIS1TAYMELSRSSDDTAVYYCARSNMGGDA-----FDIWRGRST	113
QY	122	LVTSSGGGTGGGGGGSSSLLTQDPAVSVALGQTVRTTCGDSLRSYYASWYQOKPG	181
Db	114	LVTSSGGGGGGGGGGSSSLLTQDPAVSVALGQTVRTTCGDSLRSYYASWYQOKPG	173
QY	182	QAPVLVITYGKNNRPSGIPDRFGSSSGSGNTASLTITGAQAEDADYYCNSRDSGNGHVVFG	241
Db	174	QAPVLVITYGKNNRPSGIPDRFGSSSGSGNTASLTITGAQAEDADYYCNSRDSGNGHVVFG	233
QY	242	GGTKLTVL 249	
Db	234	GGTKLTVL 241	

RESULT 7
 US-09-880-748-2046
 ; Sequence 2046, Application US/09880748
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2046
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-2046

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; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1722
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-1722

Query Match          89.3%; Score 1187; DB 1; Length 250;
Best Local Similarity 90.8%; Pred. No. 1,1e-98;
Matches 228; Conservative 6; Mismatches 13; Indels 4; Gaps

Qy 1 EVOLVQSGAEVKKPGASVKVSKRSGYFTFTGYMYVVRQAPGGGLEMMGWINPNSGGTNY 60
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 QVQLQQSGAEVKKPGASVKVSKRSGYFTFTGYTHHWVRQAPGGGLEMMGWINPNSGGTNY 60

Qy 61 AQKEFGQGVMTDRFTSICGTAYMELSRLSDDDTAVYTCAR--DRYVGSSAYHRGSYYMDVMG 118
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AQKEFGQGVMTDRFTSISITAYMELSRLSDDDTAVYCARVLPHDTITGYSQN--WFDPMG 118

Qy 119 RGLTVTVSSGGGTGGGGGGGGSSSELTQDPAYSVSALGTQVTRITCGDLSRYSYASWYQQ 178
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 RGLTVTVSSGGGGGGGGGGSSSELTQDPAYSVSALGTQVTRITCGDLSRYSYASWYQQ 178

Qy 179 KPGQAPVLVIYGNKRRSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 238
   :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 KPGQAPVLVIYGNKRRSGIPDRFGSSSGNTASLTITGAQAEDEADYYCNSRDSGNHV 238

Qy 239 VFGGQTKLTVL 249
   :||| ||| ||| |||
Db 239 VFGGQTKLTVL 249

RESULT 9
US-09-880-748-1722
; Sequence 1722, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1722
; LENGTH: 250

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Db 234 GGGTKLTVL 242

RESULT 4
PCT-US01-19110-2106
; Sequence 2106, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2106
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2106

Query Match 89.5%; Score 1189; DB 1; Length 242;
Best Local Similarity 90.4%; Pred. No. 7.3e-99;
Matches 225; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 QVOLQESGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNY 60
QY 61 AQKFGQVMTWTRDTSITGAYMELSLRSDDTAVYYCARESLTGDA-----FDIWGRS 112
Db 61 AQKFGQVMTWTRDTSITGAYMELSLRSDDTAVYYCARESLTGDA-----FDIWGRS 112
QY 121 TLVTSSGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Db 121 TLVTSSGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 173 GQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 240
Db 173 GQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 240
QY 241 GGGTKLTVL 249
Db 233 GGGTKLTVL 241

Query Match 89.5%; Score 1189; DB 1; Length 242;
Best Local Similarity 90.4%; Pred. No. 7.3e-99;
Matches 225; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 1 EVOLVQSGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNY 60
Db 1 QVOLQESGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNY 60
QY 61 AQKFGQVMTWTRDTSITGAYMELSLRSDDTAVYYCARESLTGDA-----FDIWGRS 112
Db 61 AQKFGQVMTWTRDTSITGAYMELSLRSDDTAVYYCARESLTGDA-----FDIWGRS 112
QY 121 TLVTSSGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Db 121 TLVTSSGGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
QY 173 GQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 240
Db 173 GQAPVLVIYGNKRRPSGIPDRFSGSSSGNTASLTITGAQAEADYYCNSRDSSGNHVV 240
QY 241 GGGTKLTVL 249
Db 233 GGGTKLTVL 241

Query Match 89.3%; Score 1187; DB 1; Length 242;
Best Local Similarity 90.3%; Pred. No. 1.1e-98;
Matches 224; Conservative 7; Mismatches 9; Indels 8; Gaps 1;

QY 2 VOLVQSGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNTA 61
Db 2 VOLVQSGAEVKKPGASVKASKASYFTGYMYHWVRQAPGQGLEWMGWINPNSGGTNTA 61
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-779-457-48

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Query Match	100.0%;	Score 1329;	DB 11;	Length 249;
Best Local Similarity	100.0%;	Pred. No. 1.7e-111;		
Matches 249;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVQLVQSGAEVKKPGASVKVSKCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY	60	
Db	1	EVQLVQSGAEVKKPGASVKVSKCKASGYTFTGYMYWVRQAPGQGLEWMGWINPNSGGTNY	60	
Qy	61	AQKQFQGRVTRDTRDSIGTAYMELSRLLSDDDTAVYYCARDRIYGSAYIRGSGSYMDVWGSG	120	
Db	61	AQKQFQGRVTRDTRDSIGTAYMELSRLLSDDDTAVYYCARDRIYGSAYIRGSGSYMDVWGSG	120	
Qy	121	TLTVVSSGGGTGGGGGGGGSSSELTPDPAVSVVALGQVTRITCQGDLSRYSYASWVQOKP	180	
Db	121	TLTVVSSGGGTGGGGGGGGSSSELTPDPAVSVVALGQVTRITCQGDLSRYSYASWVQOKP	180	
Qy	181	GQAPVLVIYKGNRRPSGIPDRFSGSSSGNTASLTITGAAQEADEADYVYCNRSRDSGSHVVF	240	
Db	181	GQAPVLVIYKGNRRPSGIPDRFSGSSSGNTASLTITGAAQEADEADYVYCNRSRDSGSHVVF	240	
Qy	241	GGGTKLTVL	249	
Db	241	GGGTKLTVL	249	

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RESULT      2
PCT-US01-19110-2107
; Sequence 2107, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PE523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2107
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2107

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Query Match 89.7%; Score 1191.5; DB 1; Length 243;

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Best Local Similarity   90.8%; Pred. No. 4.4e-99;
Matches 226; Conservative 7; Mismatches 9; Indels 7; Gaps 1;

QY    1 EVQLVQSGAEVKPKGASVKYSCKASGYTFFTGGYYMYWRQAPQGCGLEWMGWINPNSGGTNY 60
      :||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    1 QVOLQESGAEEVKPGASVKYSCKASGYTFFTGGYYMHVWRQAPQGCGLEWMGWINPNSGGTNY 60

QY    61 AQKQTGRVTWTRDTSIGTAYMELSRLSDDDTAVYYCARDRYGSSAYHRGSYYMDVWGNG 120
      :||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    61 AQKQFGRVTWTRDTSISITAYMELSRLSDDDTAVYYCARSLPHFDADF-----DIWGRS 113

QY    121 TLTVSVSGGGGTGGGSGGGSSSLLTDOPAVSVVALGOTVRITTCOGDSLRSYYASWYOOKP 180
      :||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    114 TLTVSVSGGGGTGGGSGGGSSSLLTDOPAVSVVALGOTVRITTCOGDSLRSYYASWYOOKP 173

QY    181 GQAPVLVIYGKNRPSGIPDRFGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHVVVF 240
      :||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    174 GQAPVLVIYGKNRPSGIPDRFGSSSGNTASLTITGAQAEDADYYCNSRDSSGNHVVVF 233

QY    241 GGGTKLIVL 249
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Db    234 GGGTKLIVL 242

RESULT 3
US-09-880-748-2107
; Sequence 2107, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2107
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2107
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	Query Match	89.7%	Score 1191.5;	DB 22:	Length 243;
	Best Local Similarity	90.8%;	Pred. No. 4.4e-99;		
	Matches 226;	Conservative 7;	Mismatches 9;	Indels 7;	Gaps 1;
Qy	1	EVQLVQSGLAEYVKPCASVKSVKCKASGYTFFTCYGMHWVRQAPGQGLEWMGWINPNSGGTNY	60		
Db	1	QVQLDSGAELVKKPCASVKSVKCKASGYTFTCYIMHWVRQAPGQGLEWMGWINPSGGTNY	60		
Qy	61	AQKFQGRVTMTDRTSIGHAYMELSLRSDDDTAVYYCARDRYVGSSAYIRGSYYMDVDWGQR	120		
Db	61	AQKFQGRVTMTDRTSISTAYMELSLRLSRDSDTAVYYCARSLHFSDAF-----DIWGRS	113		
Qy	121	TLTIVSSGGGTGGGGSGGGSSSELTQDPAYSVVALGQTVRITCGQDSLRSYYASWYQQKP	180		
Db	114	TLTVSSGGGGSGGGSGGGSSSELTQDPAYSVALGQTVRITCGQDSLRSYYASWYQQKP	173		
Qy	191	GQAPVLVIYGKNRPISGTPDRFSSSSSGNTASLTIITGAQAEDADYYICNSRDSSGNHVVF	240		
Db	174	GQAPVLVIYGKNRPISGTPDRFSSSSSGNTASLTIITGAQAEDADYYICNSRDSSGNHVVF	233		
Qy	241	GGGTKLTVL	249		

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 16:34:03 ; Search time 410.32 Seconds
(without alignments)
213.597 Million cell updates/sec

Title: US-08-779-457-48
Perfect score: 1329
Sequence: 1 EVOLVSGAEVKKPGASVKY.....SRDSSGNHVVFGGTKLTVL 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/US06_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US083_COMB.pcp.*
- 8: /cgn2_6/ptodata/2/paa/US084_COMB.pcp.*
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- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pcp.*
- 24: /cgn2_6/ptodata/2/paa/US100_COMB.pcp.*
- 25: /cgn2_6/ptodata/2/paa/US101_COMB.pcp.*
- 26: /cgn2_6/ptodata/2/paa/US102_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1329	100.0	249	11	US-08-779-457-48
2	1191.5	89.7	243	1	PCT-US01-19110-2107
3	1191.5	89.7	243	22	US-09-880-748-2107
4	1189	89.5	242	1	PCT-US01-19110-2106
5	1189	89.5	242	22	US-09-880-748-2106
6	1187	89.3	242	1	PCT-US01-19110-2046
7	1187	89.3	242	22	US-09-880-748-2046

8	1187	89.3	250	1	PCT-US01-19110-1722	Sequence 1722, Ap
9	1187	89.3	250	22	US-09-880-748-1722	Sequence 1722, Ap
10	1182.5	89.0	241	1	PCT-US01-19110-2008	Sequence 2008, Ap
11	1182.5	89.0	241	22	US-09-880-748-2008	Sequence 2008, Ap
12	1181.5	88.9	243	1	PCT-US01-19110-2014	Sequence 2014, Ap
13	1181.5	88.9	243	22	US-09-880-748-2014	Sequence 2014, Ap
14	1177	88.6	242	1	PCT-US01-19110-2021	Sequence 2021, Ap
15	1177	88.6	242	22	US-09-880-748-2021	Sequence 2021, Ap
16	1173	88.3	250	1	PCT-US01-19110-1723	Sequence 1723, Ap
17	1173	88.3	250	22	US-09-880-748-1723	Sequence 1723, Ap
18	1170.5	88.1	241	1	PCT-US01-19110-2032	Sequence 2032, Ap
19	1170.5	88.1	241	22	US-09-880-748-2032	Sequence 2032, Ap
20	1169.5	88.0	241	1	PCT-US01-19110-2031	Sequence 2031, Ap
21	1169.5	88.0	241	22	US-09-880-748-2031	Sequence 2031, Ap
22	1167	87.8	248	1	PCT-US01-19110-1721	Sequence 1721, Ap
23	1167	87.8	248	22	US-09-880-748-1721	Sequence 1721, Ap
24	1162.5	87.5	238	1	PCT-US01-19110-1907	Sequence 1907, Ap
25	1162.5	87.5	238	22	US-09-880-748-1907	Sequence 1907, Ap
26	1158.5	87.2	247	1	PCT-US01-19110-1729	Sequence 1729, Ap
27	1158.5	87.2	247	22	US-09-880-748-1729	Sequence 1729, Ap
28	1150.5	86.6	245	1	PCT-US01-19110-1919	Sequence 1919, Ap
29	1150.5	86.6	245	22	US-09-880-748-1919	Sequence 1919, Ap
30	1145.5	86.2	249	1	PCT-US01-19110-2033	Sequence 2033, Ap
31	1145.5	86.2	249	22	US-09-880-748-2033	Sequence 2033, Ap
32	1145	86.2	250	1	PCT-US01-19110-1647	Sequence 1647, Ap
33	1145	86.2	250	22	US-09-880-748-1647	Sequence 1647, Ap
34	1143.5	86.0	247	1	PCT-US01-19110-927	Sequence 927, App
35	1143.5	86.0	247	22	US-09-880-748-927	Sequence 927, App
36	1142.5	86.0	247	1	PCT-US01-19110-948	Sequence 948, App
37	1142.5	86.0	247	22	US-09-880-748-948	Sequence 948, App
38	1138	85.6	248	1	PCT-US01-19110-967	Sequence 967, App
39	1138	85.6	248	22	US-09-880-748-967	Sequence 967, App
40	1137.5	85.6	243	1	PCT-US01-19110-1947	Sequence 1947, Ap
41	1137.5	85.6	243	22	US-09-880-748-1947	Sequence 1947, Ap
42	1136	85.5	246	1	PCT-US01-19110-1638	Sequence 1638, Ap
43	1136	85.5	246	22	US-09-880-748-1638	Sequence 1638, Ap
44	1135.5	85.4	249	1	PCT-US01-19110-1730	Sequence 1730, Ap
45	1135.5	85.4	249	22	US-09-880-748-1730	Sequence 1730, Ap

ALIGNMENTS

RESULT 1
US-08-779-457-48
; Sequence 48, Application US/08779457
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodrigues, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96

Best Local Similarity 46.9%; Pred. No. 1.3e-21;
Matches 83; Conservative 25; Mismatches 38; Indels 31; Gaps 4;

Qy	1	EVOLVQSGAEVKKPGESLKISQGGSTPSSYKMMVROAPGKGLWMGGIIPFETANY	60
Db	20	QVOLKQSGAELVKPGASVKISCKASGYTFTDYYINWKQRPQGLEWIGKIGPGSGSTYY	79
Qy	61	AQKFOGRVTITADESTSTAYMELSSLRSEDTAVYYCARDRVVVPATSLRGGMD-----VM	115
Db	80	NEKFKGKATLTADKSSSTAYMOLSLTSEDSAVYFCA-----RSGYDYDWFAYW	128
Qy	116	GQGTVTVTSSGGGGGGGGGSGQSVLTQPASVSGSPGQSITISCTCTSSDVGYY	172
Db	129	GQGLVTIVS-----AAKTTAPSVYPLAPVCGGTGSSVTIGCL-----VKGYY	170

Search completed: August 15, 2002, 16:35:37
Job time: 797 sec

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GASTRIC MUCOSA;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yanashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isozaki T., Sugano S.;
*NEED human cDNA sequencing project.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK038027; BAB1633.1; -.
SQ SEQUENCE 496 AA; 53532 MW; C72BE1E247C86FED CRC64;

Query Match 30.5%; Score 396.5; DB 4; Length 496;
Best Local Similarity 40.8%; Pred. No. 2e-22;
Matches 102; Conservative 27; Mismatches 82; Indels 39; Gaps 8;

QY 1 EVLVQSGAEVKKPGESLKISQCGSGFTSSYKMNVRQAPGKGLWGGIPIFGTANY 60
Db : ||||| : || : || : || : || : || : || : || : || : || : || : ||
20 QVHLVQSGAEKMPGSSVKVSKASANPERSYFTWVRQAPCGQLWGMGIIPNFGAPNY 79
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 61 AKQFGRRVTITADESTAYMELSLRSEDYAVYCARDRVVVPATSLRGMDVMGQGT 120
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
Db 80 AQFQDRVTISADSTTVYMETLSLTFEDTAFYTCGRGLTYVGGSYV-YLQHWGQGT 138
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 121 VNVSSGGGGGGGGGSGSVLTPASV-SGSPQSITISCTGSSDVGGYVNVSWYQ 179
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
Db 139 VTVSS-----ASPTGPKVFPPLSLCTQPDGNVVIACL-----VOGF-----PP 176
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 180 QHPGKAPKLMIEYSGKRPSPGSGNR-----FSGKSGSTASLTISGLQ--AEDEADYYC 230
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
Db 177 QEP-----LSVTWSESGGVGTARNPPSPQDASGDLTYTSSQLTLPATCLAGKSVTCHV 230
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 231 SYTTRSTRV 240
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
Db 231 KHYTNPSQDV 240
: ||||| : || : || : || : || : || : || : || : || : || : || : ||

RESULT 14
QY298 PRELIMINARY; PRT; 150 AA.
AC QY298;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAA11829.1; -.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
KW SIGNAL.
FT NON_TER 150 150
FT SIGNAL 1 19
FT POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

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Query Match 29.8%; Score 388; DB 4; Length 150;
Best Local Similarity 62.4%; Pred. No. 2.2e-22;
Matches 78; Conservative 15; Mismatches 24; Indels 8; Gaps 2;

QY 1 EVLVQSGAEVKKPGESLKISQCGSGFTSSYKMNVRQAPGKGLWGGIPIFGTANY 60
Db : ||||| : || : || : || : || : || : || : || : || : || : || : ||
20 QVHLVQSGAEVKKPGASVKVSKGYTLTLPVHWGQAPGKGLWVGSFDPESGESY 79
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 61 AKQFGRRVTITADESTAYMELSLRSEDYAVYCARDRVVVPATSLRGMDVMGQGT 120
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
Db 80 AREFQGSVTTWATDTSTDIAYMELSLRSDTAVYICA-----VPDP-----AFDINGQGT 131
: ||||| : || : || : || : || : || : || : || : || : || : || : ||
QY 121 VTVSS 125
: |||||
Db 132 VTVSS 136

RESULT 15
QY298 PRELIMINARY; PRT; 473 AA.
AC QY298;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE IGG-1 OR 1810060009RIK.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003599; Iq.
DR InterPro; IPR003597; Iq-cl.
DR InterPro; IPR003600; Iq-like.
DR InterPro; IPR003006; Iq_MHC.
DR Pfam; PF00047; Iq; 4.
DR SMART; SM00409; Iq; 2.
DR SMART; SM00407; Iq; 1.
DR SMART; SM00406; Iq; 1.
DR SMART; SM00410; Iq-like; 1.
DR PROSITE; PS00290; Iq_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

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Query Match 29.7%; Score 385.5; DB 11; Length 473;

Db	80	AQXPQDRVTTITRDRSMNTAYMELLSURSEDTAMYYCARG-----SSWDADFINGQGT	135
Qy	121	VTYSSGGGGGGGGGGGGSSQSVLTQPASVSGSPG--QSITISCTG-----	164
Db	136	VTYSS-----GSASAPTLPLVSCENSPTSSTSAVAVCLAQDFLPDSITFSWKY	184
Qy	165	-TSDVG-----GYNYVSWYQ-----OHG-----	183
Db	185	KNSDSISSTRGFFSVLRGGYAAATQVLLPSPKDVMOGTDEHVVKYQHPNGNKEKNVPLP	244
Qy	184	-----KAPKLMY-----EGSKRRSGSVN-----	202
Db	245	VIAELPPKSVFVPPRPGFGFNPRKSKLLICQATGFSPRQIYSWLREGKGVGVTTDQV	304
Qy	203	RFGSKSGS-----TASLTIS-----GLQAEADAYCYSSYTRSTRV	240
Db	305	QAEAKESGPTTKYKVTSLTTIKESDWLSQSMTFCRVDRHGLTFQONASSMCVDPQDTAIRV	364
Qy	241	FG-----GGTKLTVL	250
Db	365	FAIPPSFASIFLTKSTKLCL	385

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RESULT 11
Q9GYZ2
ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
   (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP282622; AAC01452.1; -.
DR HSSP; PO1772; 2FB4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT FT 119 119
SO SPOUNCE 119 AA; 13567 MW; BA893873PFD5FA6AB CRC64;

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Query Match 30.7%; Score 399; DB 5; Length 119;
Best Local Similarity 61.7%; Pred. NO. 2.4e-23;
Matches 79; Conservative 16; Mismatches 21; Indels 12; Gaps 2;

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QY 1 EVOLVSGAEVKKPGESLKI SCQSGGFTSSYKMMNVVRQAPKGLEWMGGIIPFTANY 60
      |||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGAEVRKPGASVRVSKASGYTFTGYIMNVVRQAPGHLEWIGYINPSRGYINY 60
      |||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKPGQRTVTTADESTSTAYMELSSUEDTAYVYCAR---DRVVVPATSLRGGMDVWGQ 117
      |||:||||:||||:||||:||||:|||||:|||||:|||||:|||||:|||||
Db 61 NQKFKQRTVTTDKSFSTAYMDLRSLSADSAVYVCARYDDHYC-----LDYWGQ 111
      |||||
QY 118 GTTVTVSS 125
      |||||
Db 112 GTTVTVSS 119
      |||||

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RESULT	12	
Q9BRV0	Q9BRV0	PRELIMINARY; PRT; 500 AA.
AC	Q9BRV0;	
DT	01-JUN-2001 (Tremblrel. 17, Created)	
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)	
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)	
DE	DE HYPOTHETICAL 54.2 KDA PROTEIN.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	{1}	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=PROSTATE;	
RA	Strausberg R.;	
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC005951; AA05951.1; -	
DR	HSP; P01789; IMCP.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR003597; Ig_cl.	
DR	InterPro; IPR003600; Ig_like.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 4.	
DR	SMART; SM00409; IG; 4.	
DR	SMART; SM00407; IGcl; 2.	
DR	SMART; SM00406; IGV; 1.	
DR	SMART; SM00410; IG_like; 1.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.	
DR	Hypothetical protein.	
SK	SEQUENCE 500 AA; A09BF43F2A3CC6D9 CRC64;	

Query Match	30.6%	Score	397.5	DB	4	Length	500
Best Local Similarity	40.4%	Pred. No.	1.7e-22				
Matches	103	Conservative	30	Mismatches	77	Indels	45
Gaps							
Qy	1	EVQLVQSGAEVKKPGESLKISCSOGSGFTFSYKNNWVRQAPGKGLEWGGIIPIFGTANY	60				
Db	20	QVHLVQSGAEVMSFGASRVYCKTSGYAFITYSIIVWRQAPGGLEWGMWISPSDNTFR	79				
Qy	61	AKQFGQRTVTADBSTATYNELSLRSEDTATYYCARDVVVPATSLRGG----	MDVW	115			
Db	80	AKQFGQRTVLTDTSTVYMEKLSRSDDTAVYYCARR--YCSYSSCQNDYIIYYVMDW	137				
Qy	116	GQGTFTVTVSSGGGGGGGGGGSQSVLTPQASV--SGSPQSGITITICTGTSDDVGQNY	174				
Db	138	GKGFTTVTVSS-----ASPTSPKVFPLSLCSTQPDGNWVIACL-----VQGF--	178				
Qy	175	VSWTQOHPGRAPKIMITYEGSKRRCVCSNR-----FSGSKSGSTASLTISGLQ--AEDE	225				
Db	179	---FPQEP-----LSVTWSESGQGVYARNPPFPQDASGLYTSQTLTPATQCLAGKS	229				
Qy	226	ADYYCCSYVTRSTRV	240				
Db	230	VTCVKKHYTNPSQDY	244				

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RESULT 13
Q96DK0
ID Q96DK0 PRELIMINARY; PRT; 496 AA.
AC Q96DK0;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO
DE ALPHAI H, MYELOMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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